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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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                                                                                                                                                                                                                                                                 Set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status.
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Pred. No. 5e+02;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                            Claim 1; SEQ ID NO 94311; 29pp + Sequence Listing; German.
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Best Local Similarity
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ABC06155
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                                                                                                         SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                   Oligonucleotide SEQ ID NO 234733 for detecting SNP TSC0057297.
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC9989, ABF00010-ABF9989, ABF00010-ABF9989, ABF00010-ABF9989, ABF00010-ABF9989, and ABI0010-ABF8073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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designed to detect single-nucleotide polymorphisms and cytosine methylation status.
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designed to detect single-nucleotide polymorphisms and cytosine
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Pred. No. 5e+02;
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                                                            Claim 1; SEQ ID NO 6146; 29pp + Sequence Listing; German.
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represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences
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20-FEB-2002 (first entry)
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Best Local Similarity 83.3
Matches 10; Conservative
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                                                                                                                                                  SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                           Oligonucleotide SEQ ID NO 141877 for detecting SNP TSC0035552
                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; SEQ ID NO 141877; 29pp + Sequence Listing; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             40.0%; Score 8.8; DB 1; Length 13; 83.3%; Pred. No. Se+02; tive 0; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                       Berlin K;
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                                                         ABF41880 standard; DNA; 13 BP
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                                                                                                                                                                                                                                                                                                                 (EPIG-) EPIGENOMICS AG
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SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single-nucleotide polymorphisms and cytosine
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                         WPI; 2001-657177/75
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methylation status.
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Berlin K;

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABF82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic formmat from WIPO at the printed specification, but the wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and oytosine methylation status in chemically pretraeted genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic discorders. The oligomers are also used for detecting cell type differentiation. ABCC0010-ABC99989, ABC0010-ABC99899, ABC0010-ABC99899, ABC0010-ABC99899 ABC0010-ABC99899 and ABI0010-ABC82073 represent the oligomers described in the invention. NOTE: The sequence was obtained in electronic format from WIPO at the printed specification, but the wipo.int/pub/published_pct_sequences
                                                                                                                                           SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                          Oligonucleotide SEQ ID NO 127765 for detecting SNP TSC0031989.
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ABF27768 standard; DNA; 13 BP.
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                                                                                                                                                                                                                                                                                                                                                                                      SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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40.0%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 5e+02;
Matches 10; Conservative 0; Mismatches 2; Indels
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BP; 8 A; 4 C; 0 G; 1 T; 0 U; 0 Other;
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Matches 10; Conserv
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Sequence 13
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Berlin K;

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SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                                                                                                                                                                                          Oligonucleotide SEQ ID NO 148662 for detecting SNP TSC0037536.
/ Match 40.0%; Score 8.8; DB 1; Length 13; Local Similarity 83.3%; Pred. No. 5e+02; les 10; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                    735 GAAACAGAACAC 746
                                                                                                    12 GAAACCGAAAAC 1
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728 GCCAGGAGAAC 739

12 GCCACGAAAAC 1

RESULT 574 ABF27768/c

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                                                                                                                                                                                This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC9989, ABF00010-ABF9989, ABF00010-ABF99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                          Set of oligonucleotides, useful for diagnosis and cell typing, idesigned to detect single-nucleotide polymorphisms and cytosine methylation status.
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                                                                                                                                        Claim 1; SEQ ID NO 224295; 29pp + Sequence Listing; German.
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nes 10; Conservative
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WPI; 2001-657177/75.
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; SEQ ID NO 148662; 29pp + Sequence Listing; German.
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                           WO200177384-A2
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central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010 -ABC39989, ABF00010-ABF9989, ABF00010-ABF9989, ABF00010-ABF9989, ABF00010-ABF99989 and ABI00010-ABF82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at fitted the printed specification, but ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                                                           Sequence 13 BP; 7 A; 6 C; 0 G; 0 T; 0 U; 0 Other;
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Matches 10; Conserv
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                                                                                                                                                           SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                               Oligonucleotide SEQ ID NO 67872 for detecting SNP TSC0017721.
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                              ABC67855 standard; DNA; 13 BP.
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Matches 10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        methylation status.
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                                                                                                 21-FEB-2002
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                                                               ABC67855;
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DB 1; Length 13; e+02; es 2; Indels

Query Match
40.0%; Score 8.8; DB 1;
Best Local Similarity 83.3%; Pred. No. 5e+02;
Matches 10; Conservative 0; Mismatches

schultz1-727.rng

06-APR-2001; 2001WO-IB000713. 07-APR-2000; 2000DE-01019173.

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SNP; single nuclectide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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         Oligonucleotide SEQ ID NO 94313 for detecting SNP TSC0023541.
                                                                                                                                                                                                                                                                                                      Claim 1; SEQ ID NO 94313; 29pp + Sequence Listing; German.
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                                                                                                                                                                                                               Berlin K;
                                                                                                                                             06-APR-2001; 2001WO-IB000713.
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                                                                                                                                                                                                              Olek A, Piepenbrock C,
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                                                                                                 WO200177384-A2
                                                                            Homo sapiens
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This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genemic DNA. The oligonuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at

Sequence 13 BP; 0 A; 5 C; 0 G; 8 T; 0 U; 0 Other;

ftp.wipo.int/pub/published_pct_sequences

Set of oligonuclectides, useful for diagnosis and cell typing, idesigned to detect single-nuclectide polymorphisms and cytosine methylation status.

Berlin K;

Piepenbrock C,

olek A,

WPI; 2001-657177/75.

(EPIG-) EPIGENOMICS

Claim 1; SEQ ID NO 69714; 29pp + Sequence Listing; German.

ö This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 trepresent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at Gaps Seguence 13 BP; 1 A; 0 C; 6 G; 6 T; 0 U; 0 Other; Query Match

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· 0 40.0%; Score 8.8; DB 1; Length 13; 83.3%; Pred. No. 5e+02; tive 0; Mismatches 2; Indels 736 AAACAGAACACC 747 Local Similarity 83.3 nes 10; Conservative Matches Ś

AAACACATCACC 1 17

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ABC69697 standard; DNA; 13 21-FEB-2002 (first entry) ABC69697; RESULT 581 ABC69697/

Oligonucleotide SEQ ID NO 69714 for detecting SNP TSC0018143.

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SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.

Homo sapiens

W0200177384-A2

18-OCT-2001

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SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                Gaps
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Query Match

40.0%; Score 8.8; DB 1; Length 13;

Best Local Similarity 83.3%; Pred. No. 5e+02;

Matches 10; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Berlin K;
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                                                                                                                                                          ABC76055 standard; DNA; 13
                                                                                                                                                                                                                 21-FEB-2002 (first entry)
                                                          731 AGGAGAAACAGA 742
                                                                                     12 AGGAGAAAGAAA 1
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                                                                                                                                                                                       ABC76055;
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                                                                                                                                RESULT 582
                                                                                                                                                 ABC76055
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99899, ABF00010-ABH99989 and ABI00010-ABH82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                                                                                                                                                          40.0%; Score 8.8; DB 1; Length 13; 83.3%; Pred. No. 5e+02; tive 0; Mismatches 2; Indels
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            Claim 1; SEQ ID NO 76072; 29pp + Sequence Listing; German.
                                                                                                                                                                                                                                Sequence 13 BP; 6 A; 5 C; 0 G; 2 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                     736 AAACAGAACACC 747
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cycosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, ardiovascular and metabolic disorders. The oligomers are also used for detecting call type differentiation. ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABT00010-ABIS2073 trepresent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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                                                                                   40.0%; Score 8.8; DB 1; Length 13; 83.3%; Pred. No. 5e+02; ive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; SEQ ID NO 7293; 29pp + Sequence Listing; German.
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                                                 Sequence 13 BP; 11 A; 2 C; 0 G; 0 T; 0 U; 0 Other;
was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences
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Best Local Similarity
                                                                                                        Local Similarity
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(EPIG-) EPIGENOMICS AG.
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ABF73773/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABE9989, ABF00010-ABF9989, ABH00010-ABH99989 and ABI00010-ABH82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                     SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                               Oligonucleotide SEQ ID NO 88825 for detecting SNP TSC0022318.
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                            ABC88808 standard; DNA; 13 BP
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                                                                                  21-FEB-2002 (first entry)
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Best Local Similarity 83.3
Matches 10; Conservative
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                                                        ABC88808,
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, ardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; SEQ ID NO 124590; 29pp + Sequence Listing; German
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         40.0%; Score 8.8; DB 1; Length 13; 83.3%; Pred. No. 5e+02; ive 0; Mismatches 2; Indels
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Best Local Similarity 83.3%;
Matches 10; Conservative
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                                                                                    WO200177384-A2
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                                           Homo sapiens
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99899, ABF00010-ABF99899, ABH00010-ABH99989 and ABI00010-ABF82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but fip.wipo.int/pub/published_pot_sequences
                                                                                                            Set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status.
                                                                                                                                                                                                        Claim 1; SEQ ID NO 173770; 29pp + Sequence Listing; German.
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                        Berlin K;
                        Olek A, Piepenbrock C,
                                                                WPI; 2001-657177/75
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40.0%; Score 8.8; DB 1; Length 13; 83.3%; Pred. No. 5e+02; 2; Indels cive 0; Mismatches 2; Indels
                                                          ABH25373 standard; DNA; 13 BP
                                                                               22-FEB-2002 (first entry)
                     734 AGAAACAGAACA 745
     Local Similarity 83.3
Les 10; Conservative
                               13 AGAAATAGAAAA 2
                                                                    ABH25373;
                                               RESULT 588
                                                      ABH25373
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SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic. Oligonucleotide SEQ ID NO 225350 for detecting SNP TSC0054939.

Homo sapiens

WO200177384-A2

18-OCT-2001.

06-APR-2001; 2001WO-IB000713.

07-APR-2000; 2000DE-01019173.

(EPIG-) EPIGENOMICS AG.

Berlin K; Olek A, Piepenbrock C,

WPI; 2001-657177/75.

Set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status.

Claim 1; SEQ ID NO 225350; 29pp + Sequence Listing; German.

This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)

Sequence 13 BP; 7 A; 0 C; 5 G; 1 T; 0 U; 0 Other;

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and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Oligonucleotide SEQ ID NO 156041 for detecting SNP TSC0039372.
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                                                                                                                                                                                                                                                            40.0%; Score 8.8; DB 1; Length 13; 83.3%; Pred. No. 5e+02; 2; Indels tive 0; Mismatches 2; Indels
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Matches 10; Conservative
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nerrous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABE09989, ABF00010-ABE99989, ABF00010-ABE99989, ABF00010-ABE99989 and ABI00010-ABE32073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but the wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                        SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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   DB 1; Length 13;
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Score 8.8; DB 1;
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Query Match
Best Local Similarity 83.3%;
Matches 10; Conservative
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This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC9989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABF82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but the was obtained in electronic format from WIPO at
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                                                                                            SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                             Oligonucleotide SEQ ID NO 235977 for detecting SNP TSC0005750.
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Best Local Similarity 83.3%,
Conservative
                              22-FEB-2002 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                                                                                                                                                          Claim 1; SEQ ID NO 240237; 29pp + Sequence Listing; German.
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99899, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI32073 tapeseent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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Set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status.
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                                                                                 Claim 1; SEQ ID NO 242925; 29pp + Sequence Listing; German.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
-ABC99989, ABF00010-ABF99899, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at the printed specification ftp.wipo.int/pub/published_pot_sequences
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40.0%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 5e+02;
Matches 10; Conservative 0; Mismatches 2; Indels
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This invention describes novel oligonuclectide primers or peptide nucleic acid (FNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, contral nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC9989, ABF0010-ABF9989, ABH0010-ABH9989 and ABI0010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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                                                                                                                                                            SND; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                              Oligonucleotide SEQ ID NO 229461 for detecting SNP TSC0055973.
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0; Mismatches
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                                 ABH29484 standard; DNA; 13
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Best Local Similarity 83.3
Matches 10; Conservative
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RESULT 596
ABH29484/c
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Oligonucleotide SEQ ID NO 182669 for detecting SNP TSC0045147.

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40.0%; Score 8.8; DB 1; Length 13; ilarity 83.3%; Pred. No. 5e+02; Conservative 0; Mismatches 2; Indels

Query Match Best Local Similarity Matches 10; Conserv

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                            SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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83.3%; Pred. No. 5e+02;
live 0; Mismatches
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Matches 10; Conservative
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07-APR-2000; 2000DE-01019173
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Best Local Similarity 83.3
Matches 10; Conservative
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                       This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF9989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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AC ABH4,
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XXX SNP;
XXW SNP;
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                                                                                                                                                                                                                                                                                                                                                          SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                             40.0%; Score 8.8; DB 1; Length 13;
llarity 83.3%; Pred. No. 5e+02;
Conservative 0; Mismatches 2; Indels
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Sequence 13 BP; 2 A; 5 C; 0 G; 6 T; 0 U; 0 Other;
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Best Local Similarity 83.3'
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                             Query Match
Best Local Similarity
Matches 10, Conserv
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RESULT 602

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06-APR-2001; 2001WO-IB000713.
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                                                                                                                   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                           Oligonucleotide SEQ ID NO 67871 for detecting SNP TSC0017721.
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               ABC67854 standard; DNA; 13
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligomucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, ardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABF99989 and ABI00010-ABF82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but the was obtained in electronic format from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                                                                                                                                                                                 Claim 1; SEQ ID NO 219382; 29pp + Seguence Listing; German.
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                                                                                              Berlin K;
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07-APR-2000; 2000DE-01019173.
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                                               (EPIG-) EPIGENOMICS AG
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Best Local Similarity
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methylation status.
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a reange of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010 +ABC99989, ABF0010-ABF99889, ABH0010-ABH99989 and ABI0010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from MIPO at
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                    set or oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              set of oligonucleotides, useful for diagnosis and cell typing, : designed to detect single-nucleotide polymorphisms and cytosine methylation status.
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                                                                                                                                 Claim 1; SEQ ID NO 242776; 29pp + Sequence Listing; German.
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              central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC9989, ABF00010-ABF998989, ABH00010-ABF99898 and ABI00010-ABF98989. The sequence tepresent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at the printed in electronic format from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
gastrointestinal, respiratory
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range of diseases including immune system,
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Best Local Similarity 83.3
Matches 10, Conservative
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40.0%; Score 8.8; DB 1; Length 13; 83.3%; Pred. No. 5e+02;

Query Match Best Local Similarity

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This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, ardiovascular and metabolic disorders. The oligomers are also used for detecting call type differentiation. ABC0010-ABC9989, ABF00010-ABF99899, ABH00010-ABH99989 and ABI00010-ABH82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                              SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                                                                                                                                                                                                                                   Set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status.
                                Oligonucleotide SEQ ID NO 39734 for detecting SNP TSC0012134.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; SEQ ID NO 39734; 29pp + Sequence Listing; German.
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                                                                                                                                                                                                                                                                                    SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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40.0%; Score 8.8; DB 1; Length 13; 83.3%; Pred. No. Se+02; ive 0; Mismatches 2; Indels
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0; Mismatches
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The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABE09989, ABE00010-ABE99989, ABE00010-ABE99989, ABE00010-ABE99989, ABE00010-ABE99989, CABE00010-ABE99989, CABE00010-ABE99989, ABE00010-ABE99989, ABE00010-ABE99989, CABE00010-ABE99989, CABE00010-ABE9989, CABE00010-ABE99989, CABE00010-ABE
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Best Local Similarity 83.3%; Pred. No. 5e+02;
Matches 10; Conservative 0; Mismatches 2; Indels
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, contral nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting call type differentiation. ABC0010-ABC9989, ABF0010-ABF9989, ABH0010-ABF9989 and ABT00010-ABIS2073 trepresent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from MIPO at
                                                                                                                                                                                                                        SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                        Oligonucleotide SEQ ID NO 159004 for detecting SNP TSC0040037.
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                                                                          ABF59007 standard; DNA; 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardicvascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences
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                                                                                                          40.0%; Score 8.8; DB 1; Length 13; 83.3%; Pred. No. 5e+02; ive 0; Mismatches 2; Indels
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                    central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC001016.0199999, ABF00010-ABF99999, ABH00010-ABH99999 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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Matches 10; Conservative
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                                                                                                                                                                                                                                                                                                                                  SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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Pred. No. Se+02;
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40.0%; Score 8.8; DB 1; Length 13; 83.3%; Pred. No. 5e+02; ive 0; Mismatches 2; Indels
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                Best Local Similarity 83.3
Matches 10; Conservative
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ABF82675
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Seguence 13 BP; 9 A; 2 C; 0 G; 2 T; 0 U; 0 Other;

ABF82675

WO200177384-A2.

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC9989, ABF00010-ABF99899, ABH0010-ABF99989, and ABI00010-ABF82073 arepresent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at the printed specification, but the wipo.int/pub/published_pct_sequences
                                                                                                                     SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                      Oligonucleotide SEQ ID NO 182672 for detecting SNP TSC0045147.
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PMA) oligoners for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, candra system, cardiovascular and metabolic disorders. The oligoners are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF9989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but they wispo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
              Set of oligonucleotides, useful for diagnosis and cell typing, idesigned to detect single-nucleotide polymorphisms and cytosine methylation status.
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                                                                                          Claim 1; SEQ ID NO 23161; 29pp + Sequence Listing; German.
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oligomers are also used for detecting cell type differentiation. ABC00010-ABC9989, ABF0010-ABF99889, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pot_sequences
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Pred. No. 5e+02;
0; Mismatches 2; Indels
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40.0%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 5e+02;
Matches 10; Conservative 0; Mismatches 2; Indels
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Best Local Similarity 83.3%;
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, ardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC9989, ABF00010-ABF9989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from MIPO at
                                                                                                                                                                                                                                                                 SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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40.0%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 5e+02;
Matches 10; Conservative 0; Mismatches 2; Indels
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This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically prefraeted genemic DNA. The oligonuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and merabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99889, ABF00010-ABF99899, ABH00010-ABF99899 and ABI00010-ABF8073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but the wipo.int/pub/published_pct_sequences
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                                SNP; single nuclectide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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Oligonucleotide SEQ ID NO 94312 for detecting SNP TSC0023541.
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Local Similarity 83.3%; Pred. No. 5e+02;
tes 10; Conservative 0; Mismatches 2; Indels
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06-APR-2001; 2001WO-IB000713.

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genemic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC09989, ABF00010-ABF9989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but the was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences
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The oligonuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 tepseent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                              This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA: The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABF99989 and ABI00010-ABF82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but the was obtained in electronic format from WIPO at
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Claim 1; SEQ ID NO 31769; 29pp + Sequence Listing; German.
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acid (FNA) oligomers for detecting single nuclectide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABE09989, ABF00010-ABE9989, ABH0010-ABE9989 and ABI0010-ABE82073 represent the oligomers described in the invention. NOTE: The sequence was obtained in electronic format from WIPO at the printed specification, but the wipo.int/pub/published_pct_sequence
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                                                                                                                                                                                                                 SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single-nucleotide polymorphisms and cytosine methylation status.
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40.0%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 5e+02;
Matches 10; Conservative 0; Mismatches 2; Indels
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                                                                                                               Olek A, Piepenbrock C,
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                                                                                              (EPIG-) EPIGENOMICS AG
                                                                                                                                WPI; 2001-657177/75.
                        WO200177384-A2.
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        Homo sapiens
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligomucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC9989, ABF00010-ABF99989, ABH0010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but the wipo.int/pub/published_pct_sequences
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                                                                           Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single-nucleotide polymorphisms and cytosine methylation status.
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                                                                                                                                                                             Claim 1; SEQ ID NO 219381; 29pp + Sequence Listing; German.
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40.0%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 5e+02;
Matches 10; Conservative 0; Mismatches 2; Indels
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ABH19406/c
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oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligoners are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at fire wipo int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99889, ABF00010-ABF99889, ABF00010-ABF9989, ABF00010-ABF99899 and ABI00010-ABF3073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but the wipo.int/pub/published_pot_sequences
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     Pred. No. 5e+02;
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ABH43253;

DB 1; Length 13;

40.0%; Score 8.8;

Query Match

97US-00000805 90US-00544218.

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Human leukocyte antigen typing by amplifying a sample followed by sequence specific oligonucleotide hybridization with labeled oligonucleotide probes that hybridize with a series of known control DNA
                                                                                                                                                                                                   Disclosure; Col 11-14; 16pp; English.
                                                                    (BLOO-) BLOOD CENT RES FOUND INC.
                                                                                           Baxter-Lowe LA, Gorski JA,
                                                                                                                WPI; 2001-217923/22.
            30-DEC-1997;
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08-APR-1993;
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                                                        SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                   Oligonucleotide SEQ ID NO 243230 for detecting SNP TSC0059331,
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Conservative
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           22-FEB-2002 (first entry)
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The present invention relates to human leukocyte antigen (HLA) typing. The method involves detecting polymorphic residues by sequence specific oligonucleotide probe hybridization (SSOPH) with labeled oligonucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New mammalian agouti polypeptide useful to identify molecules that control agouti polypeptide and as immunogen to produce antibodies usefu for treating, preventing diabetes, hyperamylinemia, neoplasms, obesity.
                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                    DB 1; Length 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Exonl-exon2 junction of wild type mouse agouti cDNA clone.
                                                                                                                                                                                                                                                      2; Indels
                                                                                                                                         Sequence 13 BP; 4 A; 3 C; 4 G; 2 T; 0 U; 0 Other;
                                                                                                                                                                                              40.0%; Score 8.8; DB 1;
83.3%; Pred. No. 5e+02;
ive 0; Mismatches
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                                                                                                                                                                                                                                                      10; Conservative
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                                                                                                                                                                                                                            Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21-MAY-1993;
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                                                                                                                                                                                                    Query Match
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. 0 methods, compositions and kits for identifying compounds which are inhibitors of agout; activity, and for altering fatty acid synthetase activity and intracellular calcium levels in transformed cells. The sequences and methods of the invention are useful in the detection and treatment of diabetes, neoplasms, hyperinsulinaemia, obesity, and various forms of cancer including tumours. The present sequence representing the exon1-exon2 junction of the wild type mouse agout; cDNA clone is compared to the same junction in the agouti Ay (lethal yellow) cDNA clone Human; ss; agouti; chromosome 20; black pigment; yellow pigment; agouti coat colour; obesity; non-insulin dependent diabetes; obesity-associated diabetes; intracellular calcium level; hyperinsulinaemia; hyperglycaemia; fatty acid synthetase; metabolism; adipocyte cell; diabetes; hyperamylinaemia; cancer; gene therapy; cytostatic; antidiabetic; anorectic; intron/exon structure; AY. Gaps ô 40.0%; Score 8.8; DB 1; Length 13; 83.3%; Pred. No. 5e+02; tive 0; Mismatches 2; Indels Sequence 13 BP; 0 A; 3 C; 3 G; 7 T; 0 U; 0 Other; /*tag= a /note= "DNA break point" Wild-type human agouti cDNA fragment. Location/Qualifiers BP. 93US-00064385 98US-00034088 12-FEB-2001; 2001US-00781811 ABX11332 standard; cDNA; 13 (first entry) 734 AGAAACAGAACA 745 Query Match
Best Local Similarity 83.3
Matches 10; Conservative AGAAGCAGCACA 2 (WOYC/) WOYCHIK R P. (BULT/) BULTMAN S J. (MICH/) MICHAUD E J. US2002151463-A1 21-MAY-1993; 03-MAR-1998; Homo sapiens misc feature 30-APR-2003 17-OCT-2002 ABX11332; RESULT 639 ABX11332/c 8888888888888 ઠ

New polynucleotide comprising an isolated agouti gene, useful for diagnosing, preventing and/or treating diabetes, hyperamylinemia, cancer

Example 1; Fig 9B; 152pp; English.

obesity

Michaud EJ;

Woychik RP, Bultman SJ,

WPI; 2003-198329/19.

The invention discloses a polynucleotide comprising an isolated agouti gene and the polypeptide it encodes. The agouti locus, in chromosome 20, regulates the differential production of black and yellow pigment granules that give rise to the agouti coat colour of mice. Obesity and non-insulin dependent diabetes are genetically inherited disorders in humans and mice. The obesity-associated diabetes of the mutant agouti

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humans. Also disclosed are methods for detecting proteins which interact with the agouti polypeptide, for generating an immune response, for increasing or decreasing the intracellular calcium level in a cell, for promoting obesity, hyperinsulinaemia or hyperglycaemia in an animal and for altering fatty acid synthetase activity in a cell or increasing the metabolism in an adipocyte cell. The polynucleotide is useful in detecting and cloning of the gene in which expression of the gene product correlates with the development of diabetes, hyperamylinaemia, cancer and obesity in animals, in detecting the agouti gene and homologous DNA sequences, in detecting mutations in the gene, in early detection of animals at risk of developing the diseases and in early treatment (e.g. cene therapy) of afflicted animals. The antibody is used in isolating and regulating the activity of agouti proteins. The sequence presented is the wild-type human agouti cDNA fragment showing the DNA break point at the exon I/exon II boundary compared to the agouti AY mutation cDNA sequence (ABXI1334)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human, optineurin, ds. ophthalmological, single nucleotide polymorphism; SNP; glaucoma; progressive ocular hypertensive disorder; glaucoma related disorder; motif; repeat element; regulatory region.
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                                                                                                                                                                                                                                                                                                                                                                                                                 40.0%; Score 8.8; DB 1; Length 13; 83.3%; Pred. No. 5e+02; tive 0; Mismatches 2; Indels
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(RAYM/) RAYMOND V.
(MORI/) MORISSETTE J.
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promoter, a host cell comprising the promoter operably linked to a heterologous sequence, diagnosing or prognosing glaucoma in a sample obtained from a cell or bodily fluid (comprising detecting a polymorphism in a promoter region of the optimeurin gene, associated with a glaucoma phenotype), detecting a SNP sequence variation in a sample containing a SNP sequence variation in a sample containing DNA, determining the presence of an optimeurin promoter sequence variation in a sample containing DNA, determining the presence or increased susceptibility to glaucoma or to a progressive ocular hypertensive or progression of glaucoma or to a progressive ocular hypertensive or progression of glaucoma in a patient, comprising providing a multification reaction primers that direct amplification of a selected nucleic acid region containing the variation within the optimeurin promoter and amplifying the DNA) and detecting a polymorphism (comprising capable of detecting a SNP located within an optimeurin promoter, and detecting the polymorphism). The invention is used to diagnose and present sequence is an optimeurin promoter motif, repeat element or putative regulatory region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                                                                                                                                                                                                                                                                                                 40.0%; Score 8.8; DB 1; Length 13; 83.3%; Pred. No. Se+02; tive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                  Sequence 13 BP; 6 A; 2 C; 5 G; 0 T; 0 U; 0 Other;
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Best Local Similarity 83.3'
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oligomers are also used for detecting cell type differentiation. ABC00010 -ABC9989, ABF0010-ABF9989, ABH00010-ABH99989 and ABI00010-ABF82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at fig. wipo.int/pub/published_pot_sequences
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Best Local Similarity 88.9
Matches 8; Conservative
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The

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This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, astdowascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99999, ABF00010-ABF99999, ABH00010-ABH99999 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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                                                              SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status.
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Oligonucleotide SEQ ID NO 116959 for detecting SNP TSC0029279.
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nes 8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (EPIG-) EPIGENOMICS AG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, coingomers are also used for detecting cell type differentiation. ABC00010-ABC9989, ABF00010-ABF9989, ABH00010-ABF9989, ABH00010-ABF9989 and ABI00010-ABI82073 tarpresent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from NIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Oligonucleotide SEQ ID NO 148265 for detecting SNP TSC0037435.
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          731 AGGAGAAAC 739
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07-APR-2000; 2000DE-01019173 (EPIG-) EPIGENOMICS AG

Berlin Piepenbrock C, olek A,

WPI; 2001-657177/75

Set of oligonucleotides, useful for diagnosis and cell typing, idesigned to detect single-nucleotide polymorphisms and cytosine methylation status.

Claim 1; SEQ ID NO 148266; 29pp + Sequence Listing; German.

This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligoners for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligoners are also used for detecting cell type differentiation. ABC0010-ABE99989, ABF00010-ABE99899, ABH00010-ABE99899 and ABI00010-ABE82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form marr of the printed specification, but the wipo.int/pub/published_pct_sequences

Sequence 13 BP; 2 A; 4 C; 0 G; 6 T; 0 U; 1 Other;

Query Match
39.1%; Score 8.6; DB 1; Length 13;
Best Local Similarity 88.9%; Pred. No. 5.4e+02;
Matches 8; Conservative 1; Mismatches 0; Indels

731 AGGAGAAAC 739 AGGAGAAAY 1 à

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963/c ABF16963 standard; DNA; 13 BP. ABF16963; RESULT 646

21-FEB-2002 (first entry)

Oligonucleotide SEQ ID NO 116960 for detecting SNP TSC0029279.

SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.

Homo sapiens

WO200177384-A2.

18-OCT-2001.

06-APR-2001; 2001WO-IB000713.

07-APR-2000; 2000DE-01019173

(EPIG-) EPIGENOMICS AG.

ĸ Berlin Olek A, Piepenbrock C,

WPI; 2001-657177/75.

Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single-nucleotide polymorphisms and cytosine methylation status.

Claim 1; SEQ ID NO 116960; 29pp + Sequence Listing; German.

This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genemic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metebolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC9989, ABF00010-ABF99899, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at

Sequence 13 BP; 2 A; 3 C; 0 G; 7 T; 0 U; 1 Other; ftp.wipo.int/pub/published_pct_sequences

Gaps ö 39.1%; Score 8.6; DB 1; Length 13; 88.9%; Pred. No. 5.4e+02; ative 1; Mismatches 0; Indels Query Match
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731 AGGAGAAAC 739

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RESULT 647

AAL37783 standard; RNA; 13 BP.

AAL37783;

05-AUG-2002 (first entry)

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Gaps

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5' conserved RNA region of wild-type influenza B virus.

Cytostatic; antiviral; tumour associated antigen; TAA; dendritic cell; virus-associated antigen; VAA; recombinant influenza virus; vaccine; viral infection; immune; wild-type; influenza B virus; ss.

Influenza virus.

EP1201760-A1.

02-MAY-2002.

30-OCT-2000; 2000EP-00123687.

30-OCT-2000; 2000EP-00123687.

(ARTE-) ARTEMIS PHARM GMBH.

æ Schuler G, Hobom G, Steinkasserer A, Strobel I, Grassmann

WPI; 2002-418777/45.

Expressing tumor or viral associated antigens by dendritic cells, use for treating tumors or viral infections, comprises using recombinant influenza virus containing nucleic acid encoding the antigens.

Disclosure, Page 6; 33pp; English

The invention relates to a method for the expression of tumour associated antigens (TRA) by dendritic cells comprising: preparing a recombinant influenza virus containing a nucleotide sequence coding for the TRA or VAA; and infecting dendritic cells with the recombinant virus. The method is used for expressing TRA or VAA in dendritic cells. The cells are used for expressing TRA for treating tumours or viral infections. A vaccine can be created by using dendritic cells presenting tumour antigens to induce an immune response. This polynucleotide sequence represents a 5' conserved RNA region of the wild-type influenza B virus of the invention ALIJ763

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The present invention describes a human influenza virus (I) comprising an RNA-sequence encoding a modified RNA-polymerase that differs from the wild-type RNA-polymerase of the human influenza virus in that at least 1 of the human influenza virus in that at least 1 of the manno acid residues distinguishing the wild-type RNA-polymerase of the human influenza virus from FPV Bratislava RNA-polymerase bas been replaced with the corresponding amino acid residue(s) as present in FPV Bratislava RNA-polymerase and context and influenza virus is used in gene therapy and vaccines. The influenza virus is useful for preparing agents for: (a) gene transfer into cells, preferably into commandalian cells, particularly into human cells, by viral infection; (b) gene transfer into antigen-presenting cells, and the use of the obtained cordination, including therapeutic and prophylactic vaccination; (c) eliciting an immune response, including therapeutic and prophylactic vaccination; (c) response; (d) treating a growing tumour or a chronic infectious disease; (e) immunotherapy, preferably for autologous immunotherapy; (f) transfer and expression of foreign genes into cells infected by such viruses, or transfer and expression of RNA molecules into cells infected by such viruses, preferably the RNA molecules to be expressed are antiesnes confecules, and/or the agent is suitable for sequence-specific gene sequences or double-strand sequences relative to the target cellular mRNA molecules to be expressed are antiesnes confecules, and/or the agent is suitable for sequence-specific gene silencing, preferably by antisense RNA or RNA interference mechanisms cuted for use in vaccines against HNV, hepatitis B or C virus, herpes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Influenza virus; transcription; replication; RNA polymerase; vaccine; gene therapy; cytostatic; anti-HIV; hepatotropic; antiinflammatory; immunomodulator; virucide; infectious disease; ss.
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                                       Score 8.6; DB 1; Length 13;
Pred. No. 5.4e+02;
2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                   Influenza virus B 5' conserved region SEQ ID NO:8.
Sequence 13 BP; 5 A; 1 C; 2 G; 0 T; 1 U; 4 Other;
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                                                                                                                                                                                                                                                                                    ABQ75466 standard; RNA; 13 BP
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                                                                                       Conservative
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                                                                                                                                                                          AGUAGWAACAR 11
                       Query Match
Best Local Similarity
Local 8, Conserva
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The invention describes a recombinant influenza virus (1), stable in the absence of any helper virus, that has a viral RNA segment being a biscistronic RNA molecule coding for two genes in tandem arrangement (trandem RNA segment, TRS). (1) is useful for expression of incorporated foreign gene(s) and RNA molecules in cells. (1), preferably a recombinant influenza A virus is useful for: preventing and/or treating influenza, and for preparing a medicament for vaccination purposes; somatic gene therapy, and as immunogen for inducing antibodies; as an expression vector for producing proteins or glycoproteins; preparing agents for somatic gene therapy; immunotherapy, preferably autologous immunotherapy; constit gene therapy; immunotherapy, preferably autologous immunotherapy; infected by such viruss, where the RNA molecules into cells infected by such viruss, where the RNA molecules to be expressed include cantisense or double-stranded sequences relative to the target cell cellular mENA molecules, and/or the agent is suitable for sequence-specific gene silencing, preferably by antisense RNA or RNA interference mechanisms. (1) gives high-yield expression for foreign genes. This sequence represents the 5' conserved region of influenza B virus,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Recombinant influenza virus for transfer and expression of foreign genes and RNA molecules into cells and for preventing, treating influenza, has biscistronic viral RNAs coding for two genes in tandem arrangement.
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viruses or papilloma viruses. The present sequence represents conserved region of a wild type influenza virus, given in the exemplification of the present invention
                                                                                                                        39.1%; Score 8.6; DB 1; Length 13; llarity 72.7%; Pred. No. 5.4e+02; Conservative 2; Mismatches 1; Indels
                                                                                  Sequence 13 BP; 5 A; 1 C; 2 G; 0 T; 1 U; 4 Other;
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Matches 8; Conserv
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                                                                                                                                   Query Match
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39.1%; Score 8.6; DB 1; Length 13;

Query Match

Sequence 13 BP; 5 A; 1 C; 2 G; 0 T; 1 U; 4 Other;

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Human dendritic cell SAGE tag, SEQ ID NO:1175.
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                                                                                                                                                                                                                                                                                                                                                                                                         Attenuation of pathogenic HIV-1 strain NL4-3 involves deletion of 1 or more decanuclectides (AAQ956406-Q97018) from the nef gene and/or 1 or more decanuclectides (AAQ95019-Q97166) from the LTR region; the sequence of AAQ96406 corresponds to nucleotides 1-10 of the nef gene (AAQ95141). The response in humans, and enable the generation of therapeutic, diagnostic and targeting agents against HIV-1 infection. (Updated on 16-OCT-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                       New non-pathogenic HIV-1 strain carrying a deletion in its nef gene or LTR region - can be used in a vaccine to inhibit/reduce productive infection in an individual by a pathogenic strain.
          Gaps
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Pred. No. 5.4e+02;
2; Mismatches 1; Indels
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                                                                                                                                                  HIV-1 NL4-3 nef gene nucleotide deletion 477.
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                                                                                                                                                                                     Human immunodeficiency virus 1
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94AU-00000284.
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72.7%;
                                                                                       AAQ96882 standard; DNA; 10
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Best Local Similarity 72.7
Matches 8, Conservative
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tes 9; Conserv
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Sequences AA27573-Z79709 represent SAGE (serial analysis of gene expression) tags used to identify mRNA transcripts encoding immunostimulatory cofactor proteins which are preferentially or differentially expressed in monocyte-derived dendritic cells compared with monocytes. Some of the transcripts correspond to known genes or ESTS (expressed sequence tags) which were previously unknown to be preferentially or differentially expressed in dendritic cells, while other transcripts correspond to novel genes. Antigen-presenting cell (APC) -associated costinulatory factors play an important role in the activation of the cytotoxic inmune response, particularly against tumour cells. Tumour antigen presentation via the MHC (major histocompatibility complex) and subsequent recognition by T-cell receptors is alone insufficient to activate a robust cytotoxic immune response that can lyse the tumour cells, immunostimulatory cofactors also being required for
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SAGE tag; serial analysis of gene expression; antigen-presenting cell; APC; moncoyte-derived dendritic cell; differential gene expression; immunostimulatory cofactor; costimulatory factor; CTL; cytocoxic T-lymphocyte; tumour antigen; immunotherapy; anticancer; ss.
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98US-0089844P

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98US-0089991P

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(ROBE/) ROBERTS B L.
(SHAN/) SHANKARA S.
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efficient activation of cytotoxic T-lymphocytes (CTLs). Nucleic acid sequences identified using the SAGE tags have several potential uses. They may be used in vaccines to induce an immune response, particularly against a tumour antigen; to modulate the genotype of an APC; to screen for agents that modulate expression of differentially expressed genes in an APC; and APC; and APC; and as hybridisation probes/amplification primers for the diagnosis, prognosis and monitoring of diseases related to abnormal expressed genes. Detection of the dendritic cell differentially expressed genes, or of their encoded proteins, can be used to identify calls as belonging to the moncoyte lineage. Calls containing these genes can be used in active immunotherapy (or to stimulate production of a population of artigen-specific effector cells) and vectors containing them are used in gene therapy. Co-administration of tumour antigens and APC-associated costimulatory factors ensures adequate antigen presentation to endogenous APCs and upregulates the APCs for the presentation of co-stimulatory signals, migration to T cell-rich sites, secretion of I cell growth factors and secretion of chemokines for recruitment of immune effector cells
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98US-0089873P.
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98US-0090035P.
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Best Local Similarity 90...
Best Society 90...
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19-11-WUL-61
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Expression) tags used to identify mRNA transcripts encoding immunostimal acry cofactor proteins which are preferentially or immunostimal acry cofactor proteins which are preferentially or differentially expressed in monocyte-derived dendritic cells compared with monocytes. Some of the transcripts correspond to known genes or ESTS (expressed sequence tags) which were previously unknown to be preferentially or differentially expressed in dendritic cells, while cher transcripts correspond to novel genes. Antigen-presenting cell or the correspond to novel genes. Antigen-presenting cell or the correspond to novel genes. Antigen-presenting cell or the corporation of the cytotoxic immune response, particularly against tumour cells, mnunostimulatory datcors play an important role in the complex) and subsequent recognition by T.cell receptors is alone insufficient to activate a robust cytotoxic immune response that can lyse the tumour cells, mnunostimulatory cofactors also being required for the tumour cells, mnunostimulatory cofactors also being required for efficient activation of cytotoxic T-lymphocytes (CTLS). Nucleic acid sequences identified using the SAGE tags have several potential uses. They may be used in vaccines to induce an immune response, particularly against a tumour antigen, to modulate the genotype of an APC; to screen for agents that modulate expression of diseases related to abnormal expression of the dendritic cell differentially expressed genes, or of their encoded proteins, can be used to identify calls as belonging to the monocyte lineage. Cells containing these genes can be used in active immunotherapy (or to stimulate production of a containing them are used in gene therapy. Co-daministration of unduction of antigen-specific defector cells and each of activities of the monocyte lineage. Cells containing them are used in gene therapy. Co-daministration of costimulatory factors ensures adequate antigen presentation of costimulatory factors ensures adequate antigen presentation of costimulatory fa
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                                                         9805-0090076P.
9805-0090076P.
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ID AAZ77903 standard; DNA; 10 BP.
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Best Local Similarity 90.0
Matches 9; Conservative
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                                       SAGE tag; serial analysis of gene expression; antigen-presenting cell; APC; monocyte-derived dendritic cell; differential gene expression; mannostimulatory cofactor; costimulatory factor; CTL;
                                                                      cytotoxic T-lymphocyte; tumour antigen; immunotherapy; anticancer; ss.
                    Human dendritic cell SAGE tag, SEQ ID NO:331.
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(first entry)
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the tumour cells, immunostimulatory cofactors also being required for efficient activation of cytotoxic T-lymphocytes (CTES). Nucleic acid gequences identified using the SAGE tags have several potential uses. They may be used in vaccines to induce an immune response, particularly against a tumnour antigen; to modulate the genotype of an APC; to screen car agents that modulate expression of differentially expressed genes in an APC; and as hybridisation probes/amplification primers for the an APC; and as hybridisation probes/amplification primers for the diagnosis, prognosis and monitoring of diseases related to abnormal expression of these genes. Detection of the dendritic cell differentially expressed genes, or of their encoded proteins, can be used to identify cells as belonging to the monocyte lineage. Cells containing these genes can be used in active immunotherapy (or to stimulate production of a population of antigen-specific effector cells) and vectors containing APC-associated costimulatory factors ensures adequate antigen and presentation to endogenous APCs and upregulates the APCs for the presentation of co-stimulatory factors ensures adequate antigen presentation of T cell growth factors ensures acequate antigen correction of T cell growth factors and secretion of chemokines for recruitment of immune effector cells
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90.0%; Pred. No. 5.2e+02;
iive 0; Mismatches 1;
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that are preferentially transcribed in the metastatic breast tumour tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ86677 represent tags corresponding to distinct transcripts that are preferentially transcribed in metastatic breast tumour cells). AAZ86677 represent tags corresponding to distinct transcripts that are preferentially transcribed in the primary or non-metastatic breast tumour tissue (i.e. are downregulated in metastatic breast tumour cells). These transcripts can be used for disgnosis, prognosis, monitoring and transcripts can be used for disgnosis, prognosis, monitoring and transcripts can be used for disgnosis, prognosis, monitoring and transcripts are used to hybridisation/amplification reactions. On seful for treatment of (metastatic) breast cancer, while promoters from the transcripts are used to direct expression of the transcripts are potentially useful for treatment of direct expression, in selected cell types, of e.g. therapeutic genes (also ribozymes or antisense sequences), particularly an antigen-encoding sequence for use in gene or cell-based vaccines, for diagnosing breast cancer and for raising specific antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic and isolate populations of educated, antigen-specific immune effecter cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
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                                                                                                                                                                                                                                                                                                                                                                                                                      38.2%; Score 8.4; DB 1; Length 10; 90.0%; Pred. No. 5.2e+02;
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ROBERTS B L.
SHANKARA S.
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Best Local Similarity
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AAZ AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts that are preferentially transcribed in the metastatic breast tumour cells). AAZ83942 ct issue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942 to AAZ86677 represent tags corresponding to distinct transcripts that are preferentially transcribed in the primary or non-metastatic breast tumour cells). These crissue (i.e. are downregulated in metastatic breast tumour cells). These transcripts can be used for diagnosis, prognosis, monitoring and transcripts can be used for diagnosis, prognosis, monitoring and transcripts can be used for Mybridisation/amplification reactions. Compounds that modulate expression of the transcripts are potentially useful for treatment of (metastatic) breast cancer, while promoters from the transcripts are used to direct expression, in selected cell types, of e.g. therapeutic genes (also ribozymes or antisense sequences), particularly an antigen-encoding sequence for use in gene or cell-based vaccines, for diagnosing breast cancer and for raising specific antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic gents. Host cells that produce the polypeptides can be used to expand and isolate populations of educated, antigen-specific immune effecter cells, e.g. cytotoxic T lymphocytes, and these used for adoptive immunetherapy
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Pred. No. 5.2e+02;
0; Mismatches 1; Indels
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Claim 1; Page 59; 219pp; English.
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Best Local Similarity 90.0-
Best Local Similarity
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RESULT 658
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Compounds that modulate expression of the transcripts are potentially useful for treatment of (metastatic) breast cancer, while promoters from the transcripts are used to direct expression, in selected cell types, of e.g. therapeutic genes (also ribozymes or antisense sequences), particularly an antigen-encoding sequence for use in gene or cell-based vaccines, for diagnosing breast cancer and for raising specific antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic agents. Host cells that produce the polypeptides can be used to expand and isolate populations of educated, and these used for adoptive
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                      Claim 1; Page 131; 219pp; English.
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treatment of cancer.
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that are preferentially transcribed in the metastatic breast tumour that are preferentially transcribed in the metastatic breast tumour cells). AAZ80342 to AAZ86677 represent tags corresponding to distinct transcribts that are preferentially transcribed in metastatic breast tumour cells). AAZ8342 to AAZ86677 represent tags corresponding to distinct transcribts that are preferentially transcribed in the primary or non-metastatic breast tumour cells). These transcripts can be used for diagnosis, promotis, monitoring and transcripts can be used for diagnosis, promotis, monitoring and transcripts can be used for diagnosis, promotis monitoring and transcripts can be used for diagnosis, promotis monitoring and compounds that modulate expression of the transcripts are potentially useful for treatment of (metastatic) breast cancer, while promoters from the transcripts are used to direct expression, in selected cell types, of c.g. therapeutic genes (also ribozymes or antisense sequences), particularly an antigen-encoding sequence for use in gene or cell-based vaccines; for diagnosing breast cancer and for raising specific antibodies (bb). Ab are used to detect the polypeptides or as therapeutic and isolate populations of educated, antigen-specific immune effecter.
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Isolated polynucleotides differentially expressed between metastatic and non-metastatic breast cancer cells, useful for diagnosis, prevention and
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                                                                                                                                 Claim 1; Page 66; 219pp; English.
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Best Local Similarity 90.0-
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                                                               treatment of cancer.
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Human, metastatic breast tumour tissue; breast cancer; tag; primer; non-metastatic breast tumour tissue; gene therapy; anticancer; antimetastatic; vaccine; diagnosis; ss.
                                     Claim 1; Page 80; 219pp; English.
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98US-0089997P.
98US-0090039P.
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ROBERTS B L.
SHANKARA S.
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Best Local Similarity
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that are preferentially transcribed in the metastatic breast tumour that are preferentially transcribed in the metastatic breast tumour tissue (i.e. are upregalated in metastatic breast tumour cells). A523942 to A526677 represent tags corresponding to distinct transcripts that are preferentially transcribed in the primary or non-metastatic breast tumour cells). These crissue (i.e. are downregulated in metastatic breast tumour cells). These transcripts can be used for diagnosis, prognosis, monitoring and transcripts can be used for diagnosis, prognosis, monitoring and transcripts can be used for diagnosis, prognosis, monitoring and transcripts can be used for diagnosis of particularly where metastatic. Diagnosis is compounds that modulate expression of the transcripts are potentially compounds that modulate expression of the transcripts are potentially considered for the transcripts are used to direct expression, in selected cell types, of the transcripts are used to direct expression, in selected cell types, of articularly an antigen-encoding sequence for use in gene or cell-based vaccines, for diagnosing breast cancer and for raising specific antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic agents. Host cells that produce the polypeptides can be used to expand and isolate populations of educated, antigen-specific immune effecter cells, e.g. cytotoxic T lymphocytes, and these used for adoptive immunotherapy
                                                                                                                            Isolated polynucleotides differentially expressed between metastatic and non-metastatic breast cancer cells, useful for diagnosis, prevention and
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Roberts BL,
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WPI; 2000-106079/09.
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Human, metastatic breast tumour tissue; breast cancer, tag, primer, non-metastatic breast tumour tissue, gene therapy; anticancer, antimetastatic, vaccine; diagnosis, ss.
                                            Metastatic breast tumour cell upregulated transcript tag #1089
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98US-0090039P.
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(ROBE/) ROBERTS B L.
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19-JUN-1998;
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(GENZ ) GENZYME CORP.
(ROBE/) ROBERTS B L.
(SHAN/) SHANKARA S.
                                                          Roberts BL,
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                                                                                                                                         Claim 1; Page 87; 219pp; English.
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                             Roberts BL, Shankara
                                                        WPI; 2000-106079/09.
  (SHAN/) SHANKARA S.
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that are preferentially transcribed in the metastatic breast tumour cells. AAZ80767 to AAZ80767 to AAZ80341 represent tags corresponding to distinct transcripts that are transcribed in metastatic breast tumour cells). AAZ83342 to AAZ86677 represent tags corresponding to distinct transcripts that are preferentially transcribed in the primary or non-metastatic breast tumour cells). These can be used for diagnosis, prognosis, monitoring and transcripts can be used for diagnosis, prognosis, monitoring and transcripts can be used for diagnosis, prognosis, monitoring and transcripts can be used for diagnosis, prognosis, monitoring and compounds that modulate expression of the transcripts are potentially compounds that modulate expression of the transcripts are potentially compounds that modulate expression of the transcripts are potentially of useful for treatment of (metastatic) breast cancer, while promoters from the transcripts are used to direct expression, in selected cell types, of c.g. therapeutic genes (also ribozymes or antisense sequences), particularly an antigen-encoding sequence for use in gene or cell-based vaccines, for diagnosing breast cancer and for raising specific antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic agents. Host cells that produce the polypeptides can be used to expand and isolate populations of educated, antigen-specific immune effecter.
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Shankara S;
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to AAZ86677 represent tags corresponding to distinct transcripts that are preferentially transcribed in the primary or non-metastatic breast tumour cells). AAZ81942

to AAZ86677 represent tags corresponding to distinct transcripts that are commercially transcribed in the primary or non-metastatic breast tumour cells. These transcripts can be used for diagnosis, prognosis, monitoring and transcripts can be used for diagnosis, prognosis, monitoring and transcripts can be used for diagnosis, prognosis, monitoring and transcripts are metastatic. Diagnosis is by standard immunossays or hybridisation/amplification reactions.

Compounds that modulate expression of the transcripts are potentially useful for treatment of (metastatic) breast cancer, while promoters from the transcripts are used to direct expression, in selected cell types, of particularly an antigen-encoding sequence for use in gene or cell-based vaccines, for diagnosing breast cancer and for use in gene or cell-based and isolates nopulations of educated, antigen-epecific immune effecter

cells, e.g. cytotoxic I lymphocytes, and these used for adoptive
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                                                                                                                     Isolated polynucleotides differentially expressed between metastatic and non-metastatic breast cancer cells, useful for diagnosis, prevention and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human, metastatic breast tumour tissue; breast cancer; tag; primer; non-metastatic breast tumour tissue; gene therapy; anticancer; antimetastatic; vaccine; diagnosis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Metastatic breast tumour cell downregulated transcript tag #5791
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 10 BP; 1 A; 2 C; 1 G; 6 T; 0 U; 0 Other;
                                                                                                                                                                      Claim 1; Page 114; 219pp; English.
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 98US-0090041P
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                                                                        Roberts BL, Shankara S;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GATAAACAGA 1
                     (GENZ ) GENZYME CORP. (ROBE/) ROBERTS B L.
                                                                                               WPI; 2000-106079/09
                                                                                                                                              treatment of cancer
                                               SHANKARA S.
19-JUN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
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                                               (SHAN/)
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tasse (i.e. are upregulated in metastatic breast tumour cellals. AA280767 to AA28391 represent tags corresponding to distinct transcripts tumour cellals. AA283942 to AA286677 represent tags corresponding to distinct transcripts that are preferentially transcribed in the primary or non-metastatic breast tumour cells). These crissue (i.e. are downregulated in metastatic breast tumour cells). These transcripts can be used for diagnosis, prognosis, monitoring and transcripts can be used for diagnosis, prognosis, monitoring and transcripts can be used for diagnosis, prognosis, monitoring and compounds that modulate expression of the transcripts are potentially compounds that modulate expression of the transcripts are potentially compounds that modulate expression of the transcripts are potentially compounds that modulate expression of the transcripts are also used to direct expression, in selected cell types, of the transcripts are used to direct expression, in selected cell types, of particularly an antigen-encoding sequence for use in gene or cell-based concornes; for diagnosing breast cancer and for raising specific antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic agents: Host cells that produce the polypeptides can be used to expand and isolate populations of educated, antigen-specific immune effecter cells, e.g. cyctoxic I lymphocytes, and these used for adoptive immunotherapy
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Isolated polynucleotides differentially expressed between metastatic and non-metastatic breast cancer cells, useful for diagnosis, prevention and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; Page 211; 219pp; English.
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98US-0090039P.
                                    98US-0090040P.
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Best Local Similarity 90.0
Matches 9; Conservative
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                                                                                                                                                                                                                                                                                                        Roberts BL, Shankara
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                                                                                                                                              (GENZ ) GENZYME CORP
(ROBE/) ROBERTS B L.
(SHAN/) SHANKARA S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           treatment of cancer.
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                                    19-JUN-1998;
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99JP-00095481.

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The present invention describes a method of identifying the type of cell in a sample, involving determining which of the sequences AAH63161-AAH64724 is expressed by the cell. The transcriptomes described in the invention are cell-type specific, cancer specific or ubiquitously expressed in humans. They can also be used to screen for drugs, reduce cancer specific agene expression, standardise expression and restore the function of a diseased cell or tissue. The present sequence is one of the transcriptomes described in the exemplification of the invention

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The present invention describes a group of genes consisting of 100 genes which are highly expressed in human dendritic cells, a group of genes which are expressed at a higher frequenty in human dendritic cells than in human monocytes, and a group of genes which are expressed at lower frequency in human dendritic cells than in human monocytes. Bach group of genes are characterised in that cDNAs of these genes respectively have the base sequences of SEQ ID NO:101 to 100 (AAC74014 to AAC74013) and SEQ ID NO:201 to 300 (AAC74114 to AAC74213), each is continuous with the base sequence 5'-CATG-3' the investigation of the role and mechanism of the involvement of dendritic cells in the immune system and for the study and diagnosis of diseases in which dendritic cells play a significant role, e.g. cancers
                                                                                                        Groups of genes expressed in human dendritic cells at a greater or lesser extent than in monocytes for investigation and diagnosis of autoimmune disease and tumors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New isolated polynucleotides, useful for identifying specific cell type, such as cancer cell, comprises transcriptomes expressed in particular cell types.
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               (NISC-) JAPAN SCI & TECHNOLOGY CORP.
                                                                                                                                                                              Claim 10; Page 13; 95pp; Japanese
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Query Match

Best Local Similarity 90.00,

Best 10cal 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                              and autoimmune diseases
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                                                                              WPI; 2000-619172/59.
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                                               Hashimoto S,
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Claim 13; Page 58; 94pp; English.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New isolated polynucleotides, useful for identifying specific cell type, such as cancer cell, comprises transcriptomes expressed in particular cell types.
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                                                                                                                                                                                                               Gaps
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Best Local Similarity 90.0%
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(USSH ) US DEPT HEALTH & HUMAN SERVICES.
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       isolated polymucleotides, useful for identifying specific cell type, as cancer cell, comprises transcriptomes expressed in particular
                                                                                                                                                                                                                                                                   transcriptome, gene expression pattern, cancer; drug screening; diagnosis; cell specific gene expression; ss.
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                                                                                                          AAH64453 standard; cDNA; 10 BP
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cancer
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The present invention relates to a polymorphic variant of a reference sequence for the solute carrier family 6 neurotransmitter transporter, serotonin member 4 (SLC6A4) gene or a fragment of it or a sequence complementary to the first sequence. The invention is used in producing a recombinant organism that can be used to express SLC6A4 for protein structure analysis and binding studies. A composition comprising a genotyping oligonucleotide is used to detect a polymorphism in the SLC6A4
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                                                                                                                                                                                                                                                                                                                       New isolated polynucleotide comprising a polymorphic variant for the solute carrier family 6 neurotransmitter transporter, serotonin member 4 gene for identifying drugs for treating disorders related to expression
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                                                                                                                                                                                        Stephens JC;
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                                                                                                                                                                                           Sanchis A,
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                                                                                                                                                                                               Duda A, Nandabalan
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31-JUL-2000; 2000WO-US020638.
                                                               99US-0146290P
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                                                                                                                               (GENA-) GENAISSANCE
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nes 9; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                     of the protein.
                                                               29-JUL-1999;
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Detecting and identifying ovarian tumor, identifying increased risk for developing ovarian cancer, and determining effectiveness of ovarian cancer treatment, by measuring expression level of ovarian tumor marker
     Morin PJ, Sherman-Baust CA, Pizer ES, Hough CD;
                 WPI; 2001-626450/72
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Claim 25; Page 31; 140pp; English.

XX.

The invention relates to methods for diagnosing and prognosing ovarian tumours in an individual via the detection and measurement of the tumours in an individual via the detection and measurement of the expression of ovarian tumour marker genes (ABA83181-ABA83189, ABA83189, ABA83181 and ABA83183). The methods of the invention are useful for detecting an ovarian tumour in a patient, for identifying an individual at increased risk for developing ovarian cancer, in prognostic tests for assessing the relative severity of ovarian cancer, in prognostic tests for monitoring a patient in remission from ovarian cancer.

CC monitoring disease status in a patient being treated for ovarian cancer.

The methods can additionally be used to identify a particular tumour as being an ovarian tumour (i.e., an epithelial ovarian tumour selected from serous cystadenoma, borderline serous tumour, mucinous cystadenoma, borderline serous tumour, mucinous cystadenocarcinoma, orderline mucinous tumour, mucinous cystadenocarcinoma, endometriol darcinoma, undifferentiated carcinoma, clear cell adenocarcinoma, cystadenofibroma, and Brenner cumour. The ovarian tumour marker genes of the invention were identified overspressed in a broad variety of ovarian epithelial tumour cells crelative to normal ovarian epithelial cells. The marker genes are implicated in immune response pathways, in the regulation of cell colocalised or secreted. In addition to their use as diagnostic and protein folding, and many of these are membrane-colocalised or secreted. In addition to their use as diagnostic and protein and in protein folding, and many of these are membrane-colocalised be used as therapeuts to their tumour marker genes or their encoded content of ovarian epithelial cells. The readment and in protein cancer of prognostic markers, the ovarian tumour marker genes or their encoded content of ovarian cells content of ovarian prevention of ovarian cancer. Sequences ABA83123-ABA83169, ABA83179, ABA83181 and ABA83183 represent SAGE tags derived from the ovarian tumour marker genes of the invention

Sequence 10 BP; 5 A; 2 C; 2 G; 1 T; 0 U; 0 Other;

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0; Gaps
Query Match

38.2%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 5.2e+02;
Matches 9; Conservative 0; Mismatches 1; Indels
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RESULT 670

AAF35790 standard; DNA; 10 BP.

AAF35790;

(first entry) 23-MAR-2001

Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:2529.

Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF; nor previously assigned open reading frame; nonannocated ORF; SAGE; serial analysis of gene expression; antifungal; tag; identification; linker; PCR primer; de.

Saccharomyces cerevisiae

WO200077214-A2

21-DEC-2000.

14-JUN-2000; 2000WO-US016223.

99US-00335032 16-JUN-1999;

(UYJO) UNIV JOHNS HOPKINS.

Kinzler K; Vogelstein B, Jelculescu V,

WPI; 2001-061874/07.

Yeast gene coding sequences comprising NORF genes with serial analysis of gene expression (SAGE) tags, useful for studying, monitoring and affecting phases of the cell cycle.

Example; Page 90; 419pp; English.

The present invention describes an isolated DNA molecule comprising a coding sequence of a yeast gene selected from a group of 745 NORF (not previously assigned open reading frame, or nonamnotated ORF) genes comprising a SAGE (serial analysis of gene expression) tag. Also described are: (1) a method (M1) of using NORF genes to affect the cell corprising administering a NORF gene whose expression varies by at least 10% between any two phases of the cell cycle selected from log phase, S phase and G2/M; (2) a method (M2) for screening candidate of antifungal drugs comprising: (a) contacting east sets substance which substance with a yeast cell; and (b) monitoring expression of a NORF gene whose expression of the yeast gene is a candidate antifungal drug; (3) a method (M3) for identifying human genes which are involved in cell cycle progression of comprising contacting human DNA with a probe which comprises at least 10 contiguous nucleotides of a NORF gene whose expression varies as in M1; and (4) a method (M4) for identifying a candidate drug as a member of a class of drugs having a characteristic effect on gene expression in a yeast cell comprising contacting a yeast cell with a candidate drug and contitoring expression in the yeast cell of at least 1 NORF genes may be used to strength of the class of the cell cycle. The expression is affected by the class of the cell cycle, the differentially contacting and feet phases of the cell cycle, the differentially cycle stression is dentification of antifungal drugs. The NORF genes may be used to identify candidate drugs which affect the cell cycle are thods may be used to identify candidate drugs which affect the cell cycle are the expression of antifungal drugs. April 2016 the cell cycle are ceptered in the exemplification of the present invention.

AAF33262 to AAF33267 represent linkers and port exemple invention.

Sequence 10 BP; 6 A; 1 C; 3 G; 0 T; 0 U; 0 Other;

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0; Gaps 38.2%; Score 8.4; DB 1; Length 10; 90.0%; Pred. No. 5.2e+02; tive 0; Mismatches 1; Indels Best Local Similarity 90.0 Matches 9; Conservative Query Match

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AAF43163 standard; DNA; 10 BP. RESULT 671 AAF43163 ID AAF4

AAF43163;

23-MAR-2001 (first entry)

Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:11302.

Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF; nor previously assigned open reading frame; nonannotated ORF; SAGE; serial analysis of gene expression; antifungal; tag; identification; linker; PCR primer; ds.

Saccharomyces cerevisiae.

WO200077214-A2

Saccharomyces cerevisiae.

Kinzler K;

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Yeast gene coding sequences comprising NORF genes with serial analysis of gene expression (SAGE) tags, useful for studying, monitoring and affecting phases of the cell cycle.
                                                                                  Example; Page 353; 419pp; English
             14-JUN-2000; 2000WO-US016223.
                                           Velculescu V, Vogelstein B,
                       99US-00335032
                                  SNING OHIO JOHNS HOPKINS
                                                                                                                                                                                                                                                                           1 TGCCAGCAGA 10
                                                     WPI; 2001-061874/07.
                        16-JUN-1999;
    21-DEC-2000,
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The present invention describes an isolated DNA molecule comprising a coding sequence of a yeast gene selected from a group of 745 NORF (not previously assigned open reading frame, or nonamontated ORP) genes comprising a SAGE (serial analysis of gene expression) tag. Also described are: (1) a method (M1) of using NORF genes to affect the cell cycle comprising administering a NORF gene whose expression varies by at least 10% between any two phases of the cell cycle selected from log phase, S phase and G2/M; (2) a method (M2) for screening candidate antifungal drugs comprising: (a) contacting a test substance whose expression of varies as in M1, where a test substance which modifies the expression of varies as in M1, where a test substance which modifies the expression of the yeast gene is a candidate antifungal drug; (3) a method (M3) for identifying human genes which are involved in cell cycle progression contiguous nucleotides of a NORF gene whose expression at method (M4) for identifying a condidate drug as a member of a class of drugs having a characteristic effect on gene expression in a comprising contecting a yeast cell with a candidate drug as a member of contiguous expression in the yeast cell with a candidate drug and contecting a yeast cell with a candidate drug and contecting a yeast cell of at least 1 NORF gene whose expression is affected by the class of the cell cycle, the differentially expression is affected by the class of the cell cycle, the differentially expression is affected by the class of the cell cycle, the differentially expression in the yeast cell of at least 1 NORF gene whose expression and feet phases of the cell cycle, the differentially expressed genes may be used as markers of phases of the cell cycle of expressed genes may be used as markers of phases of the cell cycle. The expression is dentify candidate drugs which affect the cell cycle expressed to dentification of antifungal drugs. April 100 of the present invention.

Appliance of the present invention of the present invent
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Best Local Similarity 90.0
Matches 9; Conservative
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Gaps

AAF43935 standard; DNA; 10 BP. 23-MAR-2001 (first entry)

Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF; nor previously assigned open reading frame; nonannotated ORF; SAGE; serial analysis of gene expression; antifungal; tag; identification; linker; PCR primer; ds. Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:12074.

The present invention describes an isolated DNA molecule comprising a coding sequence of a yeast gene selected from a group of 745 NORF (not previously assigned open reading frame, or nonamnotated ORF) genes comprising a SAGE (serial analysis of gene expression) tag. Also described are: (1) a method (M1) of using NORF genes to affect the cell cycle comprising administering a NORF gene whose expression varies by at least 10% between any two phases of the cell cycle selected from log phase, S phase and G2/M; (2) a method (M2) for screening candidate of the yeast gene (M2) for screening candidate of the yeast gene (M3) for screening candidate antifurgal drugs comprising; (a) contacting a test substance which a yeast cell; and (M3) for identifying human genes which are involved in cell cycle progression of contiguous inucleotides of a NORF gene whose expression of contiguous inucleotides of a NORF gene whose expression in a contiguous inucleotides of a NORF gene whose expression in a control of drugs having a characteristic effect on gene expression in a cross of drugs. The NORF gene whose expression in a corpusion of a NORF gene whose expression in the yeast cell with a candidate drug as a member of substreamy monitor and affect phases of the cell cycle. The expression is affected by the class of drugs. The NORF gene whose expression is affected by the class of the cell cycle, the differentially cycles may be used to identifying a candidate drugs which affect the cycle cycle and for identifying a candidate drugs which affect the cycle cycle and for identification of a mithing a drugs. The NORF gene whose expressed genes may be used in the exemplification of the present invention.

Cycle and for identification of antifungal drugs. App33268 to App44064 cycle cycle and for identification of antifungal substribution of the present invention. Yeast gene coding sequences comprising NORF genes with serial analysis of gene expression (SAGE) tags, useful for studying, monitoring and affecting phases of the cell cycle. Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF; nor previously assigned open reading frame; nonannotated ORF; SAGE; ö Query Match

Best Local Similarity 90.0%; Pred. No. 5.2e+02;
Matches 9; Conservative 0; Mismatches 1; Indels Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:4102. method, in the exemplification of the present invention Sequence 10 BP; 1 A; 2 C; 2 G; 5 T; 0 U; 0 Other; Kinzler K; Example; Page 381; 419pp; English AAF37363 standard; DNA; 10 BP. 14-JUN-2000; 2000WO-US016223. Vogelstein B, 99US-00335032 (UYJO) UNIV JOHNS HOPKINS. 23-MAR-2001 (first entry) 729 CCAGGAGAA 738 10 CCAGTAGAAA 1 WPI; 2001-061874/07. WO200077214-A2. 16-JUN-1999; Velculescu V, 21-DEC-2000 AAF37363; 673 RESULT XXXXXXXXXX 8

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Yeast gene coding sequences comprising NORF genes with serial analysis of gene expression (SAGE) tags, useful for studying, monitoring and affecting phases of the cell cycle.
                   Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF; nor previously assigned open reading frame; nonannotated ORF; SAGE; SACE; serial analysis of gene expression; antifungal; tag; identification; linker; PCR primer; ds.
                                                                                                                                                                                                                                                                                                                             Pelculescu V, Vogelstein B,
                                                                                                                                                                                                                    14-JUN-2000; 2000WO-US016223
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                                                                                                           Saccharomyces cerevisiae.
                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-061874/07.
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                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention describes an isolated DNA molecule comprising a coding sequence of a yeast gene selected from a group of 745 NORF (not previously assigned open reading frame, or nonannotated ORF) genes comprising a SAGE (serial analysis of gene expression) tag. Also described are: (1) a method (M1) of using NORF genes to affect the cell cycle comprising administering a NORF gene whose expression varies by at least 10% between any two phases of the cell cycle selected from log phase, S phase and G2/M; (2) a method (M2) for screening candidate by an entitlengal drugs comprising: (a) contexting a test substance with a yeast cell; and (b) monitoring expression of a NORF gene whose expression of the yeast gene is a candidate antifungal drug; (3) a method (M3) for identifying human genes which are involved in cell cycle progression of contriguous nucleotides of a NORF gene whose expression of a NORF gene whose expression in a contiguous nucleotides of a NORF gene whose expression in a yeast cell comprising contacting a yeast cell with a candidate drug as a member of a yeast cell comprising contacting a yeast cell with a candidate drug and contoring expression in the yeast cell of at least 1 NORF gene whose expression is affected by the class of drugs. The NORF gene whose corpression is affect phases of the cell cycle, the differentially expression is affected by the class of drugs. The NORF gene whose corpressed genes may be used to identify candidate drugs which affect the cell cycle and for identification of antifungal drugs. Appl3268 to ApP44064.

Cycle and for identification of antifungal drugs. Bapilass of the exemplification of the present invention of the present inventi
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                                                                                                                                                                                                                                                                                                                                           Yeast gene coding sequences comprising NORF genes with serial analysis of gene expression (SAGE) tags, useful for studying, monitoring and affecting phases of the cell cycle.
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serial analysis of gene expression, antifungal, tag, identification,
linker, PCR primer, ds.
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38.2%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 5.2e+02;
Matches 9; Conservative 0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                        Kinzler
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                                                                                                                                                             14-JUN-2000; 2000WO-US016223
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ID AAF4
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AC AAF4
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Kinzler K;

99US-00335032

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The present invention describes an isolated DNA molecule comprising a coding sequence of a yeast gene selected from a group of 745 NORF (not previously assigned open reading frame, or nonamnotated ORF) genes comprising a SAGE (serial analysis of gene expression) tag. Also described are: (1) a method (M1) of using NORF genes to affect the cell cycle comprising administering a NORF gene whose expression varies by at least 10% between any two phases of the cell cycle selected from log phase, S phase and G2/M; (2) a method (M2) for screening candidate cell; and (b) monitoring expression of a NORF gene whose expression of the yeast gene whose expression of cell; and (b) monitoring expression of a NORF gene whose expression of the yeast gene is a candidate antifungal drug; (3) a method (M3) for identifying human genes which are involved in cell cycle progression of identifying human genes which are involved in cell cycle progression contiguous mucloticates of a NORF gene whose expression varies as in M1; and (4) a method (M4) for identifying a cendidate drug as a member of a class of drugs having a characteristic effect on gene expression in a contiguous mucloting expression in the yeast cell with a candidate drug and continuitor and affect phases of the cell cycle. The contiguous mucloting expression in the yeast cell of at least 1 NORF genes may be used to identify candidate drugs which affect the cell cycle and for identification of antifungal drugs, the differentially contenting and monitoring and facet phases of the cell cycle. The expression is dentification of antifungal drugs, the differentially cycle and for identify candidate drugs which affect the cell cycle and for identification of antifungal drugs. The NORF genes may be used to identify and phases of the cell cycle and for identification of antifungal drugs. The NORF genes is market system to intensity in the exemplification of the present invention.

AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ô
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 10 BP; 3 A; 4 C; 2 G; 1 T; 0 U; 0 Other;
Example; Page 265; 419pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity 90.0
nes 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     739 CAGAACACCG 748
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ID AAF3
XX
AC AAF3
XX
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Yeast, Saccharomyces cerevisiae; characterisation; cell cycle; NORF; nor previously assigned open reading frame; nonannotated ORF; SAGE; serial analysis of gene expression; antifungal; tag; identification;

Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:4132.

23-MAR-2001 (first entry)

AAF37393;

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Yeast gene coding sequences comprising NORF genes with serial analysis of gene expression (SAGE) tags, useful for studying, monitoring and affecting phases of the cell cycle.
                                  Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF; nor previously assigned open reading frame; nonannotated ORF; SAGE; serial analysis of gene expression; antifungal; tag; identification; linker; PCR primer; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 38.2%; Score 8.4; DB 1; Length 10; Best Local Similarity 90.0%; Pred. No. 5.2e+02; Matches 9; Conservative 0; Mismatches 1; Indels
                  Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:5238.
                                                                                                                                                                                                                                                                                              Example; Page 187; 419pp; English.
                                                                                                                                                                                                                Velculescu V, Vogelstein B,
                                                                                                                                                                        99US-00335032.
                                                                                                                                                    14-JUN-2000; 2000WO-US016223
                                                                                                                                                                                           (UYJO ) UNIV JOHNS HOPKINS
23-MAR-2001 (first entry)
                                                                                         Saccharomyces cerevisiae.
                                                                                                                                                                                                                                   WPI; 2001-061874/07.
                                                                                                             WO200077214-A2.
                                                                                                                                                                         16-JUN-1999;
                                                                                                                                 21-DEC-2000
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Yeast gene coding sequences comprising NORF genes with serial analysis of gene expression (SAGE) tags, useful for studying, monitoring and affecting phases of the cell cycle.

Example; Page 147; 419pp; English

Kinzler K;

Velculescu V, Vogelstein B,

WPI; 2001-061874/07.

UNJO) UNIV JOHNS HOPKINS

99US-00335032.

16-JUN-1999;

Kinzler K;

14-JUN-2000; 2000WO-US016223

Saccharomyces cerevisiae.

WO200077214-A2.

21-DEC-2000.

linker; PCR primer; ds.

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The present invention describes an isolated DNA molecule comprising a coding sequence of a yeast gene selected from a group of 745 NORF (not previously assigned open reading frame, or nonamnotated ORF) genes comprising a SAGE (serial analysis of gene expression) tag. Also described are: (1) a method (M1) of using NORF genes to affect the cell cycle comprising administering a NORF gene whose expression varies by at least 10% between any two phases of the cell cycle selected from log the cast 10% between any two phases of the cell cycle selected from log comprising: (a) contacting a test substance with a yeast cell; and (b) monitoring expression of a NORF gene whose expression of varies as in M1, where a test substance which modifies the expression of the yeast gene is a candidate antifurgal drug; (3) a method (M3) for identifying human genes which are involved in cell cycle progression of comprising contacting human DNA with a probe which comprises at least 10 contiguous nucleotides of a NORF gene whose expression varies as in M1; and (4) a method (M4) for identifying a candidate drug as a member of a class of drugs having a characteristic effect on gene expression in a feet that each 1 NORF gene whose expression is affected by the class of drugs. The NORF gene whose expression is affected by the class of the cell cycle, the differentially expressed genes may be used as markers of phases of the cell cycle. The methods may be used to identify candidate drugs which affect the cluster cycle and fert intention of antifungal drugs. Adalysing the characteristic cycle and fert dentification of antifungal drugs. The NORF gene whose cycle and for identify candidate drugs which affect the cycle and fert identification of antifungal drugs. The NORF gene in the exemplification of the present invention. AAPS3262 to AAPS3267 represent linkers and por invention of the present invention.
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The present invention describes an isolated DNA molecule comprising a coding sequence of a yeast gene selected from a group of 745 NORF (not previously assigned open reading frame; or nonannotated ORF) genes comprising a shall searial analysis of gene expression) tag. Also described are: (1) a method (M1) of using NORF genes whose expression varies by at clast 10% between any two phases of the cell cycle selected from log phase, S phase and G2/M; (2) a method (M2) for screening candidate and man for antitioning a drugs comprising; (a) contecting a test substance with a yeast call; and (b) monitoring expression of a NORF gene whose expression of the great gene is a candidate antifungal drug; (3) a method (M3) for candidate antifungal drug; (3) a method (M3) for identifying nontacting human DNA with a probe which comprises at least 10 comprising contacting whose expression varies as 10 M1; and (4) a method (M4) for identifying a candidate drug as a member of a class of drugs having a characteristic effect on gene expression in a class of drugs having a characteristic effect on gene expression in a class of drugs having a characteristic effect on gene expression in a class of drugs which are least 1 NORF gene whose expression is affected by the class of the cell cycle. The method may be used a markers of phases of the cell cycle. The methods may be used to identify candidate drugs which affect the cell cycle of the resent short and affect the call cycle of the present invention. AAF33267 represent in the exemplification of the present invention.
Sequence 10 BP; 6 A; 2 C; 2 G; 0 T; 0 U; 0 Other;
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0
                           38.2%; Score 8.4; DB 1; Length 10; 90.0%; Pred. No. 5.2e+02; tive 0; Mismatches 1; Indels
Sequence 10 BP; 6 A; 2 C; 2 G; 0 T; 0 U; 0 Other;
                                                                9; Conservative
                                                                                             729 CCAGGAGAAA 738
                                                                                                                           1 CCAGAAGAAA 10
                                  Query Match
Best Local Similarity
                                                  Best Loca
Matches
                                                                                               8
                     ö
                     Gaps
                     .
0
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AAF37393 standard; DNA; 10 BP.

RESULT 676 AAF37393 ID AAF

736 AAACAGAACA 745 AAACAGAGCA 10

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Gaps

scnurczı-/2/.rng

AAF38223 standard; DNA; 10 BP. AAF38223;

RESULT 677 AAF38223

(first entry) 23-MAR-2001

Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:4962.

reast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF; nor previously assigned open reading frame; nonamnotated ORF; SAGE; serial analysis of gene expression; antifungal; tag; identification; linker; PCR primer; ds.

Saccharomyces cerevisiae.

WO200077214-A2

21-DEC-2000.

14-JUN-2000; 2000WO-US016223.

99US-00335032. 16-JUN-1999;

(UYJO) UNIV JOHNS HOPKINS

Kinzler K; Vogelstein B, Velculescu V,

WPI; 2001-061874/07.

Yeast gene coding sequences comprising NORF genes with serial analysis of gene expression (SAGE) tags, useful for studying, monitoring and affecting phases of the cell cycle.

Example; Page 177; 419pp; English.

The present invention describes an isolated DNA molecule comprising a coding sequence of a year gene selected from a group of 745 NORF (not previously assigned open reading frame, or nonamotated ORP) genes comprising a SAGE (serial analysis of gene expression) tag. Also described are: (1) a method (M1) of using NORF genes to affect the cell cycle comprising administering a NORF gene whose expression varies by at contact of the cell cycle selected from log phase, S phase and G2/M; (2) a method (M2) for screening candidate cell; and (b) monitoring expression of a NORF gene whose expression of cell; and (b) monitoring expression of a NORF gene whose expression of the yeast gene is a candidate antifungal drug; (3) a method (M3) for cell; and (b) monitoring expression of a NORF gene whose expression of the yeast gene is a candidate antifungal drug; (3) a method (M3) for identifying a probe which comprises at least 10 comprising contacting human DNA with a probe which comprises at least 10 contiguous nucleotides of a NORF gene whose expression in a contiguous nucleotides of a NORF gene whose expression in a contiguous nucleotides of a NORF gene whose expression is affected by the class of drugs. The NORF genes may be used to startify monitoring expression in the yeast cell of at least 1 NORF genes may be used to stricting and fert phases of the cell cycle. The methods may be used to identify candidate drugs which affect the cell cycle and for identification of antifungal drugs. AAF33268 to AAF33261 represent shod; in the exemplification of the present invention.

AAF33262 to AAF33267 represent linkers and por present invention.

Sequence 10 BP; 4 A; 2 C; 3 G; 1 T; 0 U; 0 Other;

0; Gaps Query Match
38.2%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 5.2e+02;
Matches 9; Conservative 0; Mismatches 1; Indels

727 TGCCAGGAGA 736

TGCCAGGAAA 10

g

AAF42636 standard; DNA; 10 BP.

AAF42636;

(first entry) 23-MAR-2001 Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:10775.

Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF; nor previously assigned open reading frame; nonannotated ORF; SAGE; serial analysis of gene expression; antifungal; tag; identification; linker; PCR primer; ds.

Saccharomyces cerevisiae.

WO200077214-A2

21-DEC-2000

14-JUN-2000; 2000WO-US016223

99US-00335032 16-JUN-1999;

(UYJO) UNIV JOHNS HOPKINS.

Kinzler K; Vogelstein B, Velculescu V,

WPI; 2001-061874/07.

Yeast gene coding sequences comprising NORF genes with serial analysis of gene expression (SAGE) tags, useful for studying, monitoring and affecting phases of the cell cycle.

Example; Page 334; 419pp; English,

The present invention describes an isolated DNA molecule comprising a coding sequence of a yeast gene selected from a group of 745 NORF (not previously assigned open reading frame; or nonanocated OF79 genes comprising a SAGE (serial analysis of gene expression) tag. Also described are: (1) a method (M1) of using NORF genes whose expression varies by at cast 10% between any two phases of the cell cycle selected from log phase. S phase and G2/M; (2) a method (M2) for screening candidate antifungal drugs comprising: (a) contacting a test substance with a yeast cell; and (b) monitoring expression of a NORF gene whose expression of the yeast gene is a candidate antifungal drug; (3) a method (M3) for the yeast gene is a candidate antifungal drug; (3) a method (M3) for identifying human genes which a probe which cell cycle progression contiguous nucleotides of a NORF gene whose expression varies as in M1; where the yeast gene is a candidate antifungal drug; (3) a method (M3) for identifying a candidate drug as a member of a contiguous nucleotides of a NORF gene whose expression in a characteristic effect on gene expression in a cast cell comprising contacting a yeast cell with a candidate drug as a member of a cast of drugs having a characteristic effect on gene expression in a contacting a yeast cell offer the cell cycle. The contox may be used to identify candidate drugs which affect the cell cycle and for identify candidate drugs which affect the cell cycle and for identification of antifungal drugs. AAF31268 to AAF41064 represent lankers and PCC AAF331268 to AAF41064 represent lankers and present invention. method, in the exemplification of the present invention

Seguence 10 BP; 1 A; 1 C; 1 G; 7 T; 0 U; 0 Other;

Gaps .. Score 8.4; DB 1; Length 10; Pred. No. 5.2e+02; 0; Mismatches 1; Indels Query Match
Best Local Similarity 90.0%;
Matches 9; Conservative

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736 AAACAGAACA 745 10 AAACAGAATA 8 g

RESULT 679

AAF42385 standard; DNA; 10 BP.

(first entry) 23-MAR-2001

AAF42385;

Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:9124.

Yeast, Saccharomyces cerevisiae, characterisation, cell cycle, NORF, nor previously assigned open reading frame, nonannotated ORF, SAGE, serial analysis of gene expression, antifungal, tag, identification, linker; PCR primer; ds

Saccharomyces cerevisiae.

WO200077214-A2.

21-DEC-2000

14-JUN-2000; 2000WO-US016223.

99US-00335032 16-JUN-1999;

SNINGO ONIV JOHNS HOPKINS

Kinzler K; Velculescu V, Vogelstein B,

WPI; 2001-061874/07.

Yeast gene coding sequences comprising NORF genes with serial analysis of gene expression (SAGE) tags, useful for studying, monitoring and affecting phases of the cell cycle.

Example; Page 325; 419pp; English

Example; Page 82; 419pp; English

The present invention describes an isolated DNA molecule comprising a coding sequence of a yeast gene selected from a group of 745 NORF (not previously assigned open reading frame, or nonamnotated ORF) genes comprising a SAGE (serial analysis of gene expression) tag, Also described are: (1) a method (M1) of using NORF genes to affect the cell comprising administering an NORF gene whose expression varies by at least 10% between any two phases of the cell cycle selected from log phase, S phase and G2/M; (2) a method (M2) for screening candidate on this analysis of the cell cycle selected from log phase, S phase and G2/M; (2) a method (M2) for screening candidate of antifungal drugs comprising: (a) contacting a test substance which see expression of varies as in M1, where a test substance which modifies the expression of varies as in M1, where a test substance which modifies the expression of the yeast gene whose expression varies as in M1, dentifying human genes which are involved in cell cycle progression contiguous nucleotides of a NORF gene whose expression varies as in M1, and (4) a method (M4) for identifying a candidate drug as a member of a class of drugs having a characteristic effect on gene expression in a continuous nucleotides of a NORF gene whose expression is affected by the class of drugs. The NORF genes may be used to candidate drug swhich affect the cell continuous mucleoring expression in the yeast cell will expressed genes may be used to identify candidate drugs which affect the cell cycle and for identification of antifungal drugs. ARF33268 to AAF33261 represent short in the exemplification of the present invention.

AAF33262 to AAF33267 represent linkers and PCR primers used in the exemplification of the present invention

The present invention describes an isolated DNA molecule comprising a coding sequence of a yeast gene selected from a group of 745 NORF (not previously assigned open reading frame, or nonannotated ORF) genes comprising a SAGE (serial analysis of gene expression) tag. Also comprising administering a NORF gene whose expression varies by at least 10% between any two phases of the cell cycle selected from log phase, S phase and G2/M; (2) a method (M2) for screening candidate antifungal aruge comprising; (a) contacting a test substance with a yeast cell; and (b) monitoring expression of a NORF gene whose expression of varies as in M1, where a test substance which modifies the expression of varies as in M2, where a test substance which modifies the expression of the vest gene is a candidate antifungal drug; (3) a method (M3) for identifying a probe which comprising contacting human DNA with a probe which comprises at least 10 contriguous nucleotides of a NORF gene whose expression in a comprising contacting indentifying a candidate drug as a member of a class of drugs having a characteristic effect on gene expression in a comprising contacting a yeast cell of at least 1 NORF gene whose expression in the yeast cell comprising contacting a yeast cell of a comprise as in M3; and (4) a method whose expression in the yeast cell of a test 1 NORF genes may be used to study, monitor and affect phases of the cell cycle. The methods may be used to identify candidate drugs which affect the cell cycle and for identification of antitungal drugs. As 13286 to AAF31262 to A

Sequence 10 BP; 4 A; 3 C; 3 G; 0 T; 0 U; 0 Other;

ö Yeast gene coding sequences comprising NORF genes with serial analysis of gene expression (SAGE) tags, useful for studying, monitoring and affecting phases of the cell cycle. Yeast, Saccharomyces cerevisiae, characterisation, cell cycle, NORF, nor previously assigned open reading frame, nonannotated ORF, SAGE, serial analysis of gene expression, antifungal, tag; identification, linker, PCR primer, ds. Gaps ., Score 8.4; DB 1; Length 10; Pred. No. 5.2e+02; 0; Mismatches 1; Indels Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:2309. Kinzler K; AAF35570 standard; DNA; 10 BP. 38.2%; 90.0%; 99US-00335032. Velculescu V, Vogelstein B, 14-JUN-2000; 2000WO-US016223 SNINGO NIND (OLYU) (first entry) 9; Conservative Saccharomyces cerevisiae. 728 GCCAGGAGAA 737 1 GCCAGGACAA 10 WPI; 2001-061874/07. Best_Local Similarity Matches 9; Conserv WO200077214-A2. 16-JUN-1999; 23-MAR-2001 21-DEC-2000. AAF35570; Query Match RESULT 680 AAF3557 ઠે schultz1-727.rng

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The present invention describes an isolated DNA molecule comprising a coding sequence of a yeast gene selected from a group of 745 NORF (not previously assigned open reading frame, or nonamotated ORF) genes comprising a SAGE (serial analysis of gene expression) tag. Also described are: (1) a method (M1) of using NORF genes whose expression varies by at last 10% between any two phases of the cell cycle selected from log phase, S phase and G2/M, (2) a method (M2) for screening candidate antifungal drugs comprising; (a) contacting a test substance with a yeast cell; and (b) monitoring expression of a NORF gene whose expression of the yeast gene is a candidate antifungal drug; (3) a method (M3) for identifying human genes which are involved in cell cycle progression of and (4) a method (M4) for identifying a candidate drug as a member of a class of drugs having a characteristic effect on gene expression in a yeast cell comprising contacting a yeast cell with a candidate drug and yeast cell comprising contacting a yeast cell with a candidate drug and contouring expression in the yeast cell of at least 1 NORF gene whose expression in the yeast cell of the cell with a candidate drug and contouring expression in the yeast cell of contouring expression in the yeast cell of contouring expression in the yeast cell of at least 1 NORF gene may be used to study, monitor and affect phases of the cell cycle, the differentially expression is affected by the class of frugs. The NORF genes may be used to study monitor and affect phases of the cell cycle the methods may be used to identify candidate drugs which affect the cell cycle and for identification of antifungal drugs. AAFA1064
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                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF; nor previously assigned open reading frame; nonannotated ORF; SAGE; serial analysis of gene expression; antifungal; tag; identification; linker; PCR primer; ds.
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                                                                           38.2%; Score 8.4; DB 1; Length 10; 90.0%; Pred. No. 5.2e+02; Live 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:8426.
BP; 5 A; 2 C; 2 G; 1 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kinzler K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example; Page 300; 419pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Vogelstein B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14-JUN-2000; 2000WO-US016223
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAF41687 standard; DNA; 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Saccharomyces cerevisiae
                                                                                                                                                                                                                                     735 GAAACAGAAC 744
                                                                                                                                                                                                                                                                                                                 1 GAAACTGAAC 10
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                                                                                                                Local Similarity
les 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200077214-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16-JUN-1999;
        Sequence 10
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                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 681
                                                                                                                             Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAF41687
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The present invention describes a method for genotyping a human matrix metalloproteinase 3 (MMP3) gene of an individual. MMP3 has vulnerary, compostatic and antiatrelosclerotic activity, and can be used in gene therapy. The method can be used: for improving the efficacy and therapy. The method can be used: for improving the efficacy and therapy. The method can be used: for improving the efficacy and creating diseases associated with MMP3 activity, e.g., wound healing, cancer and coronary atherosclerosis; to validate MMP3 as a candidate of associated with MMP3 activity, and in the design of cilinical trials of associated with MMP3 activity, and in the design of cilinical trials of candidate drugs for treating a specific condition or disease predicted to be associated with MMP3 activity. Polymorphic variants of a reference candidate drugs for treating a specific condition or disease predicted to be associated with MMP3 activity. Polymorphic variants of a reference sequence for MMP3, and in expressing MMP3 protein for use in screening for candidate drugs to treat diseases related to MMP3 activity. ABL01225 to ABL01246 and ABL01247 to ABL01290 represent allele-specific collisouncleotide (ASO) probes and primers used in the detection of preferred primers
                                                                                                                                                                       ö
represent SAGE tags used in the exemplification of the present invention. AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE method, in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human, matrix metalloproteinase 3; MMP3; chromosome 11q22.3; SNP; haplotype; polymorphism; polymorphis; single nucleotide polymorphism; probe; primer; detection; genotyping; vulnerary; cytostatic; cancer; antiatteriosclerotic; gene therapy; coronary atherosclerosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Genotyping human matrix metalloproteinase 3 gene of an individual for determining the haplotype of the individual, comprises determining the identity of a nucleotide pair at specific polymorphic sites for two copies of the gene.
                                                                                                                                                                    Gaps
                                                                                                                                                                       .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human MMP3 gene polymorphism detection primer SEQ ID NO:74.
                                                                                                                            Length 10;
                                                                                                                       Score 8.4; DB 1; Length 10
Pred. No. 5.2e+02;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Stephens JC;
                                                                                     Seguence 10 BP; 7 A; 2 C; 1 G; 0 T; 0 U; 0 Other,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Koshy B,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 17; Page 15; 83pp; English.
                                                                                                                                                                                                                                                                                                                                              ABL01295
ID ABL01295 standard; DNA; 10 BP.
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2000US-0218092P
                                                                                                                         Query Match 38.2%;
Best Local Similarity 90.0%;
Matches 9; Conservative (
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                                                                                                                                                                                                                  735 GAAACAGAAC 744
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             wound healing; ss.
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13-JUL-2000;
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Primer-extension oligonucleotide #11 to detect human SCYA1 polymorphisms.
Sequence 10 BP; 4 A; 2 C; 3 G; 1 T; 0 U; 0 Other;
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Best Local Similarity
Matches 9; Conserv
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                                                                                                                                                                                                                                                                                                                                                                      ABL42763;
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AAS14466
ID AAS1
XX
AC AAS1
XX
DT 23-A
XX
DE Prim
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                                                                                                                                                                                                                                                                                                                                                 The present invention describes a method for genotyping a human matrix metalloproteinase 3 (MMP3) gene of an individual. MMP3 has vulnerary, cytostatic and antiarteriosclerotic activity, and can be used in gene therapy. The method can be used: for improving the efficacy and craft steps in the discovery and development of drugs for treating diseases associated with MMP3 activity, e.g., wound healing, concurred and coronary atherosclerosis; to validate MMP3 as a candidate agent for treating a specific condition or disease predicted to be associated with MMP3 activity; and in the design of clinical trials of candidate drugs for treating a specific condition or disease predicted to be associated with MMP3 activity. Polymorphic variants of a reference condidate drugs for treating a specific condition or disease predicted to be associated with MMP3 activity. Polymorphic variants of a reference sequence for MMP3, and in expressing MMP3 protein for use in screening for candidate drugs to treat diseases related to MMP3 activity, ABL01225 to ABL01247 to ABL01290 represent allele-specific oligonucleotide (ASO) probes and primers used in the detection of polymorphisms in the human MMP3 gene. ABL01291 to ABL0134 represent to MMP3 gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genotyping human matrix metalloproteinase 3 gene of an individual for determining the haplotype of the individual, comprises determining the identity of a nucleotide pair at specific polymorphic sites for two
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human, matrix metalloproteinase 3; MMP3; chromosome 11q22.3; SNP;
haplotype; polymorphism; polymorphic; single nucleotide polymorphism;
probe; primer; detection; genotyping; vulnerary; cytostatic; cancer;
antiarteriosclerotic; gene therapy; coronary atherosclerosis;
wound healing; ss.
                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gene polymorphism detection primer SEQ ID NO:89.
                                                                                           Score 8.4; DB 1; Length 10;
Pred. No. 5.2e+02;
0; Mismatches 1; Indels
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                                               Sequence 10 BP; 6 A; 2 C; 2 G; 0 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                      ABL01310 standard; DNA; 10 BP.
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13-JUL-2000; 2000US-0218092P.
                                                                                                38.2%;
90.0%;
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                                                                         Query Match
Best Local Similarity 90.0
                                                                                                                                                                                              731 AGGAGAAACA 740
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  MMP3 gene
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ABLO1310
ABLO1310
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention describes a human maturation/activation dendritic cell (DC) expression gene group consisting of 100 genes which show the highest expression among the genes expresd in human maturation/ activation DC. Also described are: (1) a protein expressed by the above human maturation/activation DC expression gene; (2) an antibody against the protein, and (3) an antagonist against the expression of each gene belonging to the above gene group. The gene group is useful for the treatment and the diagnosis of various human diseases related to human
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                                                                 Gaps
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Pred. No. 5.2e+02;
0; Mismatches 1; Indels
   Length 10;
                                                              Indels
Score 8.4; DB 1; L. Pred. No. 5.2e+02; 0; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 10; Page 13; 41pp; Japanese.
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                                                                                                                                                                                                                                                                                                                                             ABL42763 standard; cDNA; 10 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22-MAY-2000; 2000JP-00150562.
   Query Match
Best Local Similarity 90.0%;
Matches 9; Conservative
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Similarity 90.0%;
9; Conservative (
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                                                                                                                             727 TGCCAGGAGA 736
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                                                                                                                                                                                        1 TGCCAGGAAA 10
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The invention relates to SAGE (serial analysis of gene expression) tags representing groups of genes which are differentially expressed in human chronic hepatitis C (CH) liver tissue or hepatitis C-induced human liver tissue. The SAGE tags of this invention consist of a sequence of 10 nucleotides located downstream of the 5'-CATG-3' sequence motif lying nearest to the polyA region of cDNAs derived from a variety of genes. These tags serve to uniquely identify each transcript and can thus be used to analyse the pattern of gene expression in particular cell types. The invention also relates to proteins encoded by the genes expressed in chronic hepatitis C invertissue or HCC, antibodies against these proteins, and inhibitors of the expression of groups of genes that are overexpressed in chronic hepatitis C lisue or HCC. Groups of genes differentially expressed treatment of these diseases. Such appearance of their expression or activity, and antibodies against the gene products may be used in the expression or activity, and antibodies against the gene products may be used in the expression or diseases. Such speep inhibitors of their expression or activity and antibodies against the gene products may be used in the expression or diseases. Such speep inhibitors of their expression or activity and antibodies against the gene products may be used in the expression or dispassed genes out of those genes which are overexpressed in
                                                                                                Human chronic hepatitis C tissue expression exasperating gene group comprises 100 high-ranking genes.
                     (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN
                                                                                                                                                                Claim 19; Page 16; 139pp; Japanese.
                                                             WPI; 2002-631294/68.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention relates to novel single nucleotide polymorphisms (SNPs) in the human small inducible cytokine A1-1-309 (SCYA1) gene located on chromosome 17, and methods for haplotyping and/or genethe SCYA3 gene. The methods of the invention make use of allele specific oligonucleotides (ASOs) as probes and primers and/or primer-extension oligonucleotides for detecting the SCYA1 gene polymorphisms. The polymochotides and screened compounds are useful for the treatment of diseases associated with SCYA1 activity, such as atherosclerosis, human immunodeficiency virus (HIV) infection, and other inflammatory disorders. AAS14455-AAS14473 represent primer-extension oligonucleotides for detecting human SCYA1 gene polymorphisms
                 Human, single nucleotide polymorphism, SNP, SCYA1; chromosome 17;
small inducible cytokine A1-I-309; haplotyping; genotyping; gene;
atherosclerosis; human immunodeficiency virus; HIV infection; primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                 Genotyping human small inducible cytokine Al-I-309, homologous to mous
Tca-3 gene of individual, involves determining identity of nucleotide
pair at specific polymorphic sites for two copies of the gene.
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                                                                                                                                                                                                                                                                                                             (GENA-) GENAISSANCE PHARM INC
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Matches 9; Conservative
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                                                                                                                                          WO200179236-A2
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                                                      Match 38.2%; Score 8.4; DB 1; Length 10; Local Similarity 90.0%; Pred. No. 5.2e+02; es 9; Conservative 0; Mismatches 1; Indels
hepatocellular carcinoma compared with normal liver tissue
                            Sequence 10 BP; 5 A; 2 C; 2 G; 1 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN
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                                                                                                                    735 GAAACAGAAC 744
                                                                                                                                               1 GAAACTGAAC 10
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                                                                                                                                                                                                                                                       ABV84609;
                                                          Query Match
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The invention relates to SAGE (serial analysis of gene expression) tags representing groups of genes which are differentially expressed in human chronic hepatitis C (CH) liver tissue or hepatitis C cinduced hepatocellular carcinoma (HCC) compared with normal human liver tissue.

The SAGE tags of this invention consist of a sequence of 10 nucleotides looky region of the S'-CATG-3' sequence motif lying nearest to the polyh region of consa erived from a variety of genes. These tags serve to uniquely identify each transcript and can thus be used to analyse the pattern of gene expression in particular cell types. The invention also relates to proteins encoded by the genes expressed in chronic hepatitis C incromic hepatitis C incromic of these or HCC, antibodies against these proteins, and inhibitors of the expression of genes that are overexpressed in chronic hepatitis C liver tissue or HCC (groups of genes differentially expressed in chronic hepatitis C issue or HCC (groups of genes differentially expression of these diseases. Such genes, inhibitors of their expression or activity, and antibodies against the gene products may be used in the expression of analyse to treat chronic hepatitis C and/or HCC. Sequences and antibodies against the gene products may be used in the expression of analyse to treat chronic hepatitis C and/or HCC. Sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SAGE tag; serial analysis of gene expression; human; chronic hepatitis C; CH; liver tissue; hepatocellular carcinoma; cancer; tumour; HCC; expression pattern; differential expression; EST; expressed sequence tag;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     expressed genes out of those genes which are overexpressed in hepatcocallular carcinoma compared with chronic hepatitis C liver tissue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human chronic hepatitis C tissue expression exasperating gene group comprises 100 high-ranking genes.
                                                                                                                                                                                                                                                                                                                                                                                                                               ABV84591-ABV84690 are SAGE tags representing the 100 most highly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 8.4; DB 1; Length 10;
Pred. No. 5.2e+02;
0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 10 BP; 5 A; 2 C; 2 G; 1 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 10; Page 14; 139pp; Japanese.
Claim 37; Page 22; 139pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABV84344 standard; cDNA; 10 BP.
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90.0%;
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Matches 9; Conserv
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located downstream of the 5'-CATG-3' sequence motif lying nearest to the polyA region of cDNAs derived from a variety of genes. These tags serve to uniquely identify each transcript and can thus be used to analyse the pattern of gene expression in particular cell types. The invention also relates to proteins encoded by the genes expressed in chronic hepatitis C liver tissue or HCC, antibodies against these proteins, and inhibitors of the expression of genes that are overexpressed in chronic hepatitis C liver tissue or HCC groups of genes differentially expressed in chronic hepatitis C tissue or HCC may be used for the diagnosis and treatment of these diseases. Such genes, inhibitors of their expression or activity, and antibodies against the gene products may be used in the development of drugs to treat chronic hepatitis C and/or HCC. Sequences ABV84291-ABV84390 are SAGE tags representing the 100 least highly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to an isolated androgen-regulated gene (ARG) designated as PMEPA1. The invention is useful for selecting primers and probes for detecting prostate cancer cells in a biological sample by using nucleic acid amplification techniques. The present sequence is human ARG energy metabolism, apoptosis and redox regulator oligonuclectide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               useful for
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e cancer cells in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; androgen-regulated gene; ARG; PMBPAl; prostate cancer; ss.
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                                                                                                                                                                                                                                                                                                                                                              Score 8.4; DB 1; Length 10; Pred. No. 5.2e+02; 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                 expressed genes out of those genes which are underexpresse
hepatitis C liver tissue compared with normal liver tissue
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31-JAN-2000; 2000US-0179045P.
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Best Local Similarity 90.0
Matches 9; Conservative
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Score 8.4; DB 1; Length 10; Pred. No. 5.2e+02;

38.2%; 90.0%;

Best Local Similarity

Query Match

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Hofmann K;
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                                                                                                                                                                                WPI; 2002-528865/56
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                                                                                                                                                                                                                                                                                                                                                                   Identifying genes involved in skin stress and aging, useful e.g. in screening for cosmetic or therapeutic agents, based on differential gene
   Gaps
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  Indels
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  Mismatches
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                                                                                          ABQ86777 standard; cDNA; 11 BP.
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ABQ86292 standard; cDNA; 11
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9; Conservative
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                     731 AGGAGAACA 740
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The invention relates to identifying (M1) genes in vitro that, in humans or animals, are important for skin ageing and/or skin stress by serial analysis of gene expression between mixtures of transcribed and optionally translated, genetically encoded factors (A) obtained from young and aged skin, to identify that genes that show strong differential expression. (A) comprises protein or mRNAMs or their fragments. (M1) is useful for: identifying markers of skin ageing and/or stress; determining skin ageing and/or stress; and identifying or determining the effects of pharmaceutical or cosmetic agents for control of skin ageing. The present sequence is one of a group of human skin ageing/stress related expressed sequence tags (ABQ86246-ABQ87680) of the invention
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Human; skin ageing; skin stress; EST; expressed sequence
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                                                                                                                                                        The invention relates to identifying (MI) genes in vitro that, in humans or animals, are important for skin ageing and/or skin stress by serial analysis of gene expression between mixtures of transcribed and optionally translated, genetically encoded factors (A) obtained from young and aged skin, to identify that genes that show strong differential useful for: identifying maxkers of skin ageing and/or stress; determining skin ageing and/or stress; and identifying or determining the effects of pharmacoustical panels for connectic agents for control of skin ageing. The present sequence is one of a group of human skin ageing/stress related expressed sequence tags (ABQ86246-ABQ87680) of the invention
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                                                       Identifying genes involved in skin stress and aging, useful e.g. in
screening for cosmetic or therapeutic agents, based on differential gene
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Pred. No. 5.4e+02;
0; Mismatches 1; Indels
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                                                                                                                             German.
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                                                                                                                             8; Page 62; 325pp;
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Best Local Similarity
Matches 9; Conserv
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skin ageing and/or stress; and identifying or determining the effects of pharmaceutical or cosmetic agents for control of skin ageing. The present sequence is one of a group of human skin ageing/stress related expressed sequence tags (ABQ86246-ABQ87680) of the invention
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90.0%;
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Local Similarity 90.0%;
les 9; Conservative (
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Matches 9; Conservative
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ABV68185;

RESULT 695

ABV68185,

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The invention relates to in vitro identification (M1) of genes expressed in the skin of humans or animals by subjecting a mixture of genetically encoded factors from skin, to serial analytsis of gene expression (SAGE) so as to identify skin-expressed genes and quantify their expression.

(M1) is useful for identifying genes involved in skin homeostasis; to promotes skin homeostasis and to test agent (A) that maintains or promotes skin homeostasis or that can be used for treating skin disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma; ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus; rosacea; melanoma; basal cell cardinoma; and cardinoma or sarcoma of the skin. The present sequence is that of a human expressed sequence tag
                                                                                                                                                                                                                                                                                                                                                                              In vitro identification of skin-expressed genes, useful for determining homeostasis and identifying cosmetic or pharmaceutical agents against
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                                                                                                                                                                                                                                                                                             Hofmann K;
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ID ABV71340 standard; cDNA; 11
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Best Local Similarity 90.0-
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                          Homo sapiens.
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                                                                                                                                                                                                              Human, skin, dermatological, vulnerary, antipsoriatic, antiseborrhaeic, immunosuppressive, antiinflammatory, cytostatic, SAGB, neurodermattiis, psoriasis, dermatitis, skin cancer, EST, expressed sequence tag, ss.
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38.2%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 5.4e+02;
Matches 9; Conservative 0; Mismatches 1; Indels
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                                      ABV68185 standard; cDNA; 11 BP.
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Score 8.4; DB 1; Length 11; Pred. No. 5.4e+02; 0; Mismatches 1; Indels

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In vitro identification of skin-expressed genes, useful for determining homeostasis and identifying cosmetic or pharmaceutical agents against
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         WPI; 2002-590638/63
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Best Local Similarity
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                            e.g. skin cancer.
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disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
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immunosuppressive, antiinflammatory, cytostatic, SAGE, neurodermatitis,
psoriasis, dermatitis, skin cancer, EST; expressed sequence tag; ss.
so as to identify skin-expressed genes and quantify their expression. (M1) is useful for identifying genes involved in skin homeostasis; to determine skin homeostasis and to test agent (A) that maintains or promotes skin homeostasis or that can be used for treating skin
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Matches 9; Conservative
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                                                                                         In vitro identification of skin-expressed genes, useful for determining homeostasis and identifying cosmetic or pharmaceutical agents against
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                Conradt M,
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The invention relates to in vitro identification (M1) of genes expressed in the skin of humans or animals by subjecting a mixture of genetically so encoded factors from skin, to serial analysis of gene expression (SAGE) so as to identify skin-expressed genes and quantify their expression.

(M1) is useful for identifying genes involved in skin homeostasis; to determine skin homeostasis and to test agent (A) that maintains or promotes skin homeostasis or that can be used for treating skin disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma; ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus; sosacea; metalona, basal cell carcinoma; and carcinoma or sarcoma of the skin. The present sequence is that of a human expressed sequence tag (ESI) of the invention
In vitro identification of skin-expressed genes, useful for determining homeostasis and identifying cosmetic or pharmaceutical agents against e.g. skin cancer.
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38.28;

Query Match

The invention relates to in vitro identification (M1) of genes expressed in the skin of humans or animals by subjecting a mixture of genetically encoded factors from skin, to serial analysis of gene expression (SAGE)

Hofmann K;

Conradt M,

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Human, skin, dermatological, vulnerary, antipsoriatic, antiseborrhaeic, immunosuppressive, antiinflammatory; cytostatic, SAGE, neurodermatitis, psoriasis, dermatitis, skin cancer, EST, expressed sequence tag, ss.

21-OCT-2002 (first entry)

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The invention relates to in vitro identification (M1) of genes expressed in the skin of humans or animals by subjecting a mixture of genetically scooled factors from skin, to serial analysis of gene expression (SAGE) so as to identify skin-expressed genes and quantify their expression.

(M1) is useful for identifying genes involved in skin homeostasis, to promotes skin homeostasis and to test agent (A) that maintains or promotes skin homeostasis or that can be used for treating skin disorders, specifically neurodermatitis; sunburn; psoriaeis, scleroderma; ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus; rosacea, melanoma; basal cell carcinoma; and carcinoma or sarcoma of the skin. The present sequence is that of a human expressed sequence tag (EST) of the invention
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(M1) is useful for identifying genes involved in skin homeostasis; to determine skin homeostasis and to test agent (A) that maintains or promotes skin homeostasis or that can be used for treating skin disorders, specifically neurodermatitis; sunburn; psoriaeis, scleroderma; ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus; rosacea, melanoma; basal cell carcinoma; and carcinoma or sarcoma of the skin. The present sequence is that of a human expressed sequence tag
                                                                                                                                                                                                                                                                                     Human, skin, dermatological, vulnerary, antipsoriatic, antiseborrhaeic,
immunosuppressive, antiinflammatory, cytostatic, SAGE, neurodermatitis,
psoriasis, dermatitis, skin cancer, EST, expressed sequence tag; ss.
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Pred. No. 5.4e+02;
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90.08;
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Best Local Similarity
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ABV67021/c
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In vitro identification of skin-expressed genes, useful for determining homeostasis and identifying cosmetic or pharmaceutical agents against

Disclosure; Page 44; 1345pp; German.

e.g. skin cancer.

M, Hofmann K;

Petersohn D, Conradt (HENK) HENKEL KGAA

WPI; 2002-590638/63.

20-DEC-2001; 2001WO-EP015179. 03-JAN-2001; 2001DE-01000127.

WO200253774-A2.

11-JUL-2002,

Homo sapiens

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                         38.2%; Score 8.4; DB 1; Length 11; 90.0%; Pred. No. 5.4e+02; tive 0; Mismatches 1; Indels
Sequence 11 BP; 5 A; 3 C; 3 G; 0 T; 0 U; 0 Other;
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Matches
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ABV62887 standard; cDNA; 11

RESULT 701
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ABV62887;

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The invention relates to in vitro identification (M1) of genes expressed in the skin of humans or animals by subjecting a mixture of genetically encoded factors from skin, to serial analysis of gene expression (SAGE) so as to identify skin-expressed genes and quantify their expression.

(M1) is useful for identifying genes involved in skin homeostasis, to determine skin homeostasis and to test agent (A) that maintains or promotes skin homeostasis or that can be used for treating skin disorders, specifically neurodermatitis; sunburn; psoriasis, scleroderma; ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus; cosceas, melanoms; basal cell carcinoma, and carcinoma of the
                                                                                                                                                                                  In vitro identification of skin-expressed genes, useful for determining homeostasis and identifying cosmetic or pharmaceutical agents against
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                                                                                                                        Conradt M, Hofmann K;
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The invention relates to in vitro identification (M1) of genes expressed in the skin of humans or animals by subjecting a mixture of genetically encoded factors from skin, to serial analysis of gene expression (SAGE) so as to identify skin-expressed genes and quantify their expression. (M1) is useful for identifying genes involved in skin homeostasis, to promotes skin homeostasis and to test agent (A) that maintains or promotes skin homeostasis or that can be used for treating skin disorders, specifically neurodermatitis; subburn; psoriasis; scleroderma;
                                                                                  The invention relates to in vitro identification (M1) of genes expressed in the skin of humans or animals by subjecting a mixture of genetically schooled from skin, to serial analysis of gene expression (SAGE) so as to identify skin-expressed genes and quantify their expression.

(M1) is useful for identifying genes involved in skin homeostasis; to promotes skin homeostasis and to test agent (A) that maintains or promotes skin homeostasis or that can be used for treating skin disorders, specifically neurodermatitis, sunburn, psoriasis; soleroderma; inchthyosis, atophy dermatitis, acne, sebornhea; lupus ertythematosus; rosacea; melanoma; basal cell carcinoma, and carcinoma or sarcoma of the skin. The present sequence is that of a human expressed sequence tag
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homeostasis and identifying cosmetic or pharmaceutical agents against
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                                                        Disclosure; Page 146; 1345pp; German.
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The invention relates to in vitro identification (M1) of genes expressed in the skin of humans or animals by subjecting a mixture of genetically so actioned from skin, to serial analysis of gene expression (SAGE) so as to identify skin-expressed genes and quantify their expression. (M1) is useful for identifying genes involved in skin homeostasis, to promotes skin homeostasis and to test agent (A) that maintains or promotes skin homeostasis or that can be used for treating skin disorders, specifically neurodermatitis; sunburn, psoriasis, scleroderma; ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus; rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the skin. The present sequence is that of a human expressed sequence tag (EST) of the invention
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(MI) is useful for identifying genes involved in skin homeostasis; to determine skin homeostasis and to test agent (A) that maintains or promotes skin homeostasis or that can be used for treating skin disorders, specifically neurodermatitis; sunburn, psoriaais, scleroderma; ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus; rosacea, melanoma; basal cell carcinoma; and carcinoma or sarcoma of the skin. The present sequence is that of a human expressed sequence tag
ichthyosis; atopic dermatitis; acne; sebornhea; lupus erythematosus; rosacca; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the Skin. The present sequence is that of a human expressed sequence tag (EST) of the invention
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38.2%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 5.46+02;
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Hofmann K;

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                          Query Match 38.2%; Score 8.4; DB 1; Length 11; Best Local Similarity 90.0%; Pred. No. 5.4e+02; Matches 9; Conservative 0; Mismatches 1; Indels
Sequence 11 BP; 4 A; 1 C; 6 G; 0 T; 0 U; 0 Other;
                                                                                                                                                                                              BP.
                                                                                                                                                                                            ABV71647 standard; cDNA; 11
                                                                                      732 GGAGAAACAG 741
                                                                                                                    1 GGAGAGACAG 10
                                                                                                                                                                                                                                                                                 Human skin EST 9433
                                                                                                                                                                                                                                                      21-OCT-2002
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0; Gaps

736 AAACAGAACA 745

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The invention relates to in vitro identification (M1) of genes expressed in the skin of humans or animals by subjecting a mixture of genetically encoded factors from skin, to serial analysis of gene expression (SAGE) so as to identify skin-expressed genes and quantify their expression. (M1) is useful for identifying genes involved in skin homeostasis; to promotes skin homeostasis and to test agent (A) that maintains or promotes skin homeostasis or that can be used for treating skin disorders, specifically neurodermatitis; sunburn, psoriasis, scleroderma; ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus; rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the skin. The present sequence is that of a human expressed sequence tag
                                                                                                                                                                                                                                                                                                                              In vitro identification of skin-expressed genes, useful for determining homeostasis and identifying cosmetic or pharmaceutical agents against
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Human, skin, dermatological, vulnerary, antipsoriatic, antiseborrhaeic,
immunosuppressive, antiinflammatory, cytostatic, SAGE, neurodermatitis,
psoriasis, dermatitis, skin cancer, EST, expressed sequence tag, ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 11 BP; 9 A; 2 C; 0 G; 0 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                 Hofmann K;
                                                                                                                                                                                                                                                                                                                                                                                                Claim 24; Page 304; 1345pp; German.
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Matches 9, Conservative
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                                                                                                                                                                                                                                                                 Petersohn D, Conradt
                                                                                                                                                                                                                                 (HENK ) HENKEL KGAA
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                                                                                                                                                                                                                                                                                                                                                                  e.g. skin cancer.
                                                                                                    WO200253774-A2.
                                                                     Homo sapiens
                                                                                                                                   11-JUL-2002
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The invention relates to in vitro identification (M1) of genes expressed in the skin of humans or animals by subjecting a mixture of genetically encoded factors from skin, to serial analysis of gene expression (SAGE) so as to identify skin-expressed genes and quantify their expression. (M1) is useful for identifying genes involved in skin homeostasis; to promotes skin homeostasis and to test agent (A) that maintains or promotes skin homeostasis or that can be used for treating skin disorders, specifically neurodermatitis; sumburn, psoriasis, scleroderma; ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus; soacea, melahoma, basal cell carcinoma, and carcinoma or sarcoma of the skin. The present sequence is that of a human expressed sequence tag (EST) of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         In vitro identification of skin-expressed genes, useful for determining homeostasis and identifying cosmetic or pharmaceutical agents against
                                                                                                           In vitro identification of skin-expressed genes, useful for determining homeostasis and identifying cosmetic or pharmaceutical agents against
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human, skin, dermatological, vulnerary, antipsoriatic, antiseborrhaeic, immunosuppressive, antiinflammatory, cytostatic, SAGE, neurodermatitis, psoriasis, dermatitis, skin cancer, EST, expressed sequence tag, ss.
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Pred. No. 5.4e+02;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 11 BP; 0 A; 2 C; 1 G; 8 T; 0 U; 0 Other;
                                                                                                                                                                            Disclosure; Page 198; 1345pp; German.
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                                            Hofmann K;
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Best Local Similarity 90.0%;
Matches 9; Conservative (
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                                            Conradt M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      734 AGAAACAGAA 743
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11 AAAAACAGAA 2
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                                                                             WPI; 2002-590638/63.
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            (HENK ) HENKEL KGAA
                                                                                                                                             e.g. skin cancer.
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                                              Petersohn D,
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Disclosure; Page 143; 1345pp; German

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Sequence 11 BP; 4 A; 2 C; 4 G; 1 T; 0 U; 0 Other;

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The invention relates to in vitro identification (M1) of genes expressed in the skin of humans or animals by subjecting a mixture of genetically encoded factors from skin, to serial analysis of gene expression (SAGE) so as to identify skin-expressed genes and quantify their expression. (M1) is useful for identifying genes involved in skin homeostasis; to determine skin homeostasis and to test agent (A) that maintains or promotes skin homeostasis or that can be used for treating skin disorders, specifically neurodermatitis; sumburn; psoriasis; scleroderma; ichthyosis; atopic dermatitis; acne; sebornhea; lupus erythematosus; rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the skin. The present sequence is that of a human expressed sequence tag (EST) of the invention 88888888888888

Sequence 11 BP; 4 A; 3 C; 4 G; 0 T; 0 U; 0 Other;

Gaps . 0 Score 8.4; DB 1; Length 11; Pred. No. 5.4e+02; 0; Mismatches 1; Indels . 38.2%; 90.0%; Conservative Query Match Best Local Similarity '.hea 9; Conserve

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729 CCAGGAGAAA 738

CCAGGGGAAA 11 0

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RESULT 710 **ABV69554**

ABV69554 standard; cDNA; 11

BP

ABV69554;

(first entry) 21-OCT-2002

Human skin EST 7340

Human, skin, dermatological, vulnerary, antipsoriatic, antiseborrhaeic, immunosuppressive, antiinflammatory; cytostatic, SAGE, neurodermatitis, psoriasis, dermatitis, skin cancer, EST; expressed sequence tag, ss.

Homo sapiens

WO200253774-A2.

11-JUL-2002.

20-DEC-2001; 2001WO-EP015179

e.g. skin cancer.

03-JAN-2001; 2001DE-01000127

(HENK) HENKEL KGAA

Hofmann K; Σ Petersohn D, Conradt

WPI; 2002-590638/63.

In vitro identification of skin-expressed genes, useful for determining homeostasis and identifying cosmetic or pharmaceutical agents against e.g. skin cancer.

Disclosure; Page 230; 1345pp; German

The invention relates to in vitro identification (M1) of genes expressed in the skin of humans or animals by subjecting a mixture of genetically encoded factors from skin, to serial analysis of gene expression (SAGE) so as to identify skin-expressed genes and quantify their expression.

(M1) is useful for identifying genes involved in skin homeostasis; to becemine skin homeostasis and to test agent (A) that maintains or promotes skin homeostasis or that can be used for treating skin discorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma; ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus; roaceae, melanoma; basal cell carcinoma; and carcinoma or sarcoma of the skin. The present sequence is that of a human expressed sequence tag

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Length 11;
Score 8.4; DB 1; Length 11 Pred. No. 5.4e+02; 0; Mismatches 1; Indels
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38.2%;
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Query Match
Best Local Similarity 90.0
Matches 9; Conservative
                                    729 CCAGGAGAAA 738
                                                       1 CCAGGAGGAA 10
                                                                                                                                                                                                                                                                                                                                    Petersohn D, Conradt
                                                                                                                                                             Human skin EST 8094
                                                                                                                                                                                                                                                                                                                (HENK ) HENKEL KGAA
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ö The invention relates to in vitro identification (M1) of genes expressed in the skin of humans or animals by subjecting a mixture of genetically encoded factors from skin, to serial analysis of gene expression (SAGE) so as to identify skin-expressed genes and quantify their expression.

(M1) is useful for identifying genes involved in skin homeostasis, to promotes skin homeostasis and to test agent (A) that maintains or promotes skin homeostasis or that can be used for treating skin disorders, specifically neurodermatitis; sunburn, psoriasis, scleroderma; ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus; rosacea, melanoma; basal cell carcinoma, and carcinoma or sarcoma of the skin. The present sequence is that of a human expressed sequence tag Gaps ; 0 Length 11; 1; Indels Sequence 11 BP; 5 A; 3 C; 3 G; 0 T; 0 U; 0 Other; Score 8.4; DB 1; Pred. No. 5.4e+02; 0; Mismatches 1; Claim 24; Page 258; 1345pp; German. 38.2%; 90.0%; Query Match
Best Local Similarity 90.0
Best Local Similarity 90.0 ਨੇ

737 AACAGAACAC 746 2 AACAGAACGC

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RESULT 712 AAV39563

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ВЪ

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A process has been developed for determining the sequence of a target nucleic acid. The process comprises: (i) generating at least two fragments (F) from the target nucleic acid, and (ii) nallysing F by mass spectrometry (MS). The sequences in AAV3483 to AAV3592 are specifically claimed primers for use in the mass spectrometric analysis of the above process. The process is used to detect genetic diseases (e.g. haemophilia, thalassemia, Duchenne muscular dystrophy, Alzheimer's disease, cystic fibrosis and many others) or chromosomal abnormalities (or predisposition); infections and cancers; also for establishing identity and heredity. Particular applications are diagnosis of neuroblastoma, detecting telomerase, determining family relationships and HiA compatibility, and in genetic fingerprinting. Compared with known methods using MS, this process requires fewer specific reagents and is better suited to automation. Extended primers are shorter; primer annealing is more efficient and the process allows detection of many
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequencing nucleic acid by mass spectrometric analysis - for detecting nucleic acids, telomerase activity, oncogene mutations, or cancer-specific sequences, for diagnosis of disease.
                                                                                                                               Mass spectrometry; diagnosis; detection; biological sample; infection; genetic disease; chromosomal abnormality; identification; heredity; pathogenic organism; telomerase activity; oncogene mutation; cancer-specific sequence; primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tang K, Fu D, Siegert CW, Little DP, Higgins GS; Damhoffer-Demar B, Jurinke C, Van Den Boom D, Xiang G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 12 BP; 5 A; 3 C; 4 G; 0 T; 0 U; 0 Other;
                                                                                               Mass spectrometric analysis primer SEQ ID NO:86.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 48; Page 266; 478pp; English
                                                                                                                                                                                                                                                                                                                                                     96US-00744481.
96US-00744590.
96US-00746036.
97US-00786988.
97US-0078739.
97US-0093792.
                                                                                                                                                                                                                                                                                                                       97WO-US020444
AAV39563 standard; cDNA; 12
                                                                (first entry)
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Best Local Similarity 90..
Best Local 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (SEQU-) SEQUENOM INC
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23-JAN-1997;
19-SEP-1997;
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                                                                                                                                                                                                                     Synthetic.
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Lough DM;
                              AAV39563
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nucleic acid. The process comprises: (i) generating at least two regaments (F) from the target nucleic acid, analysing F by mass regurences (MS). The sequences in AAV39483 to AAV39592 are specifically claimed primers for use in the mass spectrometric analysis of the above process. The process is used to detect genetic diseases (e.g. process. The process is used to detect genetic diseases (e.g. haemophila, thalassemia, Duchenne muscular dystrophy, Alzheimer's disease, cystic fibrosis and many others) or chromosomal abnormalities (or predisposition); infections and cancers, also for establishing cidentity and heredity. Particular applications are disgnosis of neuroblastoma, detecting telomerase, determining family relationships and HA compatibility, and in genetic fingerprinting. Compared with known methods using MS, this process requires fewer specific reagants and is better suited to automation. Extended primers are shorter; primer anneance of many constants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequencing nucleic acid by mass spectrometric analysis - for detecting nucleic acids, telomerase activity, oncogene mutations, or cancer-specific sequences, for diagnosis of disease.
                                                                                                                                                 Mass spectrometry; diagnosis; detection; biological sample; infection; genetic disease; chromosomal abnormality; identification; heredity; pathogenic organism; telomerase activity; oncogene mutation; cancer-specific sequence; primer; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Little DP, Higgins GS;
, Van Den Boom D, Xiang G;
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                                                                                                                     Mass spectrometric analysis primer SEQ ID NO:81,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Koster H, Tang K, Fu D, Siegert CW, L
Braun A, Damhoffer-Demar B, Jurinke C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 48; Page 264; 478pp; English.
                  BP
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960S-00746036.
960S-00746055.
970S-00786988.
970S-00787639.
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                AAV39558 standard; cDNA; 12
                                                                                      28-SEP-1998 (first entry)
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06-NOV-1996;
06-NOV-1996;
06-NOV-1996;
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19-SEP-1997;
08-OCT-1997;
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                                                                                                                                                                                                                                             Synthetic.
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Lough DM;
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728 GCCAGGAGAA 737

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38.2%; Score 8.4; DB 1; Length 12; 90.0%; Pred. No. 5.6e+02; tive 0; Mismatches 1; Indels

737

728 GCCAGGAGAA

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GCCAGGACAA 11

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RESULT 713

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GCCAGGACAA

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The present invention describes polymer compositions comprising a plurality of covalently bound polymer segments. The segments comprise:

(a) at least one polycation segments. The segments comprise:

contonic polymer segment. The polycation segment is a cationic homo- or copolymer comprising at least three cationic amino acids or at least three cationic amino acids or at least three cationic amino acids or at least this; and (ii) at least one secondary amino monomer of formula (II), or an acid addition or quaternary salt of this. The compositions may be used for delivery of nucleic acids to cells. They may be used for delivery of nucleic acids to cells. They may be used for delivery of nucleic acids to cells. They may be used for the campositions is e.g. oral, topical, rectal, vaginal parenteral or by inhalation. The present invention

can example from the present invention
                                                                                                                                                                                                                                                                                                                                                                                                               New polymer compositions which include e.g. polycation segments.
genetic disease; neoplastic disease; cardiovascular disease; infectious disease; transplantation related disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    38.2%; Score 8.4; DB 1; Length 12; 90.0%; Pred. No. 5.6e+02; ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Seguence 12 BP; 0 A; 4 C; 3 G; 4 T; 1 U; 0 Other;
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98US-00124943.
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Best Local Similarity 90.0.
Best Social Similarity 90.0.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
                                                                                                                                                                                                                            01-AUG-1997;
                                                                                                                                                                                   31-JUL-1998;
                                                                                                                                                                                                                                                  30-JUL-1998;
                                                                                                    WO9906055-A1
                                                                                                                                                                                                                                                                                                                                   Kabanov AV,
                                                                                                                                              11-FEB-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAA87791;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 716
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAA87791
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention describes polymer compositions comprising a plurality of covalently bound polymer segments. The segments comprise:

(a) at least one polycation segment. The segments comprise:

conionic polymer segment. The polycation segment is a cationic homo- or copolymer comprising at least three cationic amino acids or at least three eationally lene monomers. The monomers are selected from: (i) at least one tertiary amino monomer of formula (I), or a quaternary salt of this; and (ii) at least one secondary amino monomer of formula (II), or an acid addition or quaternary salt of this. The compositions may be used for delivery of nucleic acids to cells. They may be used for treatment of genetic diseases, neoplastic diseases, cardiovascular diseases, infectious diseases or transplantation related disorders. Administration infectious diseases or transplantation related disorders. Administration by inhalation. The present sequence represents an oligonuclectide used in example from the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                      Cell membrane transfer; polynucleotide; polymer; polycation segment; genetic disease; neoplastic disease; cardiovascular disease; infectious disease; transplantation related disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cell membrane transfer; polynucleotide; polymer; polycation segment;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New polymer compositions which include e.g. polycation segments
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      38.2%; Score 8.4; DB 1; Length 12; llarity 90.0%; Pred. No. 5.6e+02; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 12 BP; 0 A; 5 C; 2 G; 4 T; 1 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kabanov AV, Alakov VY, Vinogradov SV;
                                                                                                                                                                   Antisense 12-chain oligonucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 9; Page 56; 94pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   669/c
AAX19669 standard; DNA; 12 BP.
                                           AAX19666 standard; DNA; 12 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                         97US-00912968.
98US-00124943.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (SUPR-) SUPRATEK PHARMA INC.
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                                                                                                                          (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12-mer oligonucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11 CAGGAGGAAC 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1999-204365/17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                   WO9906055-A1
                                                                                                                          03-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                    31-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-AUG-1997;
30-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     03-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                            11-FEB-1999.
                                                                                                                                                                                                                                                                                            Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAX19669;
                                                                                AAX19666;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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AAX19669/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Loc
Matches
    RESULT 71.
AAX19666/0
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ö Human; secreted protein; forensic procedure; gene therapy; chromosome mapping; canneer; autolimune disease; cardiovascular disorder; cystic fibrosis; hypothyroidism; immunological disorder; amyloidosis; brain disorder; skaletal muscle disorder; eye disorder; obesity; mitochondriocyropathy; diabetes; atheroseclerosis; Alzheimer's disease; neurodegenerative disorder; graft rejection; dementia; hyperlipidaemia; septic shock; impotence; promoter; Pl3H2; ds. Gaps ö Promoter P13H2 transcription factor binding site SEQ ID #145.

AXAXEXEXE X

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in the human Plant promoter. The invention relates to sequences AAAB7725-
AB7774 which encode human secreted proteins AAB5763-B25812. The proteins include signal peptides. The Plant promoter is used in the isolation of the cDNAs of the invention. Included in the invention are a host cell containing one of the cDNA sequences, and a purified antibody capable of binding to one of the secreted proteins. Also contained in the invention are methods for storing the sequence data on a computer system, and a method for identifying features of the CDNA sequences using a computer programme. The cDNAs are useful for expressing secreted proteins or ragments to obtain antibodies capable of specifically binding to the secreted proteins. The cDNAs may also be useful in diagnostic, forensic, gene therapy and chromosome mapping procedures and may be used to design expression vectors and secretion vectors. The proteins of the invention may be used to treat diseases including cancer, autoimmune diseases, cardiovascular disorders, operations immunological disorders, amyloidosis, brain disorders, appetutoring, immunological disorders, observed the invention in the contains of the invention disorders, amyloidosis, brain disorders, sheletal muscle disorders, eye disorders, observed the contains of the invention of the invention of the contains of the contains of the contains of disorders, eye disorders, amyloidosis, brain disorders, sheletal muscle disorders, eye disorders, observed the contains of contai
                                                                                                                                                                                                                                                                                                                                                                                                                                     Polynucleotides and polypeptides encoding proteins with signal peptides, useful in diagnostic, forensic, gene therapy and chromosome mapping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This sequence represents a transcription factor binding site identified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Alzheimer's disease,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                neurodegenerative disorders, graft rejection, Alzheim
dementia, hyperlipidaemia, septic shock and impotence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 12 BP; 9 A; 2 C; 0 G; 1 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                     Duclert A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 48; Fig 5; 306pp; English.
                                                                   99WO-IB002058.
                                                                                                                                      98US-0113686P
                                                                                                                                                                  99US-0141032P
                                                                                                                                                                                                                                                                                                     Dumas J,
                                                                                                                                                                                                                                                                                                                                                                     WPI; 2000-442637/38.
                                                                                                                                                                                                                                                                                                     Bougueleret L,
                                                                                                                                                                                                                                      (GEST ) GENSET
                                                                   20-DEC-1999;
                                                                                                                                      22-DEC-1998;
                                                                                                                                                                  25-JUN-1999;
29-JUN-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        procedures.
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Gaps ö 38.2%; Score 8.4; DB 1; Length 12; 90.0%; Pred. No. 5.6e+02; tive 0; Mismatches 1; Indels Query Match
Best Local Similarity 90.0
Matches 9; Conservative

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736 AAACAGAACA 745 3 AAACAAAACA 12 ò

AAA06954 standard; RNA; 12 BP. 03-JUL-2000 (first entry) AAA06954; RESULT 717

Human XIAP IRES mutant polypyrimidine tract, SEQ ID NO:18.

X-linked inhibitor of apoptosis protein; XIAP; IRES; internal ribosome entry site; human; cap-independent translation; drug screening; cancer; autoimmune disease; degenerative disease; immunorejection; gene therapy; mutant; polypyrimidine tract; ss.

sapiens Synthetic Ношо

WO200005366-A2

03-FEB-2000

Human herpesvirus 1.

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The invention relates to the identification of modulators of captidependent translation and apoptosis. The method comprises exposing a test compound to an X-linked inhibitor of apoptosis protein (XIAP) internal ribosome entry site (IRBS) reporter cistron, and determining the amount of translation from the winexposed XIAP IRBS reporter cistron exposed to the compound relative to the translation from the unexposed XIAP IRBS reporter cistron. A relative increase in translation from the exposed compound relative to the translation from the unexposed XIAP IRBS reporter cistron indicates a compound that increases XIAP IRES dependent (app independent) translation. XIAP protein plays a critical cole in the regulation of apoptosis by suppressing activation of downstream caspase-3 and caspase-7. Compounds identified by the method cole in the regulation of apoptosis by suppressing activation of compact and the fact increasing apoptosis) can be used for which decrease XIAP IRBS-dependent translation (thus leading to reduced expression of XIAP and hence increasing apoptosis) can be used for treating cancer. The methods can also be used for the identification of agents that upregulate XIAP translation and hence inhibit apoptosis, which can be used to treat autoimmune diseases, degenerative diseases or immunorejection. Such agents may, for example, be used to inhibit caple conditions such as Alzheimer's disease; islet colls in autoimmune diabetes mellitus; photoreceptor cells in retinities pigmentons and diabetic retinopathy; and cardiomycotycated into regan transplants. XIAP IRES elements can also be incorporated into corpan transplants. XIAP IRES elements can also be used to enhance the survival of cell or organ transplants. With IRES elements can also be used to enhance the survival of cell or organ transplants. With IRES elements can also be used to enhance the survival of cell or expression constructs which enode XIAP or other IAPs (Contents) e.g., TIAP: AAY81440). Such constructs may be used to react which, along with t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Block copolymer; genetic; neoplastic; cardiovascular; infectious disease; HIV; AIDS; cancer; Herpes Simplex Virus 1; HSV-1; antisense; oligonucleotide; DNA-RNA hybrid; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                       New isolated X-linked inhibitor of apoptosis internal ribosome entry site, used to develop agents for treating, e.g. cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Oligonucleotide complementary to part of Herpes Simplex Virus 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 12 BP; 2 A; 2 C; 1 G; 0 T; 7 U; 0 Other;
                                                                                                                                                                   Liston P;
                                                                                                                                                                                                                                                                                                                               Example IV; Fig 5A; 87pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAA91860 standard; DNA; 12 BP.
99WO-IB001415.
                                            98US-00121979
99US-00332319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                Holcik M,
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                                                                                                                 UYOT- ) UNIV OFTAWA
                                                                                                                                                                                                             WPI; 2000-338644/29
                                                                                                                                                              Korneluk RG,
22-JUL-1999;
                                            24-JUL-1998;
14-JUN-1999;
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HIV; A
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The present invention relates to compositions of a polynucleotide or its derivatives and at least one polyoxychylene-polyoxypropylene block copolymer. The compositions of the invention form a molecular solution or colloidal dispersion. The invention is used for delivering a polynucleotide to a cell for gene therapy of an animal. Diseases that may be treated by the invention include genetic, neoplastic, cardiovascular and infectious diseases. The use of the block copolymers reduces the immune response, so that a booster injection is not required to obtain an immune response, so that a booster injection is not required. Additionally, the risk of integration of polynucleotides into the chromosomes of the host organism is reduced and the risk of developing anti-polynucleotide antibodies is reduced. The present sequence is oligonucleotide A complementary to the splice site of the early mRNA of Herpes Simplex Virus I (HSV-1). This antisense oligonucleotide was also a proper property of the polynucleotide was an included and the risk of the contractions and the risk of the contraction of polynucleotide was an included and the risk of the contraction of polynucleotide was an included and the risk of the contraction of polynucleotide was an included and the risk of the contraction of the contr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Composition for gene therapy comprises polynucleotide and polyoxyethylene -polyoxypropylene block copolymer in amounts insufficient for gel formation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Herpes Simplex Virus 1 (HSV-1). This antisense oligonucleotide was designed to inhibit Herpes Virus. (Updated on 15-SEP-2003 to standardise
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Oligonucleotide primer SEQ ID NO 321079 for detecting SNP TSC0030058
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 38.2%; Score 8.4; DB 1; Length 12; 90.0%; Pred. No. 5.6e+02; tive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                               Lemieux PM, Vinogradov SV, Alakhov VY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Seguence 12 BP; 0 A; 4 C; 3 G; 4 T; 1 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 21; Page 68; 112pp; English.
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                                                                                                                                                                                                                                                                             99US-00227364.
                                                                                                                                                                                                                     06-JAN-2000; 2000WO-US000309.
                       /*tag= a
/label= RNA
                                                                                                                                                                                                                                                                                                                                  SUPR-) SUPRATEK PHARMA INC
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                                                                                                                                                                                                                                                                                                                                                             KABA/) KABANOV A V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2000-571847/53.
                                                                                                          WO200047186-A1
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                                                                                                                                                                                                                                                                             38-JAN-1999;
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                                                                                                                                                               17-AUG-2000
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misc_RNA
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             derivatives and at least one polyoxyerbylene-polyoxypropylene block copolymer. The compositions of the invention form a molecular solution or coloidal dispersion. The invention is used for delivering a polynucleotide to a cell for gene therapy of an animal. Diseases that may be treated by the invention include genetic, neoplastic, cardiovascular and infectious diseases. The use of the block copolymers reduces the number of polynucleotide molecules and the time required to obtain an immune response, so that a booster injection is not required. Additionally, the risk of integration of polynucleotides into the chromosomes of the host organism is reduced and the risk of developing anti-polynucleotide antibodies is reduced. The present sequence is an oligonucleotide complementary to the splicing site at 983-994 of the Herpes Simplex Virus I (HSV-1). This antisense oligonucleotide was designed to inhibit Herpes Virus. (Updated on 15-SEP-2003 to standardise
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Composition for gene therapy comprises polynuclectide and polyoxyethylene polyoxypropylene block copolymer in amounts insufficient for gel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Block copolymer; genetic; neoplastic; cardiovascular; infectious disease; HIV; AIDS; cancer; Herpes Simplex Virus 1; HSV-1; antisense; oligonuclectide; DNA-RNA hybrid; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           present invention relates to compositions of a polynucleotide or its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Vinogradov SV, Alakhov VY,
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                       Location/Qualifiers
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AAA91863 standard; DNA; 12 BP.
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.

Oligonucleotide primer SEQ ID NO 316641 for detecting SNP TSC0027537.

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                                                                                                                                                                                                                                                                                                                                                                                                                                        SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                       38.2%; Score 8.4; DB 1; Length 12; 90.0%; Pred. No. 5.6e+02; ive 0; Mismatches 1; Indels
                                                    Sequence 12 BP; 0 A; 0 C; 5 G; 7 T; 0 U; 0 Other;
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was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences
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                                                                                                         Best Local Similarity
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                                                                                                                          Matches
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Set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status.

Berlin K;

07-APR-2000; 2000DE-01019173. 06-APR-2001; 2001WO-IB000713.

Claim 1; SEQ ID NO 316641; 29pp + Sequence Listing; German.

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, ardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF99989, ABH00010-ABF99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Match 38.2%; Score 8.4; DB 1; Length 12; Local Similarity 90.0%; Pred. No. 5.6e+02; es 9; Conservative 0; Mismatches 1; Indels
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, axidovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABE99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from MIPO at
                                                                Set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status.
                                                                                                                             Claim 1; SEQ ID NO 380688; 29pp + Sequence Listing; German.
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Matches 9; Conservative
           Olek A, Piepenbrock C,
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central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                                                                                                                                                                                                                                    claim 1; SEQ ID NO 360794; 29pp + Sequence Listing; German.
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Best Local Similarity 90.00
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methylation status.
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                                Homo sapiens
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
                                                                                         SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
Oligonucleotide primer SEQ ID NO 272424 for detecting SNP TSC0002812
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38.2%; 90.0%;

Query Match
Best Local Similarity 90.0
Matches 9; Conservative

735 GAAACAGAAC 744

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and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for derecting cell type differentiation. ABC0010-ABC09989, ABF00010-ABF9989, ABF00010-ABF9989 and ABI00010-ABF9989. The sequence data for this parent did not form part of the printed specification, but was obtained in electronic format from WIPO at fire wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 90.0
Matches 9; Conservative
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06-APR-2001; 2001WO-IB000713.

WO200177384-A2. Homo sapiens.

18-OCT-2001.

07-APR-2000; 2000DE-01019173.

Olek A, Piepenbrock C,

WPI; 2001-657177/75.

(EPIG-) EPIGENOMICS AG.

SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.

Oligonucleotide primer SEQ ID NO 304044 for detecting SNP TSC0020762.

(first entry)

22-FEB-2002

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ABI04071 standard; DNA; 12 BP.

RESULT 729 ABI04071

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Pred. No. 5.6e+02;
0; Mismatches 1; Indels
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90.0%;
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Best Local Similarity 90.0
Matches 9; Conservative
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ABIS9560
ID ABIS956
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Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single-nucleotide polymorphisms and cytosine methylation status.

Seguence 12 BP; 1 A; 1 C; 2 G; 8 T; 0 U; 0 Other;

ftp.wipo.int/pub/published_pct_sequences

Berlin

Piepenbrock C,

olek A,

WPI; 2001-657177/75.

06-APR-2001; 2001WO-IB000713.

18-OCT-2001

07-APR-2000; 2000DE-01019173.

(EPIG-) EPIGENOMICS

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC9989, ABF00010-ABF9989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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                                                                                                                                                                                       SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                            Oligonucleotide primer SEQ ID NO 359533 for detecting SNP TSC0051639
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ber or origonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; SEQ ID NO 359533; 29pp + Sequence Listing; German
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99999, ABF00010-ABF99999, ABH00010-ABH99999 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                                                                                                                                                               Claim 1; SEQ ID NO 271487; 29pp + Sequence Listing; German
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Matches 9; Conservative
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC9989, ABF00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but ftp.wipo.int/pub/published_pct_sequences
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set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status.
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                                                                                             Claim 1; SEQ ID NO 344412; 29pp + Sequence Listing; German.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
-ABC99989, ABF00010-ABF99989, ABH00010-ABH99889 and ABI00010-ABI82073 represent the Oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences
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Pred. No. 5.6e+02;
0; Mismatches 1; Indels
                                                                                                                                         Length 12;
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                                                                                                      Sequence 12 BP; 0 A; 4 C; 0 G; 8 T; 0 U; 0 Other;
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                                                                                                                                         38.2%; Score 8.4; DB 1; 90.0%; Pred. No. 5.6e+02;
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90.0%;
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les 9; Conservative
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Best Local Similarity
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                                                                                                                                         Query Match
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ABI55220/c
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligomucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, ardiovascular and metholic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF99989, ABH00010-ABF99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                                           SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                                            Oligonucleotide primer SEQ ID NO 381996 for detecting SNP TSC0064673
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ABH71928/C
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AC ABH71928;
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DT 22-FEB-2002 (first entry)
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DT 20-FEB-2002 (first entry)
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                                    ABI82023 standard; DNA; 12
                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Olek A, Piepenbrock C,
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SNP, single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.

06-APR-2001; 2001WO-IB000713.

WO200177384-A2

18-OCT-2001.

Oligonucleotide primer SEQ ID NO 274637 for detecting SNP TSC0003624.

(first entry)

22-FEB-2002

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Gaps

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ABH74652;

ABH74652 standard; DNA; 12 BP.

RESULT 737

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         SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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nes 9; Conservative
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99999, ABF00010-ABE99999, ABH00010-ABH99999 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form par of the printed specification, but was obtained in electronic format from WIPO at
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   07-APR-2000; 2000DE-01019173.
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AB100098/C
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             This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, ardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but twipo.int/pub/published_pot_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, ardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99899, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABF82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but the was obtained in electronic format from WFPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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Claim 1; SEQ ID NO 300071; 29pp + Sequence Listing; German.

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(first entry)

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SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                         Oligonucleotide primer SEQ ID NO 341601 for detecting SNP TSC0008742
                            ABI41628 standard; DNA; 12 BP.
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RESULT 742
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                                                                                                                             Gaps
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                                                                        38.2%; Score 8.4; DB 1; Length 12; 90.0%; Pred. No. 5.6e+02; tive 0; Mismatches 1; Indels
                            Sequence 12 BP; 1 A; 0 C; 5 G; 6 T; 0 U; 0 Other;
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ABI39615 standard; DNA; 12 BP.
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                                                                                                                                                                  Set of oligonucleotides, useful for diagnosis and cell typing, idesigned to detect single-nucleotide polymorphisms and cytosine methylation status.
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Listing; German.

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABE99899, ABF00010-ABE99899, ABF00010-ABE99989, ABF00010-ABE99989, ABF00010-ABE99989 and ABI00010-ABE9073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                            Set of oligonucleotides, useful for diagnosis and cell typing, idesigned to detect single-nucleotide polymorphisms and cytosine methylation status.
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38.2%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 5.6e+02;
Matches 9; Conservative 0; Mismatches 1; Indels
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                                                                                                                                                       Claim 1; SEQ ID NO 377760; 29pp + Sequence
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ABH69031
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                                                                                                                                                                                                                                                                                                                                                            Set of oligonucleotides, useful for diagnosis and cell typing, idesigned to detect single-nucleotide polymorphisms and cytosine methylation status.
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PMA) oligoners for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a
                                                                                                                                               SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                        Oligonuclectide primer SEQ ID NO 269008 for detecting SNP TSC0001546
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status.
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SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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Homo sapiens

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range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99899, ABF00010-ABF99899, ABF00010-ABF99899, ABF00010-ABF99899, ABF00010-ABF99899 and ABI00010-ABF82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic form the NIPO at
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                                                                                                                                                                                                                                                   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                                                      Oligonucleotide primer SEQ ID NO 272355 for detecting SNP TSC0002794.
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ABI28308

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                                                               SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Oligonucleotide primer SEQ ID NO 279303 for detecting SNP TSC0007155.
                                Oligonucleotide primer SEQ ID NO 328281 for detecting SNP TSC0034210.
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Best Local Similarity 90.0°
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38.2%; Score 8.4; DB 1; Length 12; 90.0%; Pred. No. 5.6e+02; ive 0; Mismatches 1; Indels

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737 AACAGAACAC 746

3 AACAAAACAC 12

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Sequence 12 BP; 7 A; 4 C; 0 G; 1 T; 0 U; 0 Other;

ftp.wipo.int/pub/published_pct_sequences

This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF99899, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at

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ser or oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status.

Berlin K;

Piepenbrock C,

Olek A,

WPI; 2001-657177/75

(EPIG-) EPIGENOMICS AG

06-APR-2001; 2001WO-IB000713 07-APR-2000; 2000DE-01019173

(first entry)

22-FEB-2002

Claim 1; SEQ ID NO 279303; 29pp + Sequence Listing; German.

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SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                    Oligonucleotide primer SEQ ID NO 284553 for detecting SNP TSC0011877.
                                                                                                                                                                                                                                                                                                                                                                                     Set of oligonuclectides, useful for diagnosis and cell typing, is designed to detect single-nuclectide polymorphisms and cytosine
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                         ABH84560 standard; DNA; 12 BP.
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methylation status.

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC9989, ABF00010-ABF9989, ABF00010-ABF9989, ABF00010-ABF9989, ABF00010-ABF9989, and ABI00010-ABF82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form mart of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretracted genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABEG09989, ABE00010-ABE9989, ABE00010-ABE9989 and ABI00010-ABE82073 represent the oligomers described in the invention. NOTE: The sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                       Claim 1; SEQ ID NO 284553; 29pp + Sequence Listing; German
                                                                                                                                                                                                                                                                                                                                                                                      38.2%; Score 8.4; DB 1; Length 12; 90.0%; Pred. No. 5.6e+02; tive 0; Mismatches 1; Indels
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The properties of Conservative 1.00
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC9989, ABF00010-ABF99899, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
   the printed specification, but
                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                Sequence 12 BP; 0 A; 0 C; 3 G; 9 T; 0 U; 0 Other;
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data for this patent did not form part of the pass obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, cancer also used for addiovactular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABH99989 and ABI00010-ABH82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                              SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                                  Oligonucleotide primer SEQ ID NO 297818 for detecting SNP TSC0017786.
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                                    ABH97825 standard; DNA; 12 BP
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peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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designed to detect single-nucleotide polymorphisms and cytosine
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ABI16680 standard; DNA; 12 BP.
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This invention describes novel oligonucleotide primers or peptide nucleic
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acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABE99989, ABF00010-ABE99989, ABF0010-ABE9989, ABF0010-ABE9989, ABF0010-ABE9989, ABF0010-ABE9989, ABF001010-ABE9989, ABF001010-ABE998, ABF00101010-ABE998, ABF00101010-ABE998, ABF001010-ABE998, ABF00101010-ABE998, ABF00101010-ABE998, ABF00101010-ABE998, ABF00101010-ABE998, ABF00101010-ABE998, ABF0
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SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic. Oligonucleotide primer SEQ ID NO 343646 for detecting SNP TSC0043181

SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.

Oligonuclectide primer SEQ ID NO 371021 for detecting SNP TSC0058524.

22-FEB-2002 (first entry)

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and oytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, contral nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC9989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at fire wipo int/pub/published_pct_sequences Set of oligonucleotides, useful for diagnosis and cell typing, idesigned to detect single-nucleotide polymorphisms and cytosine Claim 1; SEQ ID NO 371021; 29pp + Sequence Listing; German. WPI; 2001-657177/75. methylation status

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Piepenbrock C,

Olek A,

(EPIG-) EPIGENOMICS AG

06-APR-2001; 2001WO-IB000713. 07-APR-2000; 2000DE-01019173

WO200177384-A2. Homo sapiens

18-OCT-2001

Sequence 12 BP; 7 A; 3 C; 0 G; 2 T; 0 U; 0 Other;

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretraeted genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic discorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF99989, ABH00010-ABF99989 and ABI00010-ABF82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but twipo.int/pub/published_pot_sequences
                                                                                                                     SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                      Oligonucleotide primer SEQ ID NO 274235 for detecting SNP TSC0003487
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                                                                                                                                                                                                                                                                                                                                        SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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ABH74250 standard; DNA; 12 BP.

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                Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single-nucleotide polymorphisms and cytosine methylation status.
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designed to detect single-nucleotide polymorphisms and cytosine
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                                                                                                                                                  Claim 1; SEQ ID NO 305402; 29pp + Sequence Listing; German.
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736 AAACAGAACA 745
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ABI20634
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oligomers are also used for detecting cell type differentiation. ABC00010 -ABC9989, ABF00010-ABF99899, ABF00010-ABF99899, ABF00010-ABF99899, ABF00010-ABF82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at fig. wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                                                                                                                          38.2%; Score 8.4; DB 1; Length 12; 90.0%; Pred. No. 5.6e+02; tive 0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, contral nervous system, cardiovascular and metabolic disorders. The coligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF9989, ABH00010-ABH99899 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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                                         SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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  Oligonucleotide primer SEQ ID NO 305010 for detecting SNP TSC0021207.
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                                                                                                                          This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a renge of diseases including immune system, gastrointestinal, respiratory, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF9989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but ftp.wipo.int/pub/published_pct_sequences
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The oligonuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF99899, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                       Gaps
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                                                                  Length 12;
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                                                              Score 8.4; DB 1; Length 12
Pred. No. 5.6e+02;
0; Mismatches 1; Indels
Sequence 12 BP; 9 A; 2 C; 0 G; 1 T; 0 U; 0 Other;
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                                                                                                                                    0; Mismatches
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ftp.wipo.int/pub/published_pct_sequences
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90.0%;
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Best Local Similarity 90.0%;
Matches 9; Conservative
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                                                                                                                                    9; Conservative
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XX ABIII:
XXX ABIII:
XXX ABIII:
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XXX COLL:
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Berlin K;

Piepenbrock C,

olek A,

WPI; 2001-657177/75.

06-APR-2001; 2001WO-IB000713.

WO200177384-A2.

18-OCT-2001

Homo sapiens.

07-APR-2000; 2000DE-01019173.

(EPIG-) EPIGENOMICS AG

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                                                                                                                                               SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                 Oligonucleotide primer SEQ ID NO 290367 for detecting SNP TSC0014319.
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                   ABH90374 standard; DNA; 12 BP.
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90.0%;
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                                                     ABH90374;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                                                                                                                                                          Set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status.
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Homo sapiens.
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                                                           Set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status.
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                                                                                                                                   Listing; German.
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90.0%; Pred. No. 5.6e+02;
live 0; Mismatches 1;
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 Berlin K;
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Piepenbrock C,
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                                                                                                                                                                                                                                                                                          was obtained in electronic format from Wl
ftp.wipo.int/pub/published_pct_sequences
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Length 12;

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38.2%; Score 8.4;

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This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99889, ABF00010-ABF99889, ABF00010-ABF99889 and ABI00010-ABF82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at fire printed specification, but fire wipo int/pub/published_pct_sequences
                                                                                                  SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                              Oligonucleotide primer SEQ ID NO 287381 for detecting SNP TSC0013065.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status.
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                     22-FEB-2002 (first entry)
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    90.0%; Pred. No. 5.6e+02; ative 0; Mismatches 1; Indels
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                                                                     733 GAGAACAGA 742
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, ardiovascular and metabolic disorders. The coingomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF9989, ABH00010-ABH99989 and ABI00010-ABF82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but the was obtained in electronic format from WIPO at
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designed to detect single-nucleotide polymorphisms and cytosine methylation status.
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                                                                                      Claim 1; SEQ ID NO 316995; 29pp + Sequence Listing; German
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             38.2%; Score 8.4; DB 1; Length 12
90.0%; Pred. No. 5.6e+02;
tive 0; Mismatches 1; Indels
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ABI67989/c
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                                                                                                                                                                                                                                        Berlin K;
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                                                      06-APR-2001; 2001WO-IB000713.
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Best Local Similarity 90...
9; Conservative
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18-OCT-2001.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; SS; central nervous system; gastrointestinal; respiratory; immune; metabolic.
represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                           Oligonucleotide primer SEQ ID NO 377571 for detecting SNP TSC0062398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status.
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Best Local Similarity 90.0%; Pred. No. 5.6e+02;
Matches 9; Conservative 0; Mismatches 1; Indels
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                                                                                           Sequence 12 BP; 2 A; 0 C; 2 G; 8 T; 0 U; 0 Other;
                                                        ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                                                                    ABI77598 standard; DNA; 12 BP.
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Best Local Similarity 90...
Local 9; Conservative
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, ardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABE9989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from NIPO at
                                                                                                                                                                                                                SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                 Oligonucleotide primer SEQ ID NO 295008 for detecting SNP TSC0016398.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Oligonucleotide primer SEQ ID NO 280268 for detecting SNP TSC0008419.
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designed to detect single-nucleotide polymorphisms and cytosine
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Pred. No. 5.6e+02;
0; Mismatches 1; Indels
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                                                                                ABH95015 standard; DNA; 12 BP.
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Matches 9, Conservative
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3 ACAAAACACC 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 methylation status.
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38.2%; Score 8.4; DB 1; Length 12; 90.0%; Pred. No. 5.6e+02; tive 0; Mismatches 1; Indels

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                                                                                                                                                                                                                                       Claim 1; SEQ ID NO 280268; 29pp + Sequence Listing; German.
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38.2%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 5.6e+02;
Matches 9; Conservative 0; Mismatches 1; Indels
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and merabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABF82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                             Set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status.
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                                        Berlin K;
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Sequence 12 BP; 8 A; 2 C; 0 G; 2 T; 0 U; 0 Other;
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC9989, ABF00010-ABF9989, ABF00010-ABF9989 and ABI0010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from MIPO at
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           38.2%; Score 8.4; DB 1; Length 12; 90.0%; Pred. No. 5.6e+02; ive 0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                   Gaps
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designed to detect single-nucleotide polymorphisms and cytosine
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38.2%; Score 8.4; DB 1; Length 12; 90.0%; Pred. No. 5.6e+02; tive 0; Mismatches 1; Indels
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RESULT 786 ABH73493/c

Mon Oct 18 14:40:07 2004

Page 353

Berlin K;

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC09989, ABF00010-ABF99899, ABF00010-ABF99899, ABF00010-ABF99899 and ABI00010-ABF82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at the printed specification, but ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                          Set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status.
                                                                                                                                                                                                                                                                                                                             Claim 1; SEQ ID NO 276891; 29pp + Sequence Listing; German.
                                                                                  06-APR-2001; 2001WO-IB000713.
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                                                                                                                                  SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                   Oligonucleotide primer SEQ ID NO 273478 for detecting SNP TSC0003201.
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ABH73493 standard; DNA; 12 BP
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                                                                                     38.2%; Score 8.4; DB 1; Length 12; 90.0%; Pred. No. 5.6e+02; ive 0; Mismatches 1; Indels
Sequence 12 BP; 10 A; 2 C; 0 G; 0 T; 0 U; 0 Other;
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SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.

Homo sapiens

Oligonucleotide primer SEQ ID NO 276891 for detecting SNP ISC0004323.

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF9989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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                                                        Set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status.
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designed to detect single-nucleotide polymorphisms and cytosine
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central neivous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABC99989, ABF00010-ABC99989, ABF00010-ABC99989, ABF00010-ABC9989, ABF00010-ABC9989, ABF00010-ABC9989, ABF00010-ABC98989, ABF00010-ABC98989, ABF00010-ABC98989, ABF00010-ABC98989, ABF00010-ABC98989, ABF00010-ABC98989, ABF0010-ABC98989, ABF00010-ABC98989, ABF000010-ABC98989, ABF0000010-ABC98989, ABF000010
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                                                                                                                                                                              Sequence 12 BP; 1 A; 0 C; 2 G; 9 T; 0 U; 0 Other;
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Query Match
38.2%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 5.6e+02;
Matches 9; Conservative 0; Mismatches 1; Indels

This invention describes novel oligonucleotide primers or peptide nucleic acid (PMA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory,

Claim 1; SEQ ID NO 306454; 29pp + Sequence Listing; German.

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SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
             Oligonucleotide primer SEQ ID NO 370262 for detecting SNP TSC0058079.
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                                                                                                                                                                                                                             SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                                  Oligonucleotide primer SEQ ID NO 345527 for detecting SNP TSC0044075.
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Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single-nucleotide polymorphisms and cytosine
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                                                                                                           Claim 1; SEQ ID NO 370262; 29pp + Sequence Listing; German.
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Pred. No. 5.6e+02;
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ABI70289 standard; DNA; 12 BP.

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(first entry)

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ABI70289;

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SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF99899, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Oligonucleotide primer SEQ ID NO 272598 for detecting SNP TSC0002872.
                 Claim 1; SEQ ID NO 297267; 29pp + Sequence Listing; German.
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38.2%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 5.6e+02;
Matches 9; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                               Sequence 12 BP; 1 A; 0 C; 2 G; 9 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                         Claim 1; SEQ ID NO 270944; 29pp + Sequence Listing; German
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 12 BP; 5 A; 5 C; 1 G; 1 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              was obtained in electronic format from W1
ftp.wipo.int/pub/published_pct_sequences
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  06-APR-2001; 2001WO-IB000713
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting call type differentiation. ABC0010-ABF59989, ABF00010-ABF9989 and ABI00010-ABF82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but
SNP, single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                        Oligonucleotide primer SEQ ID NO 352300 for detecting SNP TSC0047801
                                                                                                                                                                                                                                                                                              06-APR-2001; 2001WO-IB000713.
                                         ABI52327 standard; DNA; 12
                                                                                              22-FEB-2002 (first entry)
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              RESULT 797
                             ABI52327,
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                                                                                                                                                                                                                                                                                                                                    SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                  38.2%; Score 8.4; DB 1; Length 12; 90.0%; Pred. No. 5.6e+02; ive 0; Mismatches 1; Indels
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                                         Sequence 12 BP; 9 A; 0 C; 2 G; 1 T; 0 U; 0 Other;
was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences
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                                                      Query Match
Best Local Similarity 90.07
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Matches 9; Conserv
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                                                                                                                                                                                                                                                           oligonucleotides, useful for diagnosis and cell typing, ied to detect single-nucleotide polymorphisms and cytosine
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                                                                                                                                Berlin K;
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07-APR-2000; 2000DE-01019173.
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                                                           (EPIG-) EPIGENOMICS AG.
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                                                                                                                                                                                                                                                                                                 designed to detect methylation status.
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and oycosine methylation status in chemically pretreated genomic DNA. The oligomucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC09989, ABF00010-ABF99899, ABF00010-ABF99899, ABF00010-ABF99899 and ABI00010-ABF82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but twipo.int/pub/published_pot_sequences
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                                                                uer or oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status.
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                                                                                                                                                Claim 1; SEQ ID NO 357369; 29pp + Sequence Listing; German.
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                Piepenbrock
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 This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99889, ABF00010-ABF99889 and ABI00010-ABF82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but the was obtained in electronic format from WIPO at
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 central nervous system; gastrointestinal; respiratory; immune; metabolic.
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABF9989, ABF00010-ABF9989, ABH00010-ABH99989 and ABI00010-ABF82073 represent the oligomers described in the invention. NOTE: The sequence date for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99889, ABF00010-ABF9989, ABF00010-ABH99989 and ABI0010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence was obtained in electronic format from WIPO at fitte articles in the printed specification, but ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Oligonucleotide primer SEQ ID NO 270396 for detecting SNP TSC0002115.
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                                                                                                                                                                                                                                                      38.2%; Score 8.4; DB 1; Length 12; 90.0%; Pred. No. 5.6e+02; tive 0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABH70419 standard; DNA; 12 BP.
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Best Local Similarity 90.00,
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                                                                                                                                                                                                                                                                                                                                    SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                     Gaps
                                                                                                                                                                                                                                                                                                      Oligonucleotide primer SEQ ID NO 274349 for detecting SNP TSC0003519.
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Score 8.4; DB 1; Length 12
Pred. No. 5.6e+02;
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Best Local Similarity 90.0%;
Matches 9; Conservative 0
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 Query Match 38.2
Best Local Similarity 90.0
Matches 9; Conservative
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ID ABH7949
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Sequence 12 BP; 2 A; 0 C; 2 G; 8 T; 0 U; 0 Other;

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, ardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC9989, ABF00010-ABF9989, ABH00010-ABH99989 and ABI00010-ABI32073 tepresent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                        SNP, single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primër; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                      Oligonucleotide primer SEQ ID NO 279486 for detecting SNP TSC0007399.
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                                    22-FEB-2002 (first entry)
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in ejectronic format from WIPO at

Sequence 12 BP; 7 A; 3 C; 0 G; 2 T; 0 U; 0 Other;

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Set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status.

Berlin

Piepenbrock C,

olek A,

WPI; 2001-657177/75

(EPIG-) EPIGENOMICS

06-APR-2001; 2001WO-IB000713. 07-APR-2000; 2000DE-01019173.

18-OCT-2001.

Claim 1; SEQ ID NO 332424; 29pp + Sequence Listing; German.

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SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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38.2%; Score 8.4; DB 1; Length 12; 90.0%; Pred. No. 5.6e+02; tive 0; Mismatches 1; Indels
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ID ABH89176 standard; DNA; 12 BP.
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Matches 9; Conservative
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     Query Match
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WPI; 2001-657177/75

SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.

WO200177384-A2

Homo sapiens

Oligonucleotide primer SEQ ID NO 332424 for detecting SNP TSC0036902.

(first entry)

22-FEB-2002

ABI32451 IID ABI33451 IID ABI33451 XX ABI3 XX ABI3 XX KW SND; KW SND; KW Centr XX CONT XX NOOS HOWC

ABI32451;

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ABI32451 standard; DNA; 12

RESULT 804

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Set of oligonucleotides, useful for diagnosis and cell typing, idesigned to detect single-nucleotide polymorphisms and cytosine methylation status.
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                                                                                                                      Claim 1; SEQ ID NO 289169; 29pp + Sequence Listing; German.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            38.2%; Score 8.4; DB 1; Length 12; 90.0%; Pred. No. 5.6e+02; tive 0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at the printed specification, the ftp.wipo.int/pub/published_pct_sequences
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Best Local Similarity 90.0
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RESULT 810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           was obtained in electronic format from Wl
ftp.wipo.int/pub/published_pct_sequences
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ABI23297 standard; DNA; 12
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Matches 9; Conservative
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SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI32073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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Mon Oct 18 14:40:07 2004

Query Match

Matches

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ABI14975;

ABH92293

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligomucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                                    SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                Oligonucleotide primer SEQ ID NO 292286 for detecting SNP TSC0015155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status.
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ABH92293 standard; DNA; 12 BP
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                                         38.2%; Score 8.4; DB 1; Length 12; 90.0%; Pred. No. 5.6e+02; ative 0; Mismatches 1; Indels
Sequence 12 BP; 1 A; 0 C; 3 G; 8 T; 0 U; 0 Other;
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Matches 9; Conservative
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SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
Oligonucleotide primer SEQ ID NO 345526 for detecting SNP TSC0044075.
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99999, ABF00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at the printed specification, but fire wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SNP; single nuclectide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                                                                                                                                     set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status.
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                                                                                                                                                        This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99889, ABF00010-ABF99899, ABH00010-ABH99899 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but the was obtained in electronic format from WIPD at
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                  Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single-nucleotide polymorphisms and cytosine methylation status.
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABF82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABC0010-ABE99889, ABC0010-ABE99889 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                                                                38.2%; Score 8.4; DB 1; Length 12; 90.0%; Pred. No. 5.6e+02;
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                                                                                                                                                                                                                                                                       Sequence 12 BP; 8 A; 0 C; 2 G; 2 T; 0 U; 0 Other;
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Best Local Similarity 90...
Best Local 9, Conservative
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SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.

WO200177384-A2 Homo sapiens.

Oligonucleotide primer SEQ ID NO 285319 for detecting SNP TSC0012239.

ВЪ.

ABH85326 standard; DNA; 12

RESULT 819

ABH8532

22-FEB-2002

ABH85326;

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Best Local Similarity 90.0%; Pred. No. 5.6e+02;
Matches 9; Conservative 0; Mismatches 1; Indels
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Oligonucleotide primer SEQ ID NO 342390 for detecting SNP TSC0042520.
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                                                                                                                                                                                                                                                   Set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status.
                                                                                                                                                                                                                                                                                                                                                        Claim 1; SEQ ID NO 340597; 29pp + Sequence Listing; German.
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ABI42417/c
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                                                                                   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                             Oligonucleotide primer SEQ ID NO 315282 for detecting SNP TSC0026831.
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                                               This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleited bolymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC9989, ABF00010-ABF9989, ABH0010-ABH9989 and ABI0010-ABI82073 the represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                          Claim 1; SEQ ID NO 342390; 29pp + Sequence Listing; German.
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data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                      38.2%; Score 8.4; DB 1; Length 12; 90.0%; Pred. No. 5.6e+02; cive 0; Mismatches 1; Indels
                                                                                                                                        Seguence 12 BP; 0 A; 0 C; 5 G; 7 T; 0 U; 0 Other;
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Best Local Similarity 90.v.
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                                                                                                                                                                                                                                                                                                                                                  737 AACAGAACAC 746
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Best Local Similarity
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                                                                                                                                                                                                                                                              SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                                                                                                                     Oligonuclectide primer SEQ ID NO 373461 for detecting SNP TSC0060102.
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                                                                                   ABI73488 standard; DNA; 12 BP.
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                                   RESULT 825
AB173488/C
AB1734
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peptide nucleic acid, cytosine methylation, cardiovascular, primer, ss, central nervous system; gastrointestinal, respiratory; immune, metabolic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status.
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, ardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF9989, ABH00010-ABH99989 and ABI00010-ABI82073 tepsesent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SNP; single nuclectide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                            onucleotides, useful for diagnosis and cell typing, i detect single-nucleotide polymorphisms and cytosine
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                                                                                                                                                                Claim 1; SEQ ID NO 308129; 29pp + Sequence Listing; German.
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                                                                                              oligonucleotides, useful for
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ABI59320 standard; DNA; 12
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                                Piepenbrock C,
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(EPIG-) EPIGENOMICS
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                                                                                                                  designed to detect methylation status.
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Matches 9; Conser
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This invention describes novel oligonucleotide primers or peptide nucleic

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acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and oytosine methylation status in chemically pretreated genomic DNN. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF99899, ABH00010-ABH99989 and ABI00010-ABI82073 are present the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human, expressed sequence tag; EST; ds; promoter P15B4; acute myocardial infarction, acute ischaemic stroke; diabetes; anaemia; growth hormone deficiency; hepatitis; kidney carcinoma; multiple sclerosis; chemotherapy-induced neutropaenia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New purified 5' expressed sequence tags useful in diagnostic, forensi
gene therapy or chromosome mapping procedures, or for distinguishing
human tissues or cells from non-human tissues or cells.
                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                   Length 12;
                                                                                                                                                                                                                                                                                                                       1; Indels
                                                                                                                                                                                                                                         Sequence 12 BP; 0 A; 0 C; 4 G; 8 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                               38.2%; Score 8.4; DB 1;
90.0%; Pred. No. 5.6e+02;
trive 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Giordano J;
                                                                                                                                                                                                       ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               transcription factor binding site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Jobert S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 53; Fig 5; 90pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAS07924 standard; DNA; 12 BP.
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                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 90.0.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Dumas Milne Edwards J,
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to distinguish

cells,

human tissues or cells from non-human tissues or

between human tissues or cells that do not and do not express copyrising the 5' EST sequences, to obtain and express cDNA clones which include full protein coding sequences of the carding frames from a genomic sequence, and to obtain and express extended cDNAs encoding portions of the protein. EST-related nucleic diseases resulting from abnormal gene expression, for constructing a high resolution map of human chromosomes, and in gene therapy to control or treat genetic diseases. Proteins expressed from the cDNAs may be used in treat genetic diseases. Proteins expressed from the cDNAs may be used in treat genetic diseases. Proteins expressed from the cDNAs may be used in treating or controlling a variety of human conditions e.g acute myocardial infarction, acute ischaemic stroke, diabetes, anaemia, prowth hormone deficiency, hepatitis, kidney carcinoma, multiple sclerosis,

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polynucleotides comprising the 5' EST sequences, to obtain and express control counts which include full protein coding sequences of the corresponding gene products, to map and clone promoter regions, and open reading frames from a genomic sequence, and to obtain and express actended conNas encoding portions of the protein. EST-related mucleic diseases resulting from abnormal gene expression, for constructing a high resolution map of human chromosomes, and in gene therapy to control or treat genetic diseases. Proteins expressed from the cDNAs may be used in treating or controlling a variety of human conditions e.g acute treating or controlling a variety of human conditions e.g acute hormone deficiency, hepatitis, kidney carcinoma, multiple sclerosis, chemotherapy-induced neutropaenia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; expressed sequence tag; EST; ds; promoter P13H2; acute myocardial infarction; acute ischaemic stroke; diabetes; anaemia; growth hormone deficiency; hepatitis; kidney carcinoma; multiple sclerosis; chemotherapy-induced neutropaemia;
                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                      Sequence 12 BP; 9.A; 2 C; 1 G; 0 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      transcription factor binding site.
                                                                                                                                                                                                                                                                                                                                                                                           AAS07921 standard; DNA; 12 BP.
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                                                                                                                                                                                                                                                              9; Conservative
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Best Local Similarity
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Matches
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Gaps .; 0

38.2%; Score 8.4; DB 1; Length 12; 90.0%; Pred. No. 5.6e+02; ive 0; Mismatches 1; Indels

9; Conservative

Best Local Similarity

Matches

Query Match

736 AAACAGAACA 745 AAACAAAACA 12

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BP

ABA05981 standard; DNA; 12

ABA05981/c ID ABA059 RESULT 831

ABA05981;

Sequence 12 BP; 9 A; 2 C; 0 G; 1 T; 0 U; 0 Other;

hormone deficiency, hepatitis, kid chemotherapy-induced neutropaenia

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for dendritic
                                                                                                                      Activation; dendritic cell; immune response; rheumatoid arthritis; Crohn's disease; ulcerative colitis; thalassemia; muscular dystrophy; cystic fibrosis; osteoperrosis; tumour; cancer; cardiovascular disease; ischaemia; infectious disease; hepatitis; HIV; infection; vaccine; acquired immunodeficiency syndrome; AIDS; transplant rejection; malaria; cytostatic; antiinflammatory; antirheumatic; antiarthritic; anti-HIV; antiarteriosclerotic; ophthalmological; antialcoholism; osteopathic; dermatological; immunosuppressive; antiulcer; cardiant; protozoacide; cerebroprotective; vasotropic; virucide; hepatotropic; tuberculostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               contains
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Guerin N, Alakhov V, Vinogradov S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to an activation inducing composition deals in animals comprises a polynucleotide, viral vector or
                                                                                                                                                                                                                                                                                       HSV-1; herpes simplex virus; antisense oligonucleotide; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Inducing activation composition for dendritic cells in huma polynucleotide, viral vector, or polynucleotide derivative polyoxyethylene-polyoxypropylene block copolymer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 9; Page 62; 126pp; English.
                                                                                        HSV-1 antisense oligonucleotide 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28-APR-2000; 2000US-0200487P. 01-JAN-2001; 2001US-0260806P.
                                                                                                                                                                                                                                                                                                                                                                                                                                 30-APR-2001; 2001WO-US013921.
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                                                    (first entry)
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                                                                                                                                                                                                                                                                                                                                                           WO200183698-A2.
                                                    07-MAR-2002
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                                                                                                                                                                                                                                                                                                                         Synthetic.
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The sequence represents a transcription factor binding site from human promoter P13H2, the promoter and binding site being isolated using sequence from one of the 5' expressed sequence tags (EST) of the invention, one of 15442 nucleotide sequences not given in the specification. The 5' EST may be used to efficiently identify and isolate 5' untranslated regions (UTRS) and upstream regulatory regions which control the location, developmental stage, rate and quantity of protein synthesis, as well as the stability of the mRNA. ESTs containing the 5' ends of protein genes may include sequences for chromosome mapping and identification individuals. The EST may further be used to distinguish

New purified 5' expressed sequence tags useful in diagnostic, forensic, gene therapy or chromosome mapping procedures, or for distinguishing human tissues or cells from non-human tissues or cells.

Example 53; Fig 5; 90pp; English.

Giordano J;

Dumas Milne Edwards J, Jobert S,

(GEST) GENSET

WPI; 2001-357986/38.

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polymucleotide derivative and polyoxyethylene-polyoxypropylene block copolymer(s). The composition has cytostatic, antiinflammatory, antiarteristic, antiarteriscic antiinflammatory, antiarteritic, dermatological, immunosuppressive, antiarteristic, dermatological, immunosuppressive, antiarterispic, anti-HV, protozoacide and tuberculostatic activity. The composition is for inducing activation of dendritic cells in animals, composition is for inducing activation of dendritic cells in animals, cereponse and generates large amounts of dendritic cells in animals, response to gene expression and increasing the immune response and generates large amounts of dendritic cells in vivo or in vitro. It is also used in treating genetic diseases including rheumatoid arburins, postriasis, Crohn's disease, ulcerative collis, alpha-transsemia, beta-thalassemia, phenylketomuria, muscular dystrophy such as Duchenne Muscular Dystrophy, hypersarcosinaemia, adenomatous contestinal polyposis, arterisoslerosla and hypercholasterolaemia, cystic fibrosis, osteopetrosis, increased spontaneous tumours, T and B cell immunodeficiency, hyd cholesterol, arthritis, glaucoma or alcoholism. It is also used to treat neoplastic diseases including cancer, lymphoma and melanoma, cardiovascular diseases including stroke, myocardial schaemia, infectious diseases such as hepatitis, HIV infections and cargined immunisation, including melanoma vaccines, HIV vaccines, therapies and immunisation, including melanoma vaccines, HIV vaccines, continent of therapies and immunisation, including melanoma vaccines, including arterior of the hyperson of incomulantial and therefore such as renal transplant rejection. It is also used in vaccine and malaries of tubescipes, The the inventor.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Activation, dendritic cell; immune response; rheumatoid arthritis; Crohn's disease; ulcerative colitis; thalassemia; muscular dystrophy; cystic fibrosis; osteopetrosis; tumour; cancer; cardiovascular disease; ischaemia; infectious disease; hepatitis; HIV; infection; vaccine; acquired immunodeficiency syndrome; AIDS; transplant rejection; malaria; cytostatic; antinflammatory; antirheumatic; antiarthritic; anti-HIV; antiarteriosclerotic; ophthalmological; antiancholism; osteopathic; dermatological; immunosuppressive; antiulcer; cardiant; protozoacide; cerebroprotective; vasotropic; virucide; hepatotropic; tuberculostatic; HSV-1; herpes simplex virus; antisense oligonucleotide; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            38.2%; Score 8.4; DB 1; Length 12; ilarity 90.0%; Pred. No. 5.6e+02; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          malaria or tuberculosis. The present sequence is tlantisense oligonucleotide, useful to the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 12 BP; 0 A; 5 C; 2 G; 4 T; 1 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HSV-1 antisense oligonucleotide 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABA05984 standard; DNA; 12 BP.
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nes 9; Conserv
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Matches
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The invention relates to an activation inducing composition for dendritic cells in animals comprises a polymucleotide, viral vector or cells in animals comprises a polymucleotide, viral vector or collymer(s). The composition has cytostatic, antiinflammatory, preferably human; increasing the level of production and infiltration for dendritic cells in response to gene expression and increasing the immune ceptorial in response to gene expression and increasing the immune vitro. It is also used in treating genetic diseases including rheumator vitro. It is also used in treating genetic diseases including rheumatorial and because and generates and measomains, phenyleconaria, muscular dystrophy such as Duchenne Muscular Dystrophy, hypersarcosinaemia, adenomatous intestinal polyposis, arteriosclerosis and hypercholesterolammia, and melanoma, cardiovascular diseases including stroke, myocardial immunodeficiency syndrome (AIDS) and transplantation related acquired immunodeficiency syndrome (AIDS) and transplantation related disorders such as renal transplant rejection. It is also used in vaccine therapies and immunisation, including melanoma vaccines, therapies and immunisation, including melanoma accines, therapies and immunisation, including melanoma accines, therapies and immunisation, including melanoma accines, the present sequence is that of a HSV-1
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                                            contains
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                         Inducing activation composition for dendritic cells in human, opolynuclectide, viral vector, or polynuclectide derivative and polyoxyethylene-polyoxypropylene block copolymer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     38.2%; Score 8.4; DB 1; Length 12; 90.0%; Pred. No. 5.6e+02; ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      antisense oligonucleotide, useful to the invention
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                                                                                                                               Example 21; Page 72; 126pp; English
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WPI; 2002-097495/13.
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Best Local Similarity
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AAK99268
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                                                                                                                                                                                         The invention relates to purified nucleic acids, which comprise sequences selected from any of more than 50000 sequences not defined in the specification. The polynucleotide sequences are useful in making cDNA, polypeptides and promotor DNA, and in diagnostic, forensic, gene therapy or chromosome mapping procedures. The nucleic acid sequences are also useful for designing expression vectors and secretion vectors. This polynucleotide sequence represents a PISB4 promoter transcription binding site of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to purified nucleic acids, which comprise sequences selected from any of more than 50000 sequences not defined in the specification. The polymucleotide sequences are useful in making cDNA, polypeptides and promoter DNA, and in diagnostic, forensic, gene therapy or chromosome mapping procedures. The nucleic acid sequences are also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Promoter DNA, diagnostic, forensic, gene therapy, chromosome mapping, expression vector; secretion vector, P13H2; transcription binding site;
Bejanin S;
                                                                   New nucleic acid sequences comprising human expressed sequence tags (ESTs), useful in diagnostic, forensic, gene therapy or chromosome mapping procedures, or for designing expression vectors and secretion
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New nucleic acid sequences comprising human expressed sequence tags (ESTs), useful in diagnostic, forensic, gene therapy or chromosome mapping procedures, or for designing expression vectors and secretion
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Tanaka H,
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                                                                                                                                                                                                                                                                                                                                                                                                  Length 12;
                                                                                                                                                                                                                                                                                                                                                                                               38.2%; Score 8.4; DB 1; Length 12
90.0%; Pred. No. 5.6e+02;
tive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P13H2 promoter transcription binding site SRY_02 #1.
                                                                                                                                                                                                                                                                                                                                                            Sequence 12 BP; 9 A; 2 C; 1 G; 0 T; 0 U; 0 Other;
Giordano J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Giordano J,
Jobert S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Jobert S,
                                                                                                                                                             Disclosure; Fig 5; 163pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure, Fig 5; 163pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAK99265 standard; DNA; 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 90.0
Matches 9, Conservative
Dumas Milne Edwards JB,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       736 AAACAGAACA 745
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 AAACAAAACA 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2002-227459/29.
                              WPI; 2002-227459/29
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useful for designing expression vectors and secretion vectors. This polynucleotide sequence represents a P13H2 promoter transcription binding site of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention provides primers (AAX29501-X29679) for identifying sequences encoding structurally or functionally related proteins such as nuclear or G-protein coupled receptors, apoptosis-related or DNA repair/replication proteins. The identified sequences are broadly useful in plant biology, agriculture, human or veterinary medicine, reproduction, microbiology or environmental science, e.g. to study expression of nuclear receptors at different stages of tissue development or after treatment with particular drugs. It is also used for DNA fingerprinting (to generate products useful for differential hybridisation), or, where a 3'-anchor primer is used, to isolate the 3'-ends of mRNA sequences. Sequences AAX29630-X29679 represent claimed primers specific for human DNA repair and replication genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nucleic acid amplification, nuclear receptor; G-protein coupled receptor; applicats; DNA replantation; plant biology; agriculture; human; veterinary medicine; reproduction; microbiology; hybridisation; environmental science; DNA fingerprinting; PCR primer; ss.
                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                            38.2%; Score 8.4; DB 1; Length 12;
.larity 90.0%; Pred. No. 5.6e+02;
Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Primer for human DNA repair and replication genes.
                                                                                                                     BP; 9 A; 2 C; 0 G; 1 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (KIMM-) KIMMEL CANCER CENT SIDNEY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 29; Page 78; 92pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAX29674 standard; DNA; 8 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
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                                                                                                                                                                                                                                                                                                     736 AAACAGAACA 745
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                                                                                                                                                                                                                                                                                                                                                              AAACAAAACA
                                                                                                                                                                                                            Best Local Similarity
Matches 9; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens.
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                                                                                                                         Sequence 12
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                                                                                                                                                                                  Query Match
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The invention relates to an isolated nucleic acid (NI) comprising at least 20 but not more than 1500 consecutive nucleotides of the optineurin promoter promoter appearing as ADE1390. Also included are the optineurin promoter operably linked to a heterologous nucleic acid, a nucleic acid capable of detecting a single nucleotide polymorphism (SNP) in the optineurin promoter, a host cell comprising the promoter operably linked to a heterologous sequence, diagnosing or prognosing glaucoma in a sample containing promoter region of the optineurin gene, associated with a glaucoma promoter region of the optineurin gene, associated with a glaucoma phenotype), detecting a SNP sequence variation in a sample containing DNA, detecting the presence or increased susceptibility to glaucoma or to a progressive ocular hypertensive clascification reaction primers that direct amplification of a selected corporation or progression of glaucoma in a patient, comprising providing or promoter and amplifying the NA) and detecting a polymorphism (comprising obtaining a sample containing the variation within the optineurin promoter and detecting a sNP located within an optineurin promoter, and detecting the polymorphism of a specific capable of detecting a SNP located within an optineurin promoter, and detecting the polymorphism or progression end and adaptic the polymorphism or sused to diagnose and progresses t sequence is an optineurin promoter motif, repeat element or minerian and also to treat glaucoma related disorders. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New nucleic acid sequences of the optineurin gene are useful to detect polymorphisms particularly single nucleotide polymorphisms in the optineurin promoter to diagnose, prognose and treat glaucoma and related disorders.
                                                                                                                                                                                                     Human, optineurin; ds. ophthalmological; single nucleotide polymorphism; SNP; glaucoma; progressive ocular hypertensive disorder; glaucoma related disorder; motif; repeat element; regulatory region.
                                                                                                                                                                Optineurin promoter motif, repeat element or regulatory region #220.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            36.4%; Score 8; DB 1; Length 9; 100.0%; Pred. No. 4.1e+03; ative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 9 BP; 0 A; 2 C; 1 G; 6 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 11; SEQ ID NO 222; 159pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ξ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Si.
                                                                                                                                                                                                                                                                                                                                                                                                               06-MAR-2002; 2002US-00091281.
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                                         ADE14111 standard; DNA; 9 BP
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                                                                                                                       29-JAN-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Morissette J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (MORI/) MORISSETTE J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2003-864168/80.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SI E.
RAYMOND V.
                                                                                                                                                                                                                                                                                                                               US2003190617-A1
                                                                                                                                                                                                                                                                                          Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Raymond V,
                                                                                  ADE14111;
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Attenuation of pathogenic HIV-1 strain NI4-3 involves deletion of 1 or more decanucleotides (AAQ96406-Q97018) from the nef gene and/or 1 or more decanucleotides (AAQ991019-097166) from the LTR region; the sequence of AAQ96406 corresponds to nucleotides 1-10 of the nef gene (AAQ96141). The response in humans, and enable the generation of therapeutic, diagnostic and targeting agents against HIV-1 infection. (Updated on 16-OCT-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                New non-pathogenic HIV-1 strain carrying a deletion in its nef gene or LTR region - can be used in a vaccine to inhibit/reduce productive infection in an individual by a pathogenic strain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
0
                                                                                                                                HIV-1; AIDS; attenuation; vaccine; nef gene; avirulence; ss.
                                                                                                                                                                                                                                                                                                                                                            Cooper D;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              36.4%; Score 8; DB 1; L
100.0%; Pred. No. 6e+02;
tive 0; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                            Crowe S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HIV-1 NL4-3 nef gene nucleotide deletion 478.
                                                                                                      HIV-1 NL4-3 nef gene nucleotide deletion 479.
                                                                                                                                                                                                                                                                                                                      (MACF-) MACFARLANE BURNET CENT MEDICAL. (AURE-) AUSTRALIAN RED CROSS SOC.
                                                                                                                                                                                                                                                                                                                                                            Deacon NJ, Learmont JC, Mcphee DA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 13; Page 194; 301pp; English.
                                                                                                                                                           Human immunodeficiency virus 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAQ96883 standard; DNA; 10 BP.
            AAQ96884 standard; DNA; 10 BP.
                                                                                                                                                                                                                                                                              94AU-00004002.
94AU-00000284.
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                                                                (revised)
(first entry)
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                                                                                                                                                                                                                                                                 14-FEB-1994;
21-FEB-1994;
23-DEC-1994;
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                                                                                                                                                                                      WO9521912-A1
                                                                16-OCT-2003
26-MAR-1996
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                                       AAQ96884;
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Matches
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AAQ9688
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Local Similarity 100. nes 8; Conservative

Matches

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Gaps

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                                                                                                                                                                                                                                              more decanucleotides (AAQ94016-Q97018) from the nef gene and/or 1 or decanucleotides (AAQ94016-Q97018) from the nef gene and/or 1 or more AAQ96406 corresponds to nucleotides 1-10 of the nef gene (AAQ9611). The resulting avinulent HIV strains are still capable of inducing an immune response in humans, and enable the generation of therapeutic, diagnostic and targeting agents against HIV-1 infection. (Updated on 16-OCT-2003 to standardise OS field)
                                                                                                                                                                                      New non-pathogenic HIV-1 strain carrying a deletion in its nef gene or LTR region - can be used in a vaccine to inhibit/reduce productive infection in an individual by a pathogenic strain.
                                                                                                                                                                                                                                          Attenuation of pathogenic HIV-1 strain NL4-3 involves deletion of 1 or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SAGE tag; serial analysis of gene expression; antigen-presenting cell; APC; moncoyte-derived dendritic cell; differential gene expression; immunostimulatory cofactor; costimulatory factor; CTL; cytotoxic T-lymphocyte; tumour antigen; immunotherapy; anticancer; ss.
                                                                                                                                                                                                                                                                                                                                                               Gaps
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HIV-1; AIDS; attenuation; vaccine; nef gene; avirulence; ss
                                                                                                                                                                                                                                                                                                                                    DB 1; Lens
No. 6e+02;
O; Indels
                                                                                                                                                    Cooper D;
                                                                                                                                                                                                                                                                                                                           Sequence 10 BP; 5.A; 3 C; 2 G; 0 T; 0 U; 0 Other;
                                                                                                                                                    Crowe S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human dendritic cell SAGE tag, SEQ ID NO:537.
                                                                                                                                                                                                                                                                                                                                     36.4%; Scor.
100.0%; Pred. No. v.
0; Mismatches
                                                                                                                        (MACF-) MACFARLANE BURNET CENT MEDICAL. (AURE-) AUSTRALIAN RED CROSS SOC.
                                                                                                                                                    Deacon NJ, Learmont JC, Mcphee DA,
                                                                                                                                                                                                                          Claim 13; Page 194; 301pp; English.
                Human immunodeficiency virus 1.
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98US-0089844P.
98US-0089853P.
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94AU-00000284.
                                                                    95WO-AU000063.
                                                                                       94AU-00003864.
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Best Local Similarity 100...
Best Local 8, Conservative
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19-JUN-1998;
19-JUN-1998;
                                                                    14-FEB-1995;
                                                                                               21-FEB-1994;
                                 WO9521912-A1
                                                                                                        23-DEC-1994;
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                                                  17-AUG-1995
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expression) tags used to identify many carrespond to work carriers and tags used to identify many the preferentially or differentially expressed in monocyte-derived dendititic cells compared with monocytes. Some of the transcripts correspond to known genes or ESTS (expressed sequence tags) which were previously unknown to be preferentially or differentially expressed in dendritic cells, while preferentially or differentially expressed in dendritic cells, while correspond to novel genes. Antigen-presenting cell of the cytotoxic immune response, particularly against tumour cells. Tumour antigen presentation via the MiC (major histocompatibility complex) and subsequent recognition by T-cell receptors is alone the tumour antigen presentation via the MiC (major histocompatibility complex) and subsequency cognition by T-cell receptors that can lyse the tumour cells, immunostimulatory coffactors also being required for cefficient activation of cytotoxic T-lymphcotyes (CTEs) Nucleic acid sequences identified using the SAGE tags have several potential uses. They may be used in vaccines to induce an immune response that can lyse the tumour antigen; to modulate the general potential uses. They may be used in vaccines to induce an immune response, particularly against a tumour antigen; to modulate the general potential waye several potential wayers and modulate expression of diseases related to abnormal expression of these genes, or of their encoded proteins, can be used in active immunotherapy (or to stimulate production of a can be used in active immunotherapy (or to stimulate production of a population of antigen-specific effector cells) and vectors containing them are used in gene therapy. Co-administration of tumour antigens and approach and secretion of the dendritic of the modulate production of the presentation of co-stimulatory factors ensures adequate antigen presentation of co-stimulatory signals, migration of chemokines for recruitment of immune effector cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Isolated polynucleotides differentially expressed in antigen-presenting cells, useful in gene vaccines against cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequences AAZ77573-Z79709 represent SAGE (serial analysis of gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; Page 80; 130pp; English.
98US-0089991P
98US-0089994P
98US-0089994P
98US-0089999P
98US-0089999P
98US-0090035P
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                                                                         0; Indels
                                       Length 10;
Sequence 10 BP; 3 A; 4 C; 2 G; 1 T; 0 U; 0 Other;
                                   36.4%; Score 8; DB 1; L 100.0%; Pred. No. 6e+02;
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98US-0090039P.
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that are preferentially transcribed in the metastatic breast tumour clissumed in the are preferentially transcribed in the metastatic breast tumour cells). AAZ81942 ct. issue (i.e. are upregalated in metastatic breast tumour cells). AAZ81942 ct. AAZ86677 represent tags corresponding to distinct transcripts that are communicated in metastatic breast tumour cells). These ct. issue (i.e. are downregulated in metastatic breast tumour cells). These transcripts can be used for diagnosis, prognosis, monitoring and transcripts can be used for diagnosis, prognosis, monitoring and transcripts can be used for diagnosis, prognosis, monitoring and transcripts can be used to thybridisation/amplification reactions. Of yearly for treatment of (metastatic) breast cancer, while promoters from the transcripts are used to direct expression of the transcripts are potentially consisted to direct expression, in selected cell types, of the transcripts are used to direct expression, in selected cell types, of the particularly an antigen-encoding sequence for use in gene or cell-based vaccines, for diagnosing breast cancer and for raising specific antibodies (Ab). Ab are used to detect the polypeptides can be used to expand canter. Host cells that produce the polypeptides can be used to expand
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and isolate populations of educated, antigen-specific immune effecter cells, e.g. cytotoxic T lymphocytes, and these used for adoptive immunotherapy.
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                                                                    36.4%; Score 8; DB 1; Length 10; 100.0%; Pred. No. 6e+02; ive 0; Mismatches 0; Indels
                                            Sequence 10 BP; 2 A; 3 C; 3 G; 2 T; 0 U; 0 Other;
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(ROBE/) ROBERTS B L.
(SHAN/) SHANKARA S.
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antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic agents. Host cells that produce the polypeptides can be used to expand and isolate populations of educated, antigen-specific immune effecter cells, e.g. cytotoxic T lymphocytes, and these used for adoptive immunotherapy
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vaccines. Polypeptides encoded by the transcripts are also useful in vaccines; for diagnosing breast cancer and for raising specific antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic agents. Host cells that produce the polypeptides can be used to expand and isolate populations of educated, antigen-specific immune effecter cells, e.g. cytotoxic T lymphocytes, and these used for adoptive immunotherapy
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e.g. therapeutic genes (also ribozymes or antisense sequences), particularly an antigen-encoding sequence for use in gene or cell-based vaccines. Polypeptides encoded by the transcripts are also useful in vaccines; for diagnoship breast cancer and for raising specific antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic agents. Act cells that produce the polypeptides can be used to expand and isolate populations of educated, antigen-specific immune effecter cells, e.g. cytotoxic I lymphocytes, and these used for adoptive
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                                                                                                                                                                        Sequence 10 BP; 3 A; 2 C; 5 G; 0 T; 0 U; 0 Other;
                                                                                                                                                                                                      36.4%; Score 8; DB 1; L 100.0%; Pred. No. 6e+02; ative 0; Mismatches 0
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98US-0089937P.
98US-0090039P.
98US-0090040P.
98US-0090041P.
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19-JUN-1998;
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useful for treatment of (metastatic) breast cancer, while promoters from the transcripts are used to direct expression, in selected cell types, of e.g. therapeutic genes (also ribozymes or antisense sequences) particularly an antigen-encoding sequence for use in gene or cell-based vaccines. Polypeptides encoded by the transcripts are also useful in antibodies; for diagnosing breast cancer and for raising specific antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic and isolate populations of educated, antigen-specific immune effecter cells. immunotherapy 8866666666668888

Sequence 10 BP; 3 A; 3 C; 4 G; 0 T; 0 U; 0 Other;

Gaps ö 36.4%; Score 8; DB 1; Length 10; 100.0%; Pred. No. 6e+02; ive 0; Mismatches 0; Indels Query Match Best Local Similarity 100..

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RESULT 846

AAZ83594

AAZ83594 standard; DNA; 10 BP. AAZ83594;

Metastatic breast tumour cell upregulated transcript tag #2828.

(first entry)

07-APR-2000

Human, metastatic breast tumour tissue; breast cancer; tag; primer; non-metastatic breast tumour tissue; gene therapy; anticancer; antimetastatic; vaccine; diagnosis; ss.

Homo sapiens

WO9965928-A2

23-DEC-1999.

99WO-US013647 18-JUN-1999; 19-JUN-1998;

98US-0089853P. 98US-0089997P. 98US-0090039P. 98US-0090040P. 19-41-WUD-61 , 9661-NUT-6. 19-JUN-1998;

(GENZ) GENZYME CORP. (ROBE/) ROBERTS B L. (SHAN/) SHANKARA S.

Shankara BĽ, Roberts

WPI; 2000-106079/09.

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Isolated polynucleotides differentially expressed between metastatic and non-metastatic breast cancer cells, useful for diagnosis, prevention and treatment of cancer.

Claim 1; Page 134; 219pp; English.

AA280767 to AA283941 represent tags corresponding to distinct transcripts that are preferentially transcribed in the metastatic breast tumour tissue (i.e. are upregulated in metastatic breast tumour cells). AA283942 to AA286677 represent tags corresponding to distinct transcribts that are preferentially transcribed in the primary or non-metastatic breast tumour tissue (i.e. are downregulated in metastatic breast tumour cells). These transcribts can be used for diagnosis, prognosis, monitoring and treatment of breast cancer, particularly where metastatic. Diagnosis is

by standard immunoassays or hybridisation/amplification reactions. Compounds that modulate expression of the transcripts are potentially useful for treatment of metastatic) breast cancer, while promoters from the transcripts are used to direct expression, in selected cell types, of egg. therapeutic genes (also ribozymes or antisense sequence), particularly an antigen-encoding sequence for use in gene or cell-based vaccines. Polypeptides encoded by the transcripts are also useful in antiponding breast cancer and for raising specific agents. Host cells that produce the polypeptides can be used to expand and isolate populations of educated, antigen-specific immune effecter immunotherapy.

Sequence 10 BP; 3 A; 4 C; 2 G; 1 T; 0 U; 0 Other;

Gaps ; DB 1; Length 10; . 6e+02; ches 0; Indels Query Match
36.4%; Score 8; DB 1
Best Local Similarity 100.0%; Pred. No. 6e+
Matches 8; Conservative 0; Mismatches

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ò 셤 RESULT 847 AAZ82358,

AAZ82358 standard; DNA; 10

BP.

(first entry) 07-APR-2000 AAZ82358;

Metastatic breast tumour cell upregulated transcript tag #1592.

Human, metastatic breast tumour tissue; breast cancer; tag; primer; non-metastatic breast tumour tissue; gene therapy; anticancer; antimetastatic; vaccine; diagnosis; ss.

Homo sapiens.

WO9965928-A2

23-DEC-1999

99WO-US013647, 18-JUN-1999; 98US-0089853P. 98US-0089997P. 98US-0090039P. 98US-0090040P. 19-JUN-1998; .9-JUN-1998;

19-JUN-1998; 19-JUN-1998 19-JUN-1998

(GENZ) GENZYME CORP. (ROBE/) ROBERTS B L.

(SHAN/) SHANKARA S.

ŝ Shankara Roberts BL,

WPI; 2000-106079/09.

Isolated polynucleotides differentially expressed between metastatic and non-metastatic breast cancer cells, useful for diagnosis, prevention and treatment of cancer.

Claim 1; Page 101; 219pp; English.

AA280767 to AA283941 represent tags corresponding to distinct transcripts that are preferentially transcribed in the metastatic breast tumour tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942 to AAZ86677 represent tags corresponding to distinct transcribts that are preferentially transcribed in the primary or non-metastatic breast tumour tissue (i.e. are downregulated in metastatic breast tumour cells). These

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treatment of breast cancer, particularly where metastatic. Diagnosis is treatment of breast cancer, particularly where metastatic. Diagnosis is Compounds that modulate expression of the transcripts are potentially useful for treatment of (metastatic) breast cancer, while promoters from the transcripts are used to direct expression, in selected cell types, of e.g. therapeutic genes (also ribozymes or antisense sequences), particularly an antigen-encoding sequence for use in gene or cell-based vaccines; for diagnosing breast cancer and for raising specific antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic agence. Host cells that produce the polypeptides can be used to expand and isolate populations of educated, antigen-specific immune effecter cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
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(ROBE/) ROBERTS B L.
(SHAN/) SHANKARA S.
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                                                                                                                                                                                            immunotherapy
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AA280767 to AA283941 represent tags corresponding to distinct transcripts that are preferentially transcribed in the metastatic breast tumour tissue (i.e. are upregulated in metastatic breast tumour cells). AA283942 to AA286677 represent tags corresponding to distinct transcripts that are

Isolated polynucleotides differentially expressed between metastatic and non-metastatic breast cancer cells, useful for diagnosis, prevention and treatment of cancer.

WPI; 2000-106079/09.

Claim 1; Page 141; 219pp; English.

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preferentially transcribed in the primary or non-metastatic breast tumour tissue (i.e. are downregulated in metastatic breast tumour cells). These transcripts can be used for diagnosis, prognosis, monitoring and treatment of breast cancer, particularly where metastatic. Diagnosis is by standard immunoassays or hybridisation/amplification reactions.

Compounds that modulate expression of the transcripts are potentially useful for treatment of (metastatic) breast cancer, while promoters from the transcripts are used to direct expression, in selected cell types, of e.g. therapeutic genes (also ribozymes or antisense sequences), particularly an antisense necoding sequence for use in gene or cell-based vaccines. Polypeptides encoded by the transcripts are also useful in vaccines; for diagnosing breast cancer and for raising specific antibodies (Ab). Ab are used to defect the polypeptides or as therapeutic and isolate populations of educated, antigen-specific immune effecter centers.
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98US-0089997P.
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                                                                                                                                                                                                                                                                                                                                                    Local Similarity
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19-JUN-1998;
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tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
to AAZ8667, represent tags corresponding to distinct transcripts that are
preferentially transcribed in the primary or non-metastatic breast tumour
tissue (i.e. are downregulated in metastatic breast tumour
tissue (i.e. are downregulated in metastatic breast tumour
transcripts can be used for diagnosis, monitoring and
transcripts can be used for diagnosis, monitoring and
treatment of breast cancer, particularly where metastatic. Diagnosis is
by standard immunoassays or hybridisation/amplification reactions.
Compounds that modulate expression of the transcripts are potentially
useful for treatment of (metastatic) breast cancer while promoters from
the transcripts are used to direct expression, in selected cell types, of
e.g. therapputic genes (also ribozymes or antisense sequences),
particularly an antigen-encoding sequence for use in gene or cell-based
vaccines. Polypeptides encoded by the transcripts are also useful in
antibodies (Ab). Ab are used to detect the polypeptides can be used to expand
and isolate populations of educated, antigen-specific immune effecter
cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
immunotherapy
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(ROBE/) ROBERTS B L.
(SHAN/) SHANKARA S.
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(ROBE/)
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CC TAZ80767 to AZ83941 represent tags corresponding to distinct transcripts that are preferentially transcribed in the metastatic breast tumour cells. AAZ83942 cto AAZ86677 represent tags corresponding to distinct transcripts that are preferentially transcribed in the primary or non-metastatic breast tumour cells). AAZ83942 cto AAZ86677 represent tags corresponding to distinct transcripts that are downregulated in metastatic breast tumour cells). These transcripts can be used for diagnosis, prognosis, monitoring and transcripts can be used for diagnosis, prognosis, monitoring and transcripts can be used for diagnosis, prognosis, monitoring and corresponded that modulate expression of the transcripts are potentially compunds that modulate expression of the transcripts are potentially computed that modulate expression of the transcripts are used to direct expression, in selected cell types, of the transcripts are used to direct expression, in selected cell types, of particularly an antigen-encoding sequence for use in gene or cell-based vaccines; for diagnosing breast cancer and for raising specific antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic agents. Host cells that produce the polypeptides can be used to expand and isolate populations of educated, antigen-specific immune effecter cells, e.g. cytotoxic T lymphocytes, and these used for adoptive immunotherapy
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Best Local Similarity 100.
Matches 8; Conservative
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AAH63186
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Claim 1; Page 189; 219pp; English

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            AAH63239;
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cancer specific gene expression, standardise expression and restore the function of a diseased cell or tissue. The present sequence is one of the transcriptomes described in the exemplification of the invention
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cancer diagnosis; cell specific gene expression; ss.
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such as cancer cell, comprises transcriptomes expressed in particular
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llarity 100.0%; Pred. No. 6e+02;
Conservative 0; Mismatches 0; Indels
                                                                          Query Match 36.4%; Score 8; DB 1; Length 10; Best Local Similarity 100.0%; Pred. No. 6e+02; Matches 8; Conservative 0; Mismatches 0; Indels
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                                                   Sequence 10 BP; 6 A; 3 C; 1 G; 0 T; 0 U; 0 Other;
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Best Local Similarity
8; Conserve
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AAH63239 standard; cDNA; 10 BP

RESULT 853

AAH63239 ID AAH6

AAACAGAA 10

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The present invention describes a method of identifying the type of cell in a sample, involving determining which of the sequences AAH63161-AH64724 is expressed by the cell. The transcriptomes described in the invention are cell-type specific, cancer specific or ubsquitously expressed in humans. They can also be used to screen for drugs, reduce cancer specific gene expression, standardise expression and restore the function of a diseased cell or tissue. The present sequence is one of the transcriptomes described in the exemplification of the invention
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                                                  Human, transcriptome, gene expression pattern, cancer, drug screening;
cancer diagnosis, cell specific gene expression; ss.
Human colon epithelium specific transcriptome sequence SEQ ID NO: 79.
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Best Local Similarity 100.
Matches 8; Conservative
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                                                                                                        New isolated polynucleotides, useful for identifying specific cell type, such as cancer cell, comprises transcriptomes expressed in particular cell types.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; transcriptome; gene expression pattern; cancer; drug screening; cancer diagnosis; cell specific gene expression; ss.
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                                                                                                                                                                                                                                                                                                                         Sequence 10 BP; 0 A; 4 C; 4 G; 2 T; 0 U; 0 Other;
                                                       Kinzler KW;
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                                                                                                                                                                   Claim 13; Page 69; 94pp; English.
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                                                     Vogelstein B,
99US-00448480
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                       SNINGOH SNHOL VINU ( OLYU)
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                                                     Velculescu VE,
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24-NOV-1999;
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The present invention describes a method of identifying the type of cell in a sample, involving determining which of the sequences AAH63111-AAH64724 is expressed by the cell. The transcriptomes described in the invention are cell-type specific, cancer specific or ubiquitously

Claim 1; Page 40; 94pp; English.

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The present invention describes an isolated DNA molecule comprising a coding sequence of a yeast gene selected from a group of 745 NORF (not previously assigned open reading frame; or nonannotated ORF) genes comprising a SAGE (serial analysis of gene expression) tag. Also described are: (1) a method (M1) of using NORF genes to affect the cell cycle comprising administering a NORF gene whose expression varies by at least 10% between any two phases of the cell cycle selected from log phase, S phase and G2/M; (2) a method (M2) for screening candidate antifungal drugs comprising: (a) contacting a test substance with a yeast cell; and (b) monitoring expression of a NORF gene whose expression of the yeast gene is a candidate antifungal drug; (3) a method (M3) for identifying human genes which are involved in cell cycle progression of the yeast gene is a candidate antifungal drug; (3) a method (M3) for identifying a candidate antifungal drug as a member of a contiguous nucleotides of a NORF gene whose expression varies as in M1; and (4) a method (M4) for identifying a candidate drug as a member of a contiguous nucleotides of a NORF gene whose expression in a class of drugs having a characteristic effect on gene expression in a monitoring expression in the yeast cell order dry gene whose expression in a monitoring expression in the yeast cell of at least 1 NORF gene whose expression in a monitoring expression in the yeast cell of at least 1 NORF gene whose
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cancer specific gene expression, standardise expression and restore the function of a diseased cell or tissue. The present sequence is one of the transcriptomes described in the exemplification of the invention
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                                                                                                                                                                                    Gaps
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                                                                                                                                 Query Match 36.4%; Score 8; DB 1; Length 10; Best Local Similarity 100.0%; Pred. No. 6e+02; Matches 8; Conservative 0; Mismatches 0; Indels
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                                                                                          Sequence 10 BP; 7 A; 1 C; 2 G; 0 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                             BP.
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yeast cell comprising contacting a yeast cell with a candidate drug and monitoring expression in the yeast cell of at least 1 NORF gene whose expression is affected by the class of drugs. The NORF genes may be used to study, monitor and affect phases of the cell cycle, the differentially expressed genes may be used as markers of phases of the cell cycle. The methods may be used as markers of phases of the cell cycle. The represent of antifundate drugs which affect the cell represent SAGE tags used in the exemplification of the present invention. AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE method, in the exemplification of the present invention.

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to study, monitor and affect phases of the cell cycle, the differentially expressed genes may be used as markers of phases of the cell cycle. The methods may be used to identify candidate drugs which affect the cell cycle and for identification of antifungal drugs. AAF33268 to AAF44064 represent SAGE tags used in the exemplification of the present invention. AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE method, in the exemplification of the present invention
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                                                                                                                                                                                                                                                                                                                      Score 8; DB 1; Length 10;
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0; Mismatches 0; Indels
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8; Conservative
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AAP35950

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Gaps

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Query Match 36.4%; Score 8; DB 1; Length 10; Best Local Similarity 100.0%; Pred. No. 6e+02; Matches 8; Conservative 0; Mismatches 0; Indels

730 CAGGAGAA 737

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o,

2 CAGGAGAA

Sequence 10 BP; 4 A; 1 C; 5 G; 0 T; 0 U; 0 Other;

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Yeast gene coding sequences comprising NORF genes with serial analysis of gene expression (SAGE) tags, useful for studying, monitoring and affecting phases of the cell cycle.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention describes an isolated DNA molecule comprising a coding sequence of a yeast gene selected from a group of 745 NORF (not previously assigned open reading frame; or nonannotated ORF) gene comprising a SAGE (serial analysis of gene expression) tag. Also described are: (1) a method (M1) of using NORF genes to affect the cell cycle comprising administering a NORF gene whose expression varies by at least 10% between any two phases of the cell cycle selected from log phase, S phase and G2/M; (2) a method (M2) for screening candidate antifungal drugs comprising: (a) contacting a test substance with a yeast cell; and (b) monitoring expression of a NORF gene whose expression the yeast gene is a candidate antifungal drug; (3) a method (M3) for identifying human genes which are involved in cell cycle progression comprising contacting human DNA with a probe which comprises at least 10
                                                                                                                                                                                   Yeast, Saccharomyces cerevisiae; characterisation; cell cycle, NORF; nor previously assigned open reading frame; nonannotated ORF; SAGE; serial analysis of gene expression; antifungal; tag; identification;
                                                                                                                                                  Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:7808.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kinzler K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example; Page 278; 419pp; English.
                                     AAF41069 standard; DNA; 10 BP.
                                                                                                                                                                                                                                                                                                                                                                                                           14-JUN-2000; 2000WO-US016223.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Velculescu V, Vogelstein B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                 99US-00335032.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (UYJO ) UNIV JOHNS HOPKINS.
                                                                                                                 23-MAR-2001 (first entry)
                                                                                                                                                                                                                                                                                            Saccharomyces cerevisiae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-061874/07.
                                                                                                                                                                                                                                                                                                                               WO200077214-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 16-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                      21-DEC-2000.
                                                                            AAF41069;
                    AAF41069/
RESULT
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The present invention describes an isolated DNA molecule comprising a coding sequence of a yeast gene selected from a group of 745 NORF (not previously assigned open reading frame, or nonamnotated ORF) genes comprising a SAGE (serial analysis of gene expression) tag. Also described are: (1) a method (M1) of using NORF genes to affect the cell cycle comprising administering a NORF gene whose expression varies by at least 10% between any two phases of the cell cycle selected from log phase, S phase and G2/M; (2) a method (M2) for screening candidate antifungal drugs comprising; (a) antisting a test substance with a yeast cell; and (b) monitoring expression of a NORF gene whose expression of the yeast gene is a andidate antifungal drug; (3) a method (M3) for identifying human genes which are involved in cell cycle progression comprising contacting human DNA with a probe which comprises at least 10 comprising contacting human DNA with a probe which comprises at least 10 contacting uncelectibes of a NORF gene whose expression varies as in M3; and (4) a method (M4) for identifying a candidate drug as a member of a class of drugs having a characteristic effect on gene expression in a

Yeast gene coding sequences comprising NORF genes with serial analysis of gene expression (SAGE) tags, useful for studying, monitoring and affecting phases of the cell cycle.

Example; Page 96; 419pp; English.

Kinzler K;

Vogelstein B,

Velculescu V,

WPI; 2001-061874/07.

14-JUN-2000; 2000WO-US016223.

21-DEC-2000.

99US-00335032

16-JUN-1999;

(UYJO) UNIV JOHNS HOPKINS

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contiguous nucleotides of a NORF gene whose expression varies as in MI, and (4) a method (M4) for identifying a candidate drug as a member of a class of drugs having a characteristic effect on gene expression in a yeast cell comprising contacting a yeast cell with a candidate drug and monitoring expression in the yeast cell of at least 1 NORF gene whose expression is affected by the class of drugs. The NORF genes may be used to study, monitor and affect phases of the cell cycle, the differentially expressed genes may be used as markers of phases of the cell cycle. The methods may be used to identify candidate drugs which affect the cell cycle and for identification of antifungal drugs. AAP33268 to AAF44664 represent SAGE tags used in the exemplification of the present invention. AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE method, in the exemplification of the present invention.
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Sequence 10 BP; 0 A; 3 C; 1 G; 6 T; 0 U; 0 Other;

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0
         36.4%; Score 8; DB 1; Length 10; 100.0%; Pred. No. 6e+02; ive 0; Mismatches 0; Indels
Query Match
Best Local Similarity 100.0
                                                            736 AAACAGAA 743
                                                            ò
```

Gaps

10 AAACAGAA 3 g

AAF38498 standard; DNA; 10 BP. (first entry) 23-MAR-2001 AAF38498; RESULT 859

Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:5237.

Yeast, Saccharomyces cerevisiae, characterisation, cell cycle, NORF, nor previously assigned open reading frame, nonannotated ORF, SAGE, serial analysis of gene expression, antifungal, tag, identification, linker; PCR primer; ds.

Saccharomyces cerevisiae.

WO200077214-A2.

21-DEC-2000

14-JUN-2000; 2000WO-US016223.

99US-00335032. 16-JJN-1999;

(UYJO) UNIV JOHNS HOPKINS

Velculescu V, Vogelstein B,

WPI; 2001-061874/07.

Kinzler K;

Yeast gene coding sequences comprising NORF genes with serial analysis of gene expression (SAGE) tags, useful for studying, monitoring and affecting phases of the cell cycle.

Example; Page 187; 419pp; English.

The present invention describes an isolated DNA molecule comprising a coding sequence of a yeast gene selected from a group of 745 NORF (not previously assigned open reading frame; or nonannotated ORF) genes comprising a SAGE (serial analysis of gene expression) tag. Also described are: (1) a method (M1) of using NORF genes to affect the cell cycle comprising administering a NORF gene whose expression varies by at least 10% between any two phases of the cell cycle selected from log phase, S phase and G2/M; (2) a method (M2) for screening candidate antitungal drugs comprising: (a) contacting a test substance with a yeast cell; and (b) monitoring expression of a NORF gene whose expression of varies as in M1, where a test substance which modifies the expression of

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the yeast gene is a candidate antifungal drug; (3) a method (W3) for identifying human genes which are involved in cell cycle progression comprising contacting human DNA with a probe which comprises at least 10 contiguous nucleotides of a NORR gene whose expression varies as in M1; and (4) a method (M4) for identifying a candidate drug as a member of a class of drugs having a characteristic effect on gene expression in a yeast cell comprising contacting a yeast cell with a candidate drug and monitoring expression in the yeast cell of at least 1 NORR gene whose expression is affected by the class of drugs. The NORR genes may be used to study, monitor and affect phases of the cell cycle, the differentially captedes may be used to identify candidate drugs which affect the cell cycle and for identification of antifungal drugs. AAR33268 to AAR34064 represent SAGE tags used in the exemplification of the present invention.

AR53362 to AAF33267 represent linkers and PCR primers used in the SAGE method, in the exemplification of the present invention.
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Sequence 10 BP; 6 A; 2 C; 2 G; 0 T; 0 U; 0 Other;

Gaps ö A Score 8; DB 1; Length 10; Similarity 100.0%; Pred. No. 6e+02; 8; Conservative 0; Mismatches 0; Indels Query Match Best Local Similarity Matches 8; Conserv

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RESULT 860 AAF36885

BP. AAF36885 standard; DNA; 10

(first entry) 23-MAR-2001

AAF36885;

Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:3624.

Yeast, Saccharomyces cerevisiae, characterisation, cell cycle, NORF, nor previously assigned open reading frame; nonannotated ORF, SAGE; serial analysis of gene expression; antifungal; tag; identification; linker; PCR primer; ds.

Saccharomyces cerevisiae.

WO200077214-A2.

14-JUN-2000; 2000WO-US016223.

99US-00335032 16-JUN-1999;

(UYJO) UNIV JOHNS HOPKINS.

Kinzler K; Velculescu V, Vogelstein B,

WPI; 2001-061874/07.

Yeast gene coding sequences comprising NORF genes with serial analysis of gene expression (SAGE) tags, useful for studying, monitoring and affecting phases of the cell cycle.

Example; Page 129; 419pp; English.

The present invention describes an isolated DNA molecule comprising a coding sequence of a yeast gene selected from a group of 745 NORF (not previously assigned open reading frame; or nonannotated ORF) genes comprising a SAGE (serial analysis of gene expression) tag. Also described are: (1) a method (M1) of using NORF genes to affect the cell explanation amplitatering a NORF gene whose expression varies by at least 10% between any two phases of the cell cycle selected from log phase, S phase and G2/M; (2) a method (M2) for screening candidate

antifungal drugs comprising: (a) contacting a test substance with a yeast cell; and (b) monitoring expression of a NORF gene whose expression varies as in M1, where a test substance which modifies the expression the yeast gene is a candidate antifungal drug; (3) a method (M3) for identifying human genes which are involved in cell cycle progression comprising contacting human DNA with a probe which comprises at least 10 contiguous nucleotides of a NORF gene whose expression varies as in M1; and (4) a method (M4) for identifying a candidate drug as a member of a class of drugs having a characteristic effect on gene expression in a yeast cell comprising contacting a yeast cell with a candidate drug and monitoring expression in the yeast cell of least 1 NORF gene whose expression is affected by the class of drugs. The NORF gene may be used to study, monitor and affect phases of the cell cycle. The methods may be used as markers of phases of the cell cycle. The methods may be used to identify candidate drugs which affect the cell cycle and for identification of antifungal drugs. AAF33268 to AAF44064 represent SAGE tags used in the exemplification of the present invention.

AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE method, in the exemplification of the present invention.

Sequence 10 BP; 7 A; 1 C; 2 G; 0 T; 0 U; 0 Other;

36.4%; Score 8; DB 1; Length 10; 100.0%; Pred. No. 6e+02; tive 0; Mismatches 0; Indels Conservative 736 AAACAGAA 743 σ Local Similarity les 8; Conserv 2 AAACAGAA Query Match Best Loca Matches ઠ g

RESULT 861

Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:717. AAF33978 standard; DNA; 10 BP AAF33978;

23-MAR-2001 (first entry)

Yeast, Saccharomyces cerevisiae; characterisation; cell cycle; NORF; nor previously assigned open reading frame; nonannotated ORF; SAGE; serial analysis of gene expression; antifungal; tag; identification; linker; PCR primer; ds.

Saccharomyces cerevisiae

WO200077214-A2.

21-DEC-2000.

14-JUN-2000; 2000WO-US016223

99US-00335032 16-JUN-1999;

SNING OTHER HOPKINS

Kinzler K; Velculescu V, Vogelstein B,

WPI; 2001-061874/07.

Yeast gene coding sequences comprising NORF genes with serial analysis of gene expression (SAGE) tags, useful for studying, monitoring and affecting phases of the cell cycle.

Claim 1; Page 400; 419pp; English.

The present invention describes an isolated DNA molecule comprising a coding sequence of a yeast gene selected from a group of 745 NORF (not previously assigned open reading frame; or nonannotated ORF) genes comprising a SAGE (serial analysis of sersession) tag. Also described are: (1) a method (M1) of using NORF genes to affect the cell

cycle comprising administering a NORF gene whose expression varies by at least 10% between any two phases of the cell cycle selected from log phase. S phase and G2/M; (2) a method (M2) for screening candidate antifungal drugs comprising: (a) contacting a test substance with a yeast cell; and (b) monitoring expression of a NORF gene whose expression of the yeast gene is a candidate antifungal drug; (3) a method (M3) for the yeast gene is a candidate antifungal drug; (3) a method (M3) for comprising contacting human DNA with a probe which comprises at least 10 contiguous nucleotides of a NORF gene whose expression varies as in M1; contiguous nucleotides of a NORF gene whose expression in a class of drugs having a characteristic effect on gene expression in a cypast cell comprising contacting a yeast cell with a candidate drug and monitoring expression in the yeast cell of at least 1 NORF gene whose expression is affected by the class of drugs. The NORF genes may be used to identify candidate drugs which affect the cell cycle. The cypressed genes may be used to identify candidate drugs which affect the cell cycle. The methods may be used to identify candidate drugs which affect the cell cycle. The cypresent SAGE to AAPS13267 represent linkers and PCR primers used in the SAGE cell why in the present invention. . 0 Gaps . 0 36.4%; Score 8; DB 1; Length 10; 100.0%; Pred. No. 6e+02; cive 0; Mismatches 0; Indels Sequence 10 BP; 4 A; 1 C; 5 G; 0 T; 0 U; 0 Other; Local Similarity 100. nes 8; Conservative

Query Match Matches

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Gaps

.. 0

730 CAGGAGAA 737 CAGGAGAA 9 N

g

AAF35089 standard; DNA; 10 BP. AAF35089; RESULT 862 AAF35089/c

Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:1828. 23-MAR-2001 (first entry)

Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF; nor previously assigned open reading frame; nonannotated ORF; SAGE; serial analysis of gene expression; antifungal; tag; identification; linker; PCR primer; ds.

Saccharomyces cerevisiae.

WO200077214-A2.

21-DEC-2000.

14-JUN-2000; 2000WO-US016223

99US-00335032 16-JUN-1999; SNINGO UNIV (OLYU)

Kinzler K;

Vogelstein B,

WPI; 2001-061874/07. Velculescu V,

Yeast gene coding sequences comprising NORF genes with serial analysis of gene expression (SACE) tags, useful for studying, monitoring and affecting phases of the cell cycle.

Example; Page 65; 419pp; English.

The present invention describes an isolated DNA molecule comprising a coding sequence of a yeast gene selected from a group of 745 NORF (not

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comprising a SAGE (serial analysis of gene expression) tag. Also described are: (1) a method (MI) of using Norge genes to affect the cell cycle comprising administerings of gene expression) tag. Also cycle comprising administerings of gene expression varies by at least 10% between any two phases of the cell cycle selected from log phase, S phase and G2/M; (2) a method (M2) for screening candidate antifungal drugs comprising: (a) contacting a test substance with a yeast cell; and (b) monitoring expression of a NORF gene whose expression of the yeast gene is a candidate antifungal drug; (3) a method (M3) for identifying human genes which are involved in cell cycle progression of the yeast gene is a candidate antifungal drug; (3) a method (M3) for identifying human genes which are involved in cell cycle progression contiguous nuclecides of a NORF gene whose expression varies as in M1; and (4) a method (M4) for identifying a candidate drug as a member of a class of drugs having a characteristic effect on gene expression in a yeast cell with a candidate drug and conticoring expression in the yeast cell of at least 1 NORF gene whose expression is affected by the class of drugs. The NORF gene may be used to identify candidate drugs which affect the cell cycle to study, monitoring expression in the yeast cell cycle, the differentially expressed genes may be used as markers of phases of the cell cycle. The methods may be used to identify candidate drugs which affect the cell cycle and for identification of antifungal drugs. Affect the cell cycle and for identification of antifungal drugs which affect the cell cycle and for identification of the present invention.

AAF33262 to AAF33267 represent linkers and PCR primers used in the exemplification of the present invention.
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Sequence 10 BP; 1 A; 2 C; 2 G; 5 T; 0 U; 0 Other;

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36.4%; Score 8; DB 1; Length 10; 100.0%; Pred. No. 6e+02; ive 0; Mismatches 0; Indels
                      Local Similarity 100.
nes 8; Conservative
  Query Match
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734 AGAAACAG 741 8 AGAAACAG 1 ò

ABK24254 standard; DNA; 10 BP. ABK24254; RESULT 863

(first entry) 09-APR-2002

Human, retinaldehyde-binding protein 1; ss; RLBP1; haplotype; primer; genotyping; probe; autosomal recessive retinitis pigmentosa; arRP; PCR; chromosome 15q26; transgenic; ASO; allele specific oligonucleotide.

Retinaldehyde-binding protein 1 ASO primer extension primer #27.

Homo sapiens,

WO200192278-A2

06-DEC-2001.

29-MAY-2001; 2001WO-US017252.

26-MAY-2000; 2000US-0207618P.

(GENA-) GENAISSANCE PHARM INC.

Koshy B; Choi JY, Kazemi A,

WPI; 2002-122053/16.

New genetic variants having polymorphisms in the retinaldehyde-binding protein 1 gene, useful for studying the function of and for expressing RLBP1 protein for use in screening drugs for treating diseases related RLBP1 activity.

Claim 18; Page 14; 107pp; English.

The invention relates to an isolated polynuclectide, which comprises genes and haplotypes of the retinaledwide-binding protein I (RLBP1) gene. The polynuclectide comprises polymorphic aites in the RLBP1 gene, which cored in the gene. Also included are methods for haplotyping or located in the gene. Also included are methods for haplotyping or cored in the RLBP1 gene of an individual, a method for predicting a haplotype pair for the RLBP1 gene of an individual, a method for predicting an association between a trait and at least one haplotype or individual comprising at least one of periotyping or pair of the RLBP1 gene of an individual comprising at least one of periotyping or comprising a set of cigomorcheoide designed to genotyping at each of comprising a set of cigomorcheoides designed to genotyping or comprising a set of cigomorcheoides designed to genotyping or protein encoded by the first nucleoide sequence or expresses a RLBP1 protein encoded by the first nucleoide sequence or expresses a RLBP1 protein encoded by the first nucleoide sequence or expresses a RLBP1 protein encoded by the polymorphic variant sequence, an isolated polymorphic or screening for drugs targeting the artitate antibody, a method for screening for drugs targeting the artitate polymorphic and accomputer system for storing and analysing polymorphics, and a computer system for storing and analysing polymorphics and function of RLBP1, and in expressing RLBP1 protein for use in screening candidated drugs for the RLBP1 gene is useful in studying the expression and function of RLBP1, and in expressing RLBP1 protein for use in screening candidated drugs in the drug discovery and development process, including target or steps in the drug discovery and development process, including target or steps in the drug discovery and development process, including target or predicted to be associated with RLBP1 accidited to general apportance or expension of the RLBP1 isogenes in well for determining whether an individual has one of the halp or present ö Gaps . 0 36.4%; Score 8; DB 1; Length 10; 100.0%; Pred. No. 6e+02; ative 0; Mismatches 0; Indels Sequence 10 BP; 2 A; 4 C; 2 G; 2 T; 0 U; 0 Other; the primer extension method Ouery Match Best Local Similarity 100.، اماد 8; Conservative

à g RESULT 864 ABK68700

ABK68700 standard; DNA; 10 BP.

ABK68700;

02-JUL-2002 (first entry)

Human SCYA2 gene allele-specific oligonucleotide PCR primer #8.

Human, small inducible cytokine A2; SCYA2; primer; ss; haplotype pair; haplotyping; atherosclerosis; antiarteriosclerotic; gene therapy; single nucleotide polymorphism; genotyping; drug screening; PCR; chromosome 17q11.2-q21.1.

Homo sapiens.

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WO200218413-A2

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The invention relates to single nuclectide polymorphisms in the gene encoding human small inducible cytokine A2 (SCYA2) polypeptide. A method for haplotyping the SCYA2 gene in an individual comprises identifying the nuclectide at one or more polymorphic sites and determining whether one of the specification or whether both copies are defined by a haplotypes given in the specification or whether both copies are defined by a haplotype pair. This method is useful in gencyping, whereby all possible haplotype pair. This method is useful in gencyping, whereby all possible haplotype can be assigned to specific genctypes. An association between a trait and a haplotype or haplotype pair of the haplotype or haplotype pair in a reference population, where a higher haplotype or rapit may be a propulation indicates the trait is associated with the haplotype pair in a reference population, where a higher haplotype or haplotype pair. SCYA2 and its corresponding DNA are used for studying the expression and function of SCYA2, and in screening for candidate drugs to treat diseases related to SCYA2 and ilele-specific coligonucleotide PCR primers used for detecting SCYA2 gene polymorphisms
                                                                                                                                                                                                                                                                               New genetic variants having polymorphisms in the small inducible cytokine A1 (SCYA2 ) gene, useful for studying the function of SCYA2 , and for treating disorders affected by expression or function of the SCYA2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 10 BP; 5 A; 1 C; 4 G; 0 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                         Claim 19; Page 13; 58pp; English
                                                                                                                                         (GENA-) GENAISSANCE PHARM INC.
                                                                                             28-AUG-2000; 2000US-0228496P.
                                                28-AUG-2001; 2001WO-US026899.
                                                                                                                                                                                           Anastasio AE, Finkel K,
                                                                                                                                                                                                                                         WPI; 2002-339655/37.
07-MAR-2002
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Score 8; DB 1; Length 10;
Pred. No. 6e+02;
0; Mismatches 0; Indels
  36.4%; S
100.0%;
                               8; Conservative
                                                          730 CAGGAGAA 737
Query Match
Best Local Similarity
Matches 8; Conserv
                                                                                     CAGGAGAA
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Human maturation/activation dendritic cell expression gene tag #162 ABL42788 standard; cDNA; 10 BP (first entry) 12-APR-2002 ABL42788 RESULT 865
ABL42788
XX
AC
ABL4278
DT
12-APRXX
EW
Human
XX
Human

Human, maturation/activation dendritic cell expression gene, tag, maturation, activation, dendritic cell; ss.

sapiens

JP2001327293-A.

27-NOV-2001

22-MAY-2000; 2000JP-00150562.

22-MAY-2000; 2000JP-00150562

(KAGA-) KAGAKU GLJUTSU SHINKO JIGYODAN.

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The present invention describes a human maturation/activation dendritic cell (DC) expression gene group consisting of 100 genes which show the highest expression among the genes expressed in human maturation/ activation DC. Also described are: (1) a protein expressed by the above the muman maturation/activation DC expression gene; (2) an antibody against the protein, and (3) an antagonist against the expression of each gene belonging to the above gene group. The gene group is useful for the treatment and the diagnosis of various human diseases related to human DC. Abi4267 to Abi4226 represent specifically claimed human maturation/activation DC expression gene tags from the present invention
                                                            Human maturation/activation dendritic cell expression gene group.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                .
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                                                                                                                                                                                                                                                                                                                                                                                                                 Score 8; DB 1; Length 10;
Pred. No. 6e+02;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                           Sequence 10 BP; 2 A; 3 C; 4 G; 1 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                    36.4%; SCUL
100.0%; Pred
0; N
                                                                                                    Claim 10; Page 13; 41pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                               Ouery Match
Best Local Similarity luv...
1.00 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        728 GCCAGGAG 735
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 GCCAGGAG 8
                 WPI; 2002-127070/17
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Lee HH;

Kumar AM,

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Gaps

RESULT 866 AAL48074/C

AAL48074 standard; DNA; 10 BP.

AAL48074;

(first entry) 27-SEP-2002 Human CSF3 gene allele specific primer extension oligo SEQ ID NO: 52

Human; colony stimulating factor 3(granulocyte); CSF3; SNP; isogene; chromosome 17q11-12; single nucleotide polymorphism; immunostimulant; neutropenia; promyelocytic leukaemia; haematological disorder; gene therapy; PCR; primer extension oligonucleotide; ss.

Homo sapiens

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Gaps

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WO200194364-A2

13-DEC-2001.

11-JUN-2001; 2001WO-US018813.

09-JUN-2000; 2000US-0210380P.

(GENA-) GENAISSANCE PHARM INC.

Sausker EA; Messer C, Kazemi A, Duda A,

WPI; 2002-566435/60.

for New variants of colony stimulating factor 3 (CSF3) isogenes, useful fimproving efficiency and reliability in the development of drugs for treating diseases associated with CSF3 activity e.g. neutropenia.

Claim 19; Page 13; 68pp; English.

The present invention provides the protein, gene and cDNA sequences of human colony stimulating factor 3 (granulocyte) CSF3. Also described are single nucleotide polymorphisms (SNBs) identified within these sequences. The sequences can be used in the treatment of neutropenia, promyelocytic leukaemia and haematological disorders. The present sequence is an allele specific primer extension oligonucleotide used to isolate the coding sequences of the invention

(first entry)

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SAGE tag; serial analysis of gene expression; human; Th1 cell; activated T cell; T lymphocyte; immune response; expression pattern; preferential expression; immune disorder; ss.
                                                                                                                                                                                                                                                                                                                               Human activated Th1 and Th2 cell expression gene group, diagnosis and treatment of Th1 and Th2-related diseases.
                                                                                                                                                                                                                                                                             (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
                                                     Human COP9 SAGE tag, SEQ ID NO:204.
                                                                                                                                                                                                                                                                                                                                                                          Claim 19; Page 11; 60pp; Japanese.
                                                                                                                                                                                                                       19-DEC-2000; 2000JP-00385816.
                                                                                                                                                                                                                                                 19-DEC-2000; 2000JP-00385816.
                                                                                                                                                                                                                                                                                                      WPI; 2002-594261/64.
                                                                                                                                                                JP2002186482-A.
                                                                                                                                      Homo sapiens.
                         29-NOV-2002
ABV78493;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to a novel human 6-phosphofructo-2-kinase/ fructose -2,6-biphosphatase 2 (PFKFE2) isogene. The PFKFE2 of the invention has cytostatic and antidiabetic activity. The polymucleotides may have a use in gene therapy. The identified candidate agents targeting PFKFE2, are useful for treating cancer and diabetes. The methods of the invention are useful for improving the efficiency and reliability of several steps in the discovery and development of Gungs for treating diseases associated with PFKFE2 activity. The present sequence represents a PCR primer used in the invention to detect PFKFE2 gene polymorphisms by primer extension
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gene
nt of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New 6-phosphofruoto-2-kinase/fructose-2,6-bisphosphatase 2 (PFKFB2) gene variants, for improving efficiency and reliability in the development of drugs for treating diseases associated with PFKFB2 activity e.g. cancer.
                                                                                                                                                                                                                                                                                                  Human; 6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 2; PFKFB2; cytostatic; antidiabetic; gene therapy; cancer; diabetes; ss; PCR; primer; polymorphism.
                                                                  Gaps
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                                    Query Match
Best Local Similarity 100.0%; Pred. No. 6e+02;
Matches 8; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     36.4%; Score 8; DB 1; Length 10; 100.0%; Pred. No. 6e+02; Live 0; Mismatches 0; Indels
           Sequence 10 BP; 1 A; 4 C; 1 G; 4 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 10 BP; 5 A; 2 C; 2 G; 1 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 17; Page 14; 95pp; English
                                                                                                                                                                                         ABV99817 standard; DNA; 10 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (GENA-) GENAISSANCE PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                              07-JUN-2001; 2001WO-US018458.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        07-JUN-2000; 2000US-0209935P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Koshy B;
                                                                                                                                                                                                                                                                            Human PFKFB2 PCR primer #19.
                                                                                                                                                                                                                                                (first entry)
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Best Local Similarity 100.
Matches 8; Conservative
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                                                                                            730 CAGGAGAA 737
                                                                                                                     10 CAGGAGAA 3
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                                                                                                                                                                                                                                                                                                                                                                                       WO200194363-A2.
                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
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                                                                                                                                                                                                                    ABV99817;
                                                                                                                                                               RESULT 867
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The invention relates to SAGE (serial analysis of gene expression) tags representing groups of genes which are expressed in activated human Th1 and/or Th2 cells. The SAGE tags of this invention consist of a sequence of 10 nucleotides located downstream of the 5'-CATG-3' sequence motif lying nearest to the polyA region of cDNAs derived from a variety of genes. These tags serve to uniquely identify each transcript and can thus be used to analyse the pattern of gene expression in particular cell types. The invention also relates to proceins encoded by the genes expressed in Th1 and/or Th2 cells, antibodies against these proteins, and inhibitors of the expression of groups of genes that are expressed in cither or both the two cell types. Groups of genes expressed in Th1 and/or Th2 cell types may be used for the diagnosis and treatment of Th1 and/or Th2 cells sequences ABV78390-ABV78560 are SAGE tags representing 171 genes which are more highly expressed in Th1 cells
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         36.4%; Score 8; DB 1; Length 10; 100.0%; Pred. No. 6e+02; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 10 BP; 4 A; 2 C; 4 G; 0 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          729 CCAGGAGA 736
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ABK23469/c
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ABV78493 standard; cDNA; 10 BP.

RESULT 868 ABV78493 ID ABV7 XX

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The present invention relates to a nucleic acid library comprising mycdependent downstream genes or their functional fragments essentially capable of supporting a neoplastic character of cancer such as growth, invasion or spread. These myc target or tag sequences are identified by SAGE (serial analysis of gene expression). The library is useful to new diagnoses and treatments for cancer. The invention is also useful to enhance production of recombinant proteins in a production system with high expression of endogenous or transfected myc oncogenes. ABK23412-ABK23328 represent transcript tag DNA sequences that are activated or repressed by N-myc in human neuroblastoma
                                                                                                                                                                                                                               A new nucleic acid library of myc-dependent downstream genes capable of supporting a necplastic characteristic of cancer is useful to find new therapies and diagnoses for cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; ss; primer; interleukin-6; ILG; myeloma; arthritis; CAD; Kaposi sarcoma; coronary artery disease; inflammatory cytokine; hypercalcaemia; bone disease; inflammatory disease; HIV; PCR; human immunodeficiency virus infection; stunted growth; isogene; systemic onset juvenile chronic arthritis; haplotype; genotype; chromosome 7p21-p15; gene therapy; primer extension; SNP; single nucleotide polymorphism.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 36.4%; Score 8; DB 1; Length 10; 100.0%; Pred. No. 6e+02; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 10 BP; 0 A; 4 C; 4 G; 2 T; 0 U; 0 Other;
                                                                                                                              (UYAM-) UNIV AMSTERDAM ACAD ZIEKENHUIS BIJ VAN
                                                                                                                                                                                                                                                                                                 Disclosure; Page 50; 69pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABK96609 standard; DNA; 10 BP.
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21-AUG-2001; 2001US-0313963P.
                                               11-MAY-2001; 2001WO-NL000361.
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                                                                              11-MAY-2000; 2000EP-00201698
29-JUN-2000; 2000EP-00202284
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Best Local Similarity 100...
Best as 8; Conservative
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                                                                                                                                                                 Caron HN;
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                                                                                                                                                                                                 WPI; 2002-066603/09.
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                                                                                                                                                                 Versteeg R,
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               15-NOV-2001
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The invention relates to a polymucleotide comprising a first nucleotide sequence (NS1) comprising a IL6 (interleukin-6, an inflammatory cytokine) isogenes salected from isogenes 1-11 and 13-18 given in the specification, where each isogene comprises the regions of NS1 and is further defined by the corresponding sequence of polymorphisms whose locations and identifies are defined in the specification (PS2-PS6, PS8 and PS10-PS17), or a second nucleotide sequence of NS2 complementary to NS1.

Consider the corresponding sequence comprises a coding sequence for an IL6 predicting the haplotype/genotype) of the IL6 gene of an individual, or isogene. Also included are methods of haplotyping of an employe pair of the IL6 gene, a recombinant non-human organism (II) cramploxype pair of the IL6 gene, a recombinant non-human organism (III) cramploxype pair of the IL6 gene, a recombinant non-human organism (III) cramploxype pair of the IL6 gene, a recombinant non-human organism (III) cramploxype pair of the IL6 gene, a recombinant non-human organism (III) cramploxype pair of the IL6 gene, a recombinant non-human organism (III) cramploxype pair of the IL6 gene, a recombinant non-human organism (III) cramploxype pair of the IL6 gene, a recombinant non-human organism (III) cramploxype pair of the IL6 gene, and a least 10 and containing one of the identified single-nucleotide polymorphisms (SNP), an isolated polymorphism (III) are polymorphisms (SNP), an isolated containing one of polymorphic variant of IL6, an isolated monoclonal antibody specific for the IL6 gene, and a genome anthology for the IL6 gene which is a polymorphic variant is useful in screening for drugs targeting the reficiency and reliability in the discovery and development of drugs and in the validation of IL6 are useful for improving the efficiency and reliability in the discovery and development of drugs and in the validation of IL6 and in expressing the method of chromosome of polymorphism using the method of primer extension craft of the IL6 isogene is usef
                                                                                                          Genetic variants of interleukin-6 isogenes for improving efficiency and reliability in drug development for treating myeloma, coronary artery disease, arthritis and Kaposi sarcoma.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; ss; primer; interleukin-6; IL6; myeloma, arthritis; CAD; Kapos; sarcoma; coronary artery disease; inflammatory ortokine; hypercalcaenia, bone disease; inflammatory disease, HIV; PCR; human immunodeficiency virus infection; stunted growth; isogene; systemic onset juvenile chronic arthritis; haplotype; genotype; chromosome 7p21-p15; gene therapy; primer extension; SNP; single nucleotide polymorphism.
Lachowicz M;
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Denton RR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 10 BP; 0 A; 3 C; 4 G; 3 T; 0 U; 0 Other;
  KM, Chew A,
Sausker EA;
                                                                                                                                                                                                               Claim 17; Page 16; 86pp; English
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  Bieglecki
Parks KE,
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                                                                     WPI; 2002-519290/55.
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ses 8; Conserv
  Bentivegna SC,
Nandabalan K,
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Primer-extension oligonucleotide #14 to detect human DNAL4 polymorphisms.
                                                                                                                     Human, single nucleotide polymorphism; SNP; DNAL4; chromosome 22q13.1;
dynein axonemal light polypeptide chain 4; haplotyping; genotyping;
neuroprotective; neurological disorder; primer; ss.
                                                                                                                                                                                                                                                                                                                                                                         (GENA-) GENAISSANCE PHARM INC.
                                                                                                                                                                                                                                                                                                   16-APR-2001; 2001WO-US012304.
                                                                                                                                                                                                                                                                                                                                     17-APR-2000; 2000US-0197460P.
                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2002-075065/10.
                                                                                                                                                                                                                              WO200179235-A2
                                                                                                                                                                                                                                                                                                                                                                                                          Bentivegna SC,
                                                                                                                                                                                              Homo sapiens.
                                                    26-MAR-2002
                                                                                                                                                                                                                                                                  25-OCT-2001
                  AAS19962;
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to a polynucleotide comprising a first mucleotide sequence (NSI) comprising a ILG (interleukin-6, an inflammatory cytokine) sequence (NSI) comprising a ILG (interleukin-6, an inflammatory cytokine) there each isogene selected from isogenes 1-11 and 13-18 given in the specification, where each isogene comprises the regions of NSI and is further defined by the corresponding sequence of polymorphisms whose locations and chief in the sequence of NS2. complementary to NSI.

Alternatively, the sequence comprises a codaing sequence for an ILG predicting the haplotype/genotype) of the ILG gene of an individual, identifying an association between a trait and at least one haplotype or haplotype pair of the ILG gene, a recombinant non-human organism (III) remainsformed or transfected with the ILG polymorlocide to detecting a polymorphism in the ILG gene, a recombinant non-human organism (III) applying polymorphism in the ILG gene, a recombinant non-human organism (III) ragment of the ILG seque comprising at least 10 and containing one of the identified single- nucleotide polymorphisms (SNP), an isolated corresponding to the identified single- nucleotide polymorphisms (SNP), an isolated corresponding to the ILG gene, and a genome anthology for the ILG gene, The ILG gene, and a genome anthology for the ILG gene, The ILG gene, and a genome anthology for the ILG gene, and a genome anthology for the ILG gene, The ILG gene, and a genome anthology for the ILG gene, The ILG gene, and a genome anthology for the ILG gene, and a genome anthology for the ILG gene, The ILG gene, are useful for improving myeloma, correnty arrey disease (CAD), are useful for improving the efficiency and reliability in the discovery and development of causing the efficiency and reliability in the discovery and development of drugs and in the variation of ILG as a drug target. The ILG isogene is useful in diagnostic, prognostic and therapeutic methods and in expressing and in the variation of ILG isogene is useful in diagnostic, prog
                                                                                                                                                                                                                                                                                                                                 Genetic variants of interleukin-6 isogenes for improving efficiency an reliability in drug development for treating myeloma, coronary artery disease, arthritis and Kaposi sarcoma.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 10 BP; 0 A; 4 C; 1 G; 5 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                        Claim 17; Page 16; 86pp; English.
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                                                                                                                                                                                                             (GENA-) GENAISSANCE PHARM INC
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21-AUG-2001; 2001US-0313963P.
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Parks KE,
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Nandabalan K,
                                                    WO200238586-A2.
                  Homo sapiens.
                                                                                    16-MAY-2002.
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Choi JY,

Chew A,

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                                                                                                                                                                                     The present invention relates to novel single nucleotide polymorphisms (SNPs) in the human dynein, axonemal light polypeptide chain 4 (DNAL4) gene located on chromosome 22q13.1, and methods for haplotyping and/or genotyping the DNAL4 gene. The methods of the invention make use of allele-specific oligonucleotides (ASOS) as probes and primers and/or primer-extension oligonucleotides for detecting the DNAL4 gene polymorphisms. The polymucleotides and screened compounds are useful for the treatment of diseases associated with DNAL4 activity, such as neurological disorders. AAS19949-AAS19976 represent primer-extension
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human, PCR; ss, allele-specific, SNP, single nucleotide polymorphism, cerberus 1 homologue; cysteine knot superfamily, CER1; drug screening; developmental disorder; polymorphic site; CER1 haplotyping; primer.
Genotyping human dynein, axonemal light polypeptide chain 4 gene of individual, useful for determining haplotype of individual, comprises determining identity of nucleotide pair at specific polymorphic sites
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 10;
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100.0%; Pred. No. 6e+02;
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                                                                                                                                 Claim 18; Page 14; 79pp; English.
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Best Local Similarity 100.
Matches 8; Conservative
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                                                                                   two copies of gene.
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Local Similarity 100. Les 8; Conservative 730 CAGGAGAA 737

Matches

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10 CAGGAGAA

AAS19962 standard; DNA; 10 BP.

RESULT 872

AAS19962 ID AAS1

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Human; matrix metalloproteinase 13 (collagenase 3); MMP13; cancer;
arthritis; haplotype; single nucleotide polymorphism; SNP; enzyme;
cytostatic; antiarthritic; gene therapy; chromosome 11q22.3; PCR primer;
                                                                                                                                                                                                                                                                                                                                                                              Human MMP13 gene allele specific primer extension oligo SEQ ID NO: 92.
                                                                                                                                                                                                                                                                                                                                   ABL45804 standard; DNA; 10 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (GENA-) GENAISSANCE PHARM INC
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17-AUG-2000; 2000WO-US022693.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13-JUL-2001; 2001WO-US022238
                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                8; Conservative
                                                                                                                                                                                                                                                                               739 CAGAACAC 746
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Finkel K, Kliem SE,
                                                                                 WPI; 2002-435527/46.
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Best Local Similarity
Matches 8; Conserv
                                                                 Shah N;
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       25-APR-2002
                                                                  Kazemi A,
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The present invention provides the cDNA, protein and gene fragments of the human matrix metalloproteinase 13 (collagenase 3) (MMP13). Also provided are single nucleotide polymorphisms (SNPs) identified within the sequences. The sequences can be used to haplotype an individual and in the treatment of cancer and arthritis, including metastatic cancers. The present sequence is a primer extension oligonucleotide for the MMP13 gene, which is found on chromosome 11q22.3
                   Novel genetic variants of matrix metalloproteinase 13 (collagenase 3) gene useful in studying expression and function of the protein, and for screening drugs to treat diseases e.g. cancer and arthritis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   36.4%; Score 8; DB 1; Length 10; 100.0%; Pred. No. 6e+02; artive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 10 BP; 2 A; 1 C; 1 G; 6 T; 0 U; 0 Other;
                                                                                                                                                  Claim 18; Page 15; 110pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               736 AAACAGAA 743
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10 AAACAGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABN81268;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 875
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABN81268/
The invention relates to the identification of 13 novel polymorphic sites superfamily) (CER1) gene. The invention also comprises the amino acciding sequence of CER1. The CER1 protein is useful for screening and coding sequence of CER1. The CER1 protein is useful for screening drugs that target CER1 - for the treatment of developmental disorders. The CER1 for screening and testing of drugs targeted against CER1 isogenes, for screening the efficacy of therapeutic agents for treating developmental useful for supplicitive in the invention are useful for haplotyping the CER1 gene of an individual. The present DNA sequence represents a human CER1 gene primer-extension oligonucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                             Novel genetic variants of Cerberus 1 (Xenopus laevis) Homolog (Cysteine Knot Superfamily) (CER1) isogenes, useful for improving efficiency and reliability in drug development for treating developmental disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 10 BP; 1 A; 1 C; 3 G; 5 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 16; Page 14; 75pp; English.
                                                                                                                                                                                                                    (GENA-) GENAISSANCE PHARM INC
                                                                                           19-OCT-2001; 2001WO-US046100.
                                                                                                                                                         19-OCT-2000; 2000US-0241634P.
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Gaps

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The present invention relates to a novel isolated polymucleotide comprising a nucleotide sequence which is a polymorphic variant of a reference sequence for cytochrome P450, subfamily I (dioxin-inducible), polypeptide 1 (glaucoma 3, primary infantile), (CYPIBI) gene or its fragment, or a polymorphic variant of a reference sequence for a CYPIBI cDNA or its fragment. The polypeptide of the invention has cytostatic and ophthalmological activity. The polymucleotide may have a use in gene therapy, and antisense gene therapy. The polymorphism and haplotype data of the invention are useful for validating whether CYPIBI is a suitable target for drugs to treat breast cancer and primary congenital glaucoma,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New genetic variants of cytochrome P450, subfamily I dioxin-inducible, polypeptide 1, glaucoma 3, primary infantile gene, CYPIB1 for treatment and expressing CYPIB1 protein for use in identifying drugs to breast
                                                                                                              Oligonucleotide primer #19 for detecting CYP1B1 gene polymorphisms
                                                                                                                                                   Cytochrome P450; dioxin-inducible, glaucoma 3; CYP1B1; cytostatic; ophthalmological; gene therapy; polymorphism; breast cancer; PCR; primary congenital glaucoma; primer extension; primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 17; Page 16; 96pp; English.
ABN81268 standard; DNA; 10 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                             (GENA-) GENAISSANCE PHARM INC.
                                                                                                                                                                                                                                                                                                                                                   15-OCT-2001; 2001WO-US042726.
                                                                                                                                                                                                                                                                                                                                                                                    13-OCT-2000; 2000US-0240211P.
                                                                         16-AUG-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2002-426265/45.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Han J, Kliem SE,
                                                                                                                                                                                                                                                                        WO200230951-A2
                                                                                                                                                                                                                                     Homo sapiens.
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Tanguay DA;

Messer C,

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RESULT 877
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to a reporter construct comprising: (a) an estrogen response segment having 5 or more estrogen response elements (ERE); (b) a promoter segment having at least one promoter nucleic acid sequence; and (c) a nucleotide sequence that encodes a reporter polyapptide, where the nucleotide sequence is operably linked to the promoter segment and the estrogen response segment. The reporter construct and vector are useful in identifying and isolating estrogen-responsive cells. The methods are useful in inhibiting the proliferation or survival of estrogen-responsive breast cancer calls or in enhancing the proliferation or survival of estrogen-receptor non-expressing, estrogen-non-responsive cells.

Sequences ACCT8140-75 represent SAGE tags for transcripts specifically or most abundantly expressed in normal estrogen responsive cells
screening for such drugs and reducing bias in clinical trials of such drugs. The sequence represents an oligonucleotide primer, used in the invention to detect polymorphisms in the CYPIB1 gene by primer extension
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New reporter construct for identifying and isolating estrogen-responsive cells comprises an estrogen response segment, a promoter segment and a nucleotide sequence that encodes a reporter polypeptide.
                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                             ERE; reporter construct; estrogen response element; cytostatic; rat; gene therapy; breast cancer; SAGE; ds.
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0
                                                                                                        0; Indels
                                                                           36.4%; Score 8; DB 1; Length 10; 100.0%; Pred. No. 6e+02;
                                                                                                                                                                                                                                                                                                    Normal estrogen responsive cells derived SAGE tag.
                                                    Sequence 10 BP; 0 A; 4 C; 0 G; 6 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       36.4%; Score 8; DB 1; L
100.0%; Pred. No. 6e+02;
tive 0; Mismatches 0
                                                                                     100.0%; Prec. ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (DAND ) DANA FARBER CANCER INST INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 4; Page 32; 51pp; English.
                                                                                                                                                                                                                        ACC78771 standard; DNA; 10 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          09-NOV-2001; 2001US-0338136P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                08-NOV-2002; 2002WO-US035901
                                                                                                                                                                                                                                                                          (first entry)
                                                                                         Best Local Similarity 100.
Matches 8; Conservative
                                                                                                                                731 AGGAGAAA 738
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Best Local Similarity
Matches 8; Conservat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pankaj S;
                                                                                                                                                       10 AGGAGAAA 3
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                                                                                                                                                                                                                                                                                                                                                                                           WO2003042364-A2.
                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
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                                                                                                                                                                                                                                                   ACC78771;
                                                                                Query Match
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Making small interfering RNA useful for treating Huntington's chorea by incorporating nucleotides into siRNA such that the siRNA has a sequence substantially identical to at least a portion of selected target gene.

Claim 38; Fig 3; 85pp; English.

Pasloske

Pallotta V,

Jarvis R,

Ford LP,

Brown D,

(AMBI-) AMBION INC.

WPI; 2003-689529/65.

31-JAN-2003; 2003WO-US003023. 01-FEB-2002; 2002US-035332P.

WO2003064621-A2

07-AUG-2003

Small interfering RNA; siRNA; RNA interference application; anti-viral; transplant rejection; autosomal dominant genetic disease; anti-tumour; inherited disorder; Huntington's chorea; therapy; ds.

Leader DNA #2 used in the synthesis of siRNA of increased potency.

(first entry)

20-NOV-2003

AAD58112;

BP.

AAD58112 standard; DNA; 10

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The invention relates to a method for making small interfering RNA (siRNA) of increased potency. The method involves obtaining nuclectides and incorporating the nucleotides into siRNA as chat RNA duplex of 15-30 contiguous nucleotides is formed, where the siRNA has a sequence substantially identical to at least a portion of a selected target gene. The method is also useful for attenuating the expression of a target gene in a cell. The siRNA is useful in RNA interference applications which materials and applications. Medical applications include an include a wide range of research, industrial and medical processes, materials and applications and therapies, and compositions and therapies, and compositions and therapies for inherited disorders. siRNA is also useful in therapies for treating autosomal dominant genetic disease such as Huntington's chorea and management of transplant rejection. The present sequence is a leader DNA used in the synthesis of siRNA of increased potency
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Stimulus-responsive DNA organization oligonucleotide #3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 10 BP; 4 A; 2 C; 4 G; 0 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADD71433 standard; DNA; 10 BP.
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ID ADD714
XX ADD714
XX IS-JAN
DT 15-JAN
XX DE Stimul
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Gaps ö

0; Indels Length 10;

Conservative

729 CCAGGAGA 736

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CCAGGAGA 1

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Example; Page 12; 32pp; English.
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                                                                                                                                                                                                                                                                  99US-0150637P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABA01034 standard; DNA; 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8, Conservative
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         *tag=
                                                                        *tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           731 AGGAGAAA 738
                                                                                                                                                                                                                                                                                                                                 WPI; 2001-265835/27
                                                                                                                                                                                                                                                                                      (GARN/) GARNER P P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                     WO200114398-A1
                                                                                                                                                                                                                                                                    25-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unidentified
                                                              Misc binding
Misc_binding
                                                                                                                           Misc_binding
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                                                                                                                                                                                                                         01-MAR-2001
                                                                                                                                                                                                                                                                                                            Garner PP;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complex
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ABA01034/
SXXXXXXXXXX
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                                                                                                                                                                                                                                                                           The invention relates to a stimulus-responsive DNA organization undergoing formation/dissociation of a supercoil or rotation in response to an external stimulus and comprises a number of plasmid DNAs ligated in it. The DNA organization is applicable in various materials and body parts or medical micromachines e.g. artificial muscles. This sequence represents an oligonucleotide used in the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /bound_moiety= "Alpha-helical peptide nucleic acid
(alphaPNA) shown in AAB74017"
/note= "this nucleotide hybridises to the thymine at
position 15 of AB74017 to form an alphaPNA.DNA complex"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AlphaPNA, alpha-helical peptide nucleic acid, alphaPNA.DNA complex; solid-phase peptide synthesis; molecular switching; diagnosis; therapy; backbone 2; b2; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /bound_moiety= "Alpha-helical peptide nucleic acid
(alphaPNA) shown in AAB74017"
(hote= "this nucleotide hybridises to the thymine at
position 19 of AB74017 to form an alphaPNA.DNA complex"
                                                                                                                                                                                                     Stimulus-responsive DNA organization of highly compatible functional material undergoing reversible formation/dissociation of supercoil or rotation in response to external stimulus, useful as e.g. artificial
                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                  ö
  ss; stimulus-responsive DNA organization; supercoil; rotation; external stimulus; medical micromachines; artificial muscle.
                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                                            Length 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA sequence that forms complex with alphaPNA CTCCT(b2)
                                                                                                                                                                                                                                                                                                                                                      Sequence 10 BP; 0 A; 3 C; 0 G; 7 T; 0 U; 0 Other;
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100.0%; Pred. No. 6e+
tive 0; Mismatches
                                                                                                                                                                                                                                                          Example 3; SEQ ID NO 4; 29pp; Japanese.
                                                                                                                                        (NISC-) JAPAN SCI & TECHNOLOGY CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                28-AUG-2002; 2002WO-JP008656
                                                                                                                    27-FEB-2002; 2002JP-00051927
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                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
les 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                             AGGAGAAA
                                                                                                                                                              Ootani T;
                                                      WO2003072772-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Misc_binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Misc binding
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                                                                            04-SEP-2003
                                  Synthetic
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Matches
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/bound_molety= "Alpha-helical peptide nucleic acid (alphaPhA) shown in ABB74017"
/note= "this nucleotide hyboridises to the thymine at position 11 of AB74017 to form an alphaPNA.DNA complex"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New peptide-based nucleic acid surrogate (PNAs) for use in therapeutic, diagnostic and molecular switching applications e.g. alpha-PNA chips.
                                                                                                                                                                                                                                                      /bound_moiety= "Alpha-helical peptide nucleic acid (alphaPhA) shown in AAB74017" hoote= "this nucleotide hybridises to the thymine at footien in of AB74017 to form an alphaPNA.DNA complex"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /*tag= e
/bound_molety= "Alpha-helical peptide nucleic acid
(alphaPNA) shown in AAB74017"
/note= "this nucleotide hybridises to the thymine at
position 3 of AB74017 to form an alphaPNA.DNA complex"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 11 BP; 8 A; 0 C; 3 G; 0 T; 0 U; 0 Other;
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The sequence is the polypyrimidine rich region of the capture reverse phase triplex forming oligonucleotide, RP-TFO used to analyse the CSFIPO locus using the method of the invention. The invention relates to analysing target nucleic acid sequences comprising restricting isolated adding at least one triplex forming oligonucleotide (TFO), (PNAS) tail structure, hybridising the captured structure with a single nucleotide polymorphisms (SNP) identification probe and determining the Sequences, especially genomic DNA sequences, to determine if they contain SNPs or short tandem repeats (STRS). The methods can be used to detect shows to use in population genetics, drug development, forensics, cancer, genetic disease research, genomic analysis, diagnostics and therapeutics in humans, plants and animals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The sequence is the polypyrimidine rich region of a reverse phase triplex
Analyzing target nucleic acid sequences, useful for population genetics, drug development and diagnosing cancer, comprises hybridizing triple forming oligonuclectide and probe to target sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Analyzing target nucleic acid sequences, useful for population genetics, drug development and diagnosing cancer, comprises hybridizing triple forming oligonuclectide and probe to target sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      reverse phase triplex forming oligonuclectide; RP-TFO; protected nucleic acid sequence; PNAS; single nuclectide polymorphism; SNP; short tandem repeat; cancer; CSF1PO; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 36.4%; Score 8; DB 1; Length 11; Best Local Similarity 100.0%; Pred. No. 6.2e+02; Matches 8; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 11 BP; 6 A; 0 C; 5 G; 0 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Polypyrimidine-rich RP-TFO sequence.
                                                                        Example 4; Page 69; 141pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 4; Page 70; 141pp; English.
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03-NOV-1999; 99US-0163416P.
21-DEC-1999; 99US-0171348P.
07-JUL-2000; 2000US-0216579P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4 AGGAGAAA 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200132929-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAS05726;
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AAS05726/c
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                                                                                                                                                                                                                                                                                                                                                                            The invention relates to a method for detecting mutations in the base sequences of nucleic acids. The method comprises using ion pair chromatography involving a reversed phase column as a separation column, and setting the separation column at temperature that causes differences in stability between hetero- and homoduplexes. The present sequence is an exon from a mutated DNA sequence that can be analysed by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        reverse phase triplex forming oligonucleotide; RP-TFO; protected nucleic acid sequence; PNAS; single nucleotide polymorphism; SNP; short tandem repeat; cancer; CSF1PO; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                   Detecting mutations in the base sequences of nucleic acids comprises using ion pair chromatography and reversed phase separation columns.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Match 36.4%; Score 8; DB 1; Length 11; Local Similarity 100.0%; Pred. No. 6.2e+02; es 8; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 11 BP; 1 A; 3 C; 1 G; 6 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Polypyrimidine-rich capture RP-TFO sequence.
                                                                                                                                                                                                                                                                                                                                           Disclosure; Fig 3; 10pp; English
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                                                                                                                             19-APR-2000; 2000JP-00118587.
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21-DEC-1999; 99US-0171348P.
07-JUL-2000; 2000US-0216579P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the method of the invention
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                                                                                                                                                               (SHMA ) SHIMADZU CORP
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              US2001034029-A1.
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                                                  25-OCT-2001
                                                                                                                                                                                                      Fujiwake H;
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ABQ87632 standard; cDNA; 11 BP

RESULT 884

ABQ87632

4 AGGAGAAA 11

10-SEP-2002 (first entry)

ABQ87632;

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forming oligonucleotide, RP-TFO, used to analyse the CSF1PO locus using the method of the invention. The invention relates to analysing target ancleic acid sequences comprising restricting isolated DNA, hybridising at least one triplex forming oligonucleotide (TFO), adding a 3' to 5' exonuclease to form a protected nucleic acid sequence (PNAS) tail structure, hybridising the captured structure with a single nucleotide polymorphisms (SNP) identification probe and determining the SNP score. The methods can be used for analysing target nucleic acid sequences, especially genomic DNA sequences, to determine if they contain SNPs or use in population genetics, drug development, forensics, cancer, genetic disease research, genetics drug development, forensics, cancer, genetic humans, plants and animals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention relates to the coding sequence of human Creaml, which is a protein containing a repetitive 86 amino acid motif. The protein is a transcriptional control factor, and is a conjugate of retinoblastoma protein (Rb). The present sequence is the an intron-exon junction in the coding sequence of the invention
                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                       Query Match 36.4%; Score 8; DB 1; Length 11; Best Local Similarity 100.0%; Pred. No. 6.2e+02; Matches 8; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                             0; Indels
                                                                                                                                                                                                                                                                        Seguence 11 BP; 0 A; 5 C; 0 G; 6 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAI64929 standard; DNA; 11 BP
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Best Local Similarity 100.
Matches 8; Conservative
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The invention relates to identifying (M1) genes in vitro that, in humans or animals, are important for skin ageing and/or skin stress by scrial analysis of gene expression between mixtures of transcribed and optionally translated, genetically encoded factors (A) obtained from young and aged skin, to identify that genes that show strong differential useful for: identifying markers of skin ageing and/or stress; determining skin ageing and/or stress; and identifying or determining the effects of pharmaceutical or cosmetic agents for control of skin ageing. The present sequence is one of a group of human skin ageing/stress related expressed sequence tags (ABQ866246-ABQ87680) of the invention
                                                                                                                                                                                                                                                                                                                                                                                                          Identifying genes involved in skin stress and aging, useful \epsilon.g. in screening for cosmetic or therapeutic agents, based on differential gene
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                                                                                                                        Human; skin ageing; skin stress; EST; expressed sequence tag; ss.
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                                                                                          Human skin stress/ageing related EST SEQ ID NO 1387.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 8; Page 96; 325pp; German.
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Matches 8; Conservative
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Homo sapiens

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The invention relates to identifying (M1) genes in vitro that, in humans or animals, are important for skin ageing and/or skin stress by serial analysis of gene expression between mixtures of transcribed and optionally translated, genetically encoded factors (A) obtained from young and aged skin, to identify that genes that show strong differential useful for: omprises protein or mRNAMs or their fragments. (M1) is useful for: identifying markers of skin ageing and/or stress; determining skin ageing and/or stress; and identifying or determining the effects of planamecutical or commettic agents for control of skin ageing. The present sequence is one of a group of human skin ageing/stress related expressed sequence tags (ABQ87680) of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to in vitro identification (M1) of genes expressed in the skin of humans or animals by subjecting a mixture of genetically encoded factors from skin, to serial analysis of gene expression (SAGE) so as to identify skin-expressed genes and quantify their expression.

(M1) is useful for identifying genes involved in skin homeostasis; to determine skin homeostasis and to test agent (A) that maintains or promotes skin homeostasis or that can be used for treating skin disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma; ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
   screening for cosmetic or therapeutic agents, based on differential gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human, skin, dermatological, vulnerary, antipsoriatic, antiseborrhaeic, immunosuppressive, antiinflammatory, cytostatic, SAGE, neurodermatitis, psoriasis, dermatitis, skin cancer, EST, expressed sequence tag, ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        In vitro identification of skin-expressed genes, useful for determining homeostasis and identifying cosmetic or pharmaceutical agents against
                                                                                                                                                                                                                                                                                                                               Match 36.4%; Score 8; DB 1; Length 11; Local Similarity 100.0%; Pred. No. 6.2e+02; les 8; Conservative 0; Mismatches 0; Indels
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                                                     Claim 8; Page 55; 325pp; German
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                      expression.
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Matches
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                                                                                                                                                                                                                                                                                                                                                             The invention relates to identifying (M1) genes in vitro that, in humans or animals, are important for skin ageing and/or skin stress by serial analysis of gene expression between mixtures of transcribed and optionally translated, genetically encoded factors (A) obtained from young and aged skin, to identify that genes that show strong differential expression. (A) comprises protein or mRNAMs or their fragments. (M1) is useful for: identifying markers of skin ageing and/or stress; determining skin ageing and/or stress; and identifying or determining the effects of pharmacoutical or cosmettic agents for control of skin ageing. The present sequence is one of a group of human skin ageing/stress related expressed sequence tags (ABQ86246-ABQ87680) of the invention
                                                                                                                                                                                                                                                             Identifying genes involved in skin stress and aging, useful e.g. in screening for cosmetic or therapeutic agents, based on differential gene
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                                                                                    20-DEC-2001; 2001WO-EP015178
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                                                                                                                                                       (HENK ) HENKEL KGAA
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                  WO200253773-A2
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ABV71675 standard; cDNA; 11
                                                                                                  21-OCT-2002 (first entry)
                                                                                                                           Human skin EST 9461
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                                                                          ABV71675;
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                      RESULT 889
ABV71675/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           In vitro identification of skin-expressed genes, useful for determining homeostasis and identifying cosmetic or pharmaceutical agents against
                                                                                                                                                                                                                                                                                                                     Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic; immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis; psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
rosacea, melanoma, basal cell carcinoma, and carcinoma or sarcoma of
skin. The present sequence is that of a human expressed sequence tag
(EST) of the invention
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                                                                        36.4%; Score 8; DB 1; Length 11; 100.0%; Pred. No. 6.2e+02; Atlive 0; Mismatches 0; Indels
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                                                   Sequence 11 BP; 4 A; 4 C; 1 G; 2 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 24; Page 255; 1345pp; German.
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ABV70231 standard; cDNA; 11 BP.
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                                                                                                                                                                                                                                                                     (first entry)
                                                                Query Match
Best Local Similarity 100...
Since 8; Conservative
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Best Local Similarity 100.
Matches 8; Conservative
                                                                                                                              739 CAGAACAC 746
                                                                                                                                                     CAGAACAC 10
                                                                                                                                                                                                                                                                                             Human skin EST 8017.
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The invention relates to in vitro identification (MI) of genes expressed in the skin of humans or animals by subjecting a mixture of genetically encoded factors from skin, to serial analysis of gene expression (SAGE) so as to identify skin-expressed genes and quantify their expression. (MI) is useful for identifying genes involved in skin homeostasis, to determine skin homeostasis and to test agent (A) that maintains or promotes skin homeostasis or that can be used for treating skin disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ichthyosis; atopic dermatiiis; acne; seborrhea; lupus erythematosus; rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the skin. The present sequence is that of a human expressed sequence tag
Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic; immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis; psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          In vitro identification of skin-expressed genes, useful for determining homeostasis and identifying cosmetic or pharmaceutical agents against
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 disorders, specifically neurodermatitis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hofmann K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 24; Page 305; 1345pp; German.
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(M1) is useful for identifying genes involved in skin homeostasis; to promotes skin homeostasis and to test agent (A) that maintains or promotes skin homeostasis or that can be used for treating skin disorders, specifically neurodermatitis; sunburn; psoriaals, scleroderma; ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus; rosacea, melanoma; basal cell carcinoma, and carcinoma or sarcoma of the skin. The present sequence is that of a human expressed sequence tag
immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis; psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
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                                                                                                               20-DEC-2001; 2001WO-EP015179.
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8; Conservative
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                                      Homo sapiens.
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The invention relates to in vitro identification (M1) of genes expressed in the skin of humans or animals by subjecting a mixture of genetically encoded factors from skin, to serial analysis of gene expression (SAGE) so as to identify skin-expressed genes and quantify their expression.

(M1) is useful for identifying genes involved in skin homeostasis; to promotes skin homeostasis and to test agent (A) that maintains or promotes skin homeostasis or that can be used for treating skin disorders, specifically neurodermatitis; sunburn; psoriasis, scleroderma; ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus; sosceea, melanoma; basal cell carcinoma; and carcinoma or sarcoma of the skin. The present sequence is that of a human expressed sequence tag
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                                                                                 In vitro identification of skin-expressed genes, useful for determining homeostasis and identifying cosmetic or pharmaceutical agents against e.g. skin cancer.
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                                                                                                                                                                              Disclosure; Page 182; 1345pp; German
Hofmann K;
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Petersohn D, Conradt M,
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Best Local Similarity 100.0%; Pred. No. 6.2e+02;
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in the skin of humans or animals by subjecting a mixture of genetically encoded factors from skin, to serial analysis of gene expression (SAGE) so as to identify skin-expressed genes and quantify their expression.

(MI) is useful for identifying genes involved in skin homeostasis, to determine skin homeostasis and to test agent (A) that maintains or promotes skin homeostasis or that can be used for treating skin disorders, specifically neurodermatitis, sunburn, psoriasis, scleroderma; ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus; scoacea, melanoma; basal cell carcinoma, and carcinoma or sarcoma of the skin. The present sequence is that of a human expressed sequence tag Human, skin, dermatological, vulnerary, antipsoriatic, antiseborrhaeic, immunosuppressive, antiinflammatory, cytostatic, SAGB, neurodermatitis, psoriasis, dermatitis, skin cancer, EST, expressed sequence tag, ss. In vitro identification of skin-expressed genes, useful for determining homeostasis and identifying cosmetic or pharmaceutical agents against Gaps ö 36.4%; Score 8; DB 1; Length 11; 100.0%; Pred. No. 6.2e+02; tive 0; Mismatches 0; Indels Sequence 11 BP; 7 A; 1 C; 2 G; 1 T; 0 U; 0 Other; Hofmann BP. 20-DEC-2001; 2001WO-EP015179. 03-JAN-2001; 2001DE-01000127. ABV64703 standard; cDNA; 11 21-OCT-2002 (first entry) Query Match
Best Local Similarity luv...
8; Conservative Conradt M, 736 AAACAGAA 743 AAACAGAA 10 Human skin EST 2489. (HENK) HENKEL KGAA WPI; 2002-590638/63 WO200253774-A2. Petersohn D, Homo sapiens 11-JUL-2002 ABV64703; m ABYOLT 893
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                                                                                                          Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic; immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis; psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
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                                               21-OCT-2002 (first entry)
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                                                                              Human skin EST 2926.
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ABV62451/c ID ABV62451 standard; cDNA; 11 BP.

The invention relates to in vitro identification (M1) of genes expressed in the skin of humans or animals by subjecting a mixture of genetically encoded factors from skin, to serial analysis of gene expression (SAGE) so as to identify skin-expressed genes and quantify their expression. (M1) is useful for identifying genes involved in skin homeostasis; to promotes skin homeostasis and to test agent (A) that maintains or promotes skin homeostasis or that can be used for treating skin disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma; inchthyosis; atopic dermatitis, acne, seborrhea; lupus erythematosus; rosaces, melanoma; basal cell carcinoma; and carcinoma or sarcoma of the skin. The present sequence is that of a human expressed sequence tag

Disclosure; Page 94; 1345pp; German.

e.g. skin cancer.

Seguence 11 BP; 3 A; 5 C; 2 G; 1 T; 0 U; 0 Other;

the invention

ABV62451;

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The invention relates to in vitro identification (MI) of genes expressed in the skin of humans or animals by subjecting a mixture of genetically encoded factors from skin, to serial analysis of gene expression (SAGE) so as to identify skin-expressed genes and quantify their expression. (MI) is useful for identifying genes involved in skin homeostasis; to promotes skin homeostasis and to test agent (A) that maintains or promotes skin homeostasis or that can be used for treating skin disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma; ichthyosis; atopic dermatitis; anne, seborrhea; lupus expremences, rosacea; melanoma; basal cell carcinoma ar sarcoma of the skin. The present sequence is that of a human expressed sequence tag
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immunosuppressive, antiinflammatory, cytostatic, SAGE, neurodermatitis,
psoriasis, dermatitis, skin cancer, EST, expressed sequence tag, ss.
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ID ABV62810 standard; cDNA; 11
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The invention relates to in vitro identification (M1) of genes expressed in the skin of humans or animals by subjecting a mixture of genetically encoded factors from skin, to serial analysis of gene expression (\$AGE\$) so as to identify skin-expressed genes and quantify their expression. (M1) is useful for identifying genes involved in skin homeostasis; to promotes skin homeostasis and to test agent (A) that maintains or promotes skin homeostasis or that can be used for treating skin disorders, specifically neurodermatitis; sunburn; psoriais; scleroderma; ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus; rosacea, melanoma; basal cell carcinoma, and carcinoma or sarcoma of the skin. The present sequence is that of a human expressed sequence tag In vitro identification of skin-expressed genes, useful for determining homeostasis and identifying cosmetic or pharmaceutical agents against Disclosure; Page 41; 1345pp; German. e.g. skin cancer.

36.4%; Score 8; DB 1; Length 11; 100.0%; Pred. No. 6.2e+02; tive 0; Mismatches 0; Indels Sequence 11 BP; 1 A; 4 C; 2 G; 4 T; 0 U; 0 Other; 8; Conservative 729 CCAGGAGA 736 8 CCAGGAGA 1 Query Match Best Local Similarity Matches ò

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> ABV65528 standard; cDNA; 11 ABV65528; RESULT 898 ABV65528/c

21-OCT-2002 (first entry) Human skin EST 3314.

Human, skin, dermatological, vulnerary, antipsoriatic, antiseborrhaeic, immunosuppressive, antiinflammatory; cytostatic, SAGE, neurodermatitis, psoriasis, dermatitis, skin cancer, EST; expressed sequence tag; ss.

Homo sapiens

WO200253774-A2.

11-JUL-2002

03-JAN-2001; 2001DE-01000127.

20-DEC-2001; 2001WO-EP015179.

(HENK) HENKEL KGAA.

M, Hofmann K;

Conradt

Petersohn D,

In vitro identification of skin-expressed genes, useful for determining homeostasis and identifying cosmetic or pharmaceutical agents against WPI; 2002-590638/63. e.g. skin cancer.

Disclosure; Page 117; 1345pp; German.

The invention relates to in vitro identification (MI) of genes.expressed in the skin of humans or animals by subjecting a mixture of genetically encoded factors from skin, to serial analysis of gene expression (SAGE) so as to identify skin-expressed genes and quantify their expression. (MI) is useful for identifying genes involved in skin homeostasis, to determine skin homeostasis and to test agent (A) that maintains or

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36.4%; Score 8; DB 1; Length 11; larity 100.0%; Pred. No. 6.2e+02; Conservative 0; Mismatches 0; Indels

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Sequence 11 BP; 1 A; 3 C; 2 G; 5 T; 0 U; 0 Other;

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promotes skin homeostasis or that can be used for treating skin disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma; ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus; rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the skin. The present sequence is that of a human expressed sequence tag (EST) of the invention
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                                                                     ABV69872 standard; cDNA; 11 BP.
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(M1) is useful for identifying genes involved in skin homeostasis; to promotes skin homeostasis and to test agent (A) that maintains or promotes skin homeostasis or that can be used for treating skin ichthyosis, specifically neurodermatitis; sunburn; psoriasis, scleroderma; ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus; rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the skin. The present sequence is that of a human expressed sequence tag
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Human, skin, dermatological, vulnerary, antipsoriatic, antiseborrhaeic, immunosuppressive, antiinflammatory, cytostatic, SAGE, neurodermatitis, psoriasis, dermatitis, skin cancer, EST, expressed sequence tag, ss.
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immunosuppressive, antiinflammatory, cytostatic, SAGE, neurodermatitis,
psoriasis, dermatitis, skin cancer, EST; expressed sequence tag, ss.
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Best Local Similarity
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                                                                                                                                                      Homo sapiens.
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03-JAN-2001; 2001DE-01000127
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The invention relates to in vitro identification (MI) of genes expressed in the skin of humans or animals by subjecting a mixture of genetically encoded factors from skin, to serial analysis of gene expression ($AGE) so as to identify skin-expressed genes and quantify their expression. (MI) is useful for identifying genes involved in skin homeostasis, to determine skin homeostasis and to test agent (A) that maintains or promotes skin homeostasis or that can be used for treating skin disorders, specifically neurodermatitis, sunburn; psoriasis; scleroderma; inchthyosis; atopic dermatitis, acne, seborrhea; lupus expresseds incomes incomes, and call carcinoma or sarcoma of the skin. The present sequence is that of a human expressed sequence tag
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(EST) of the invention
                                                                                        Conradt
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(HENK ) HENKEL KGAA
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Similarity 100.0%; Pred. No. 6.2e+02; 8; Conservative 0; Mismatches 0; Indels
   Query Match
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Matches 8; Conserv
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ABV69727 standard; cDNA; 11 BP (first entry) 736 AAACAGAA 743 AAACAGAA 10 Human skin EST 7513. 21-OCT-2002 ABV69727;

Human, skin, dermatological, vulnerary, antipsoriatic; antiseborrhaeic; immunosuppressive, antiinflammatory; cytostatic; SAGE; neurodermatitis; psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.

Homo sapiens

WO200253774-A2

03-JAN-2001; 2001DE-01000127

(HENK) HENKEL KGAA

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WPI; 2002-590638/63

In vitro identification of skin-expressed genes, useful for determining homeostasis and identifying cosmetic or pharmaceutical agents against e.g. skin cancer.

The invention relates to in vitro identification (M1) of genes expressed in the skin of humans or animals by subjecting a mixture of genetically seconded factors from skin, to serial analysis of gene expression (\$AGE) so as to identify skin-expressed genes and quantify their expression. (M1) is useful for identifying genes involved in skin homeostasis; to promotes skin homeostasis and to test agent (A) that maintains or promotes skin homeostasis or that can be used for treating skin disorders, specifically neurodermatitis, sunburn, psoriasis; scleroderma; inchthyosis; atopic dermatitis, acne, sebornhea; lupus erythematosus; rosacca; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the skin. The present sequence is that of a human expressed sequence tag

In vitro identification of skin-expressed genes, useful for determining homeostasis and identifying cosmetic or pharmaceutical agents against

Disclosure; Page 155; 1345pp; German.

e.g. skin cancer.

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               The invention relates to in vitro identification (M1) of genes expressed in the skin of humans or animals by subjecting a mixture of genetically encoded factors from skin, to serial analysis of gene expression (SAGE) so as to identify skin-expressed genes and quantify their expression. (M1) is useful for identifying genes involved in skin homeostasis, or determine skin homeostasis and to test agent (A) that maintains or promotes skin homeostasis or that can be used for treating skin disorders, specifically neurodermatitis; sumburn, psoriasis, scleroderma; ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus; rosace; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the skin. The present sequence is that of a human expressed sequence tag
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 Claim 24; Page 237; 1345pp; German.
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100.0%; Pre
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In vitro identification of skin-expressed genes, useful for determining homeostasis and identifying cosmetic or pharmaceutical agents against
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                           ABV62306 standard; cDNA; 11
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100.0%; Pred. No. 6.2
tive 0; Mismatches
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Best Local Similarity 100.
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(EST) of the invention
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The invention relates to in vitro identification (M1) of genes expressed in the skin of humans or animals by subjecting a mixture of genetically encoded factors from skin, to serial analysis of gene expression (SAGE) so as to identify skin-expressed genes and quantify their expression. (M1) is useful for identifying genes involved in skin homeostasis, to promotes skin homeostasis and to test agent (A) that maintains or promotes skin homeostasis or that can be used for treating skin disorders, specifically neurodermatitis; sunburn, psoriasis, scleroderma; ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus; rosacea; melanoma; basal cell carcinoma, and carcinoma or sarcoma of the skin. The present sequence is that of a human expressed sequence tag (EST) of the invention
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Disclosure; Page 202; 1345pp; German.
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The invention relates to in vitro identification (M1) of genes expressed in the skin of humans or animals by subjecting a mixture of genetically encoded factors from skin, to serial analysis of gene expression (SAGE) so as to identify skin.expressed genes and quantify their expression (M1) is useful for identifying genes involved in skin homeostasis; to promotes skin homeostasis and to test agent (A) that maintains or promotes skin homeostasis or that can be used for treating skin disorders, specifically neurodermatitis; subburn; psoriasis; scleroderma;
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In vitro identification of skin-expressed genes, useful for determining homeostasis and identifying cosmetic or pharmaceutical agents against
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6.2e+02;

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(M1) is useful for identifying genes involved in skin homeostasis, to promotes skin homeostasis and to test agent (A) that maintains or promotes skin homeostasis or that can be used for treating skin disorders, specifically neurodermatitis; sunburn; psoriasis, scleroderma; ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus; rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the skin. The present sequence is that of a human expressed sequence tag
so as to identify skin-expressed genes and quantify their expression. (M1) is useful for identifying genes involved in skin homeostasis; to determine skin homeostasis and to test agent (A) that maintains or promotes skin homeostasis or that can be used for treating skin identifications is pecifically neurodermatitis; sunburn; psoriasis; scleroderma; ichthyosisis atopic dermatitis; acnes; seborncha; lupus erythematosus; rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the skin. The present sequence is that of a human expressed sequence tag
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36.4%; Score 8; DB 1; Ler
Best Local Similarity 100.0%; Pred. No. 6.2e+02;
Matches 8; Conservative 0; Mismatches 0;
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Best Local Similarity 100.
Matches 8; Conservative
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ABV64254/c
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DB 1; Length 11;

36.4%; Score 8;

Query Match

In vitro identification of skin-expressed genes, useful for determining homeostasis and identifying cosmetic or pharmaceutical agents against

Conradt M, Hofmann K;

Petersohn D,

WPI; 2002-590638/63

20-DEC-2001; 2001WO-EP015179. 03-JAN-2001; 2001DE-01000127 Disclosure; Page 120; 1345pp; German.

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Hofmann

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e.g. skin cancer.

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Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic; immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis; psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
                                                                                                                                                                                                                                                          In vitro identification of skin-expressed genes, useful for determining homeostasis and identifying cosmetic or pharmaceutical agents against
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        21-OCT-2002 (first entry)
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                            Human skin EST 2040.
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The invention relates to in vitro identification (M1) of genes expressed in the skin of humans or animals by subjecting a mixture of genetically senced from skin, to serial analysis of gene expression (SAGE) so as to identify skin-expressed genes and quantify their expression.

(M1) is useful for identifying genes involved in skin homeostasis; to determine skin homeostasis and to test agent (A) that maintains or promotes skin homeostasis or that can be used for traating skin disorders, specifically neurodermatitis; sumburn; psoriasis; scleroderma; ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus; rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the skin. The present sequence is that of a human expressed sequence tag (EST) of the invention
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Matches 8; Conservative
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36.4%; Score 8; DB 1; Length 11; 100.0%; Pred. No. 6.2e+02; Itive 0; Mismatches 0; Indels

735

728 GCCAGGAG

Sequence 11 BP; 3 A; 2 C; 5 G; 1 T; 0 U; 0 Other;

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Human, mouse, rat, TEM, tumour endothelial marker, NEM, PEM; cytostatic; normal endothelial marker; pan-endothelial marker; immunostimulant; antiangiogenic; tumour, necamgiogenesis; vascularised tumour; polycystic kidney disease; diabetes; retinopathy; rheumatoid arthritis;
                                                                                                                                           Human Pan-Endothelial Marker SEQ ID NO 65.
                                                                                                                                                                                                                                                                                                                                                                                                                                    St Croix B, Kinzler KW, Vogelstein B;
                                                         .967/c
ABL91967 standard; cDNA; 11 BP.
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11-AUG-2000; 2000US-0224360P.
11-APR-2001; 2001US-0282850P.
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                                                                                                                    30-MAY-2002 (first entry)
3 GCCAGGAG 10
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                                                                                                                                                                                                                           psoriasis; ss
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                                                                                           ABL91967;
                                         RESULT 914
                                                      ABL91967/
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An isolated molecule comprising an antibody variable region which specifically binds to an extracellular domain of a tumor endothelial marker (TBM) protein, useful for inhibiting tumor growth. WPI; 2002-291856/33.

Example 4; Page 326; 331pp; English.

The invention relates to an isolated molecule comprising an antibody variable region which specifically binds to an extracellular domain of a tumour endothelial marker (TEM) protein selected from ABB90732, ABB90749, ABB90749, ABB90750 and ABB90769. The antibodies which bind to TEM proteins have cytostatic, immunostimulant and antiangiogenic activity. They are useful for inhibiting tumour growth, neoangiogensis in subjects bearing a vascularised tumour, polycystic kidney disease, diabetic retinopathy, rheumatoid archritis and psoriasis Human, mouse and rat TEM genes and the encoded proteins (ABL92075-ABL92141 and ABB90712-ABB90789) are disclosed, as are marker oligonucleotide sequences: tumour endothelial markers (TEM) ABL91904-ABL92014 and ABL92143-ABL92191; normal endothelial markers (MEM) ABL920044, and pan-endothelial markers oligonucleotide marker useful to the invention

Sequence 11 BP; 1 A; 4 C; 4 G; 2 T; 0 U; 0 Other;

36.4%; Score 8; DB 1; Length 11; 100.0%; Pred. No. 6.2e+02; ive 0; Mismatches 0; Indels Query Match
Best Local Similarity 100.00 728 GCCAGGAG 735 ठे

11 GCCAGGAG 4 g

RESULT 915

ABQ81877 standard; DNA; 11 BP. 19-NOV-2002 (first entry) ABQ81877; ABQ01877

XX ABQ0

XX ABQ0

XX ABQ0

XX ABQ0

XX E BD1

Kaposi's Sarcoma SAGE library Tag No.7 SEQ ID NO:27.

Human; Kaposi's sarcoma; tumour; angiogenesis; tag; ss

Homo sapiens

EP1225233-A2.

23-JAN-2002; 2002EP-00075264. 24-JUL-2002.

23-JAN-2001; 2001EP-00200228. 28-SEP-2001; 2001EP-00203703. 28-SEP-2001; 2001US-0325722P.

(AMST-) AMSTERDAM SUPPORT DIAGNOSTICS

BV.

Cornelissen M; Kuyl AC, Van Der

WPI; 2002-668396/72.

Determining presence of a tumor cell or angiogenesis, and the effectiveness of treatment, by detecting the presence of marker genes is useful to detect and monitor treatment of Karposi's Sarcoma.

Claim 12; Page 8; 38pp; English.

The present invention describes a method for determining if an individual has a tumour cell or site of angiogenesis, or if a treatment is effective

in changing angiogenesis or changing a status of a set of target cells, comprising determining if a sample of the subject has an expression product of at least one marker gene. Also described is a compound capable of altering the expression or activity of Keratin 14, TIE 1, Salioadhesin or Siglec in a cell. Peripheral blood mononuclear cell (PBMC)-expressed Keratin 14, TIE 1, Salioadhesin or Siglec, and kits containing them from the present invention can be used in a diagnostic method, particularly as an indicator of anglogenesis or to determine presence of a tumour cell. The method of the invention is suitable to determine within a few days if a certain treatment against Kaposi's Sarcoma is successful. ABQ81851 to ABQ82006 represent nucleotide sequence used in the exemplification of the present invention

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Sequence 11 BP; 5 A; 3 C; 3 G; 0 T; 0 U; 0 Other;

Gaps ; 36.4%; Score 8; DB 1; Length 11; 100.0%; Pred. No. 6.2e+02; ive 0; Mismatches 0; Indels Query Match Best Local Similarity 100.00 Best Local Similarity 100.00

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730 CAGGAGAA 737 4 CAGGAGAA 11 원 à

ABX71892 standard; DNA; 11 RESULT 916 ABX71892/c

ABX71892;

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BP.

DNA tag used to identify human gene encoding PEM 65. (first entry) 12-MAR-2003

Human; endothelial cell; EC; tumour endothelial cell; TEM; NEM; Tumour endothelial marker; normal endothelial marker; PEM; pan-endothelial marker; polycystic kidney disease; psoriasis; diabetic retinopathy; rheumatoid arthritis; tumour angiogenesis; necangiogenesis; immune response; cytostatic; antidiabetic; ophthalmological; antirheumatic; antiarthritic; antipsoriatic; ds.

Homo sapiens.

WO200283874-A2.

24-OCT-2002,

10-APR-2002; 2002WO-US008253.

11-APR-2001; 2001US-0282850P. 06-FEB-2002; 2002US-0354262P.

(UYJO) UNIV JOHNS HOPKINS.

Vogelstein Kinzler KW, St Croix B, Carson-Walter E,

m

WPI; 2003-093016/08.

New purified human transmembrane protein, designated as tumor endothelial marker (TEM) 3, useful for detecting, diagnosing or treating tumors, polycystic kidney disease, diabetic retinopathy, rheumatoid arthritis or psoriasis.

Disclosure; Page 97; 374pp; English.

The present invention relates to a novel method for the isolation of endothelial cells (ECB), and the identification of genes expressed in normal and tumour ECS. Thmour endothelial marker (TEM), normal endothelial marker (TEM), normal identified in human ECs. The human EC marker proteins and the polynucleotide sequences encoding them are useful for detecting diagnosing or treating tumours as well as polycystic kidney disease, diabetic retinopathy, rheumatoid arthritis, and psoriasis. They are also

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RESULT 918

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Oligo:nucleotide contg. human protein kinase A gene sequence - useful as carcinostatic agent.
useful for inhibiting necanglogenesis or tumour angiogenesis, for inducing an immune response to tumour endichbelial cells in a patient, or for identifying candidate drugs for treating tumours. ABX71828-ABX71999 represent DNA tags for human PEM, TEM or NEM genes
                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                      Antisense oligonucleotide targeted to protein kinase A-RI-alpha gene.
                                                                                                                                                                                                                                                                                                                                                                                                                   Human protein kinase A-RI-alpha gene; antisense oligonucleotide; carcinostatic; leukemia; large intestinal cancer; rectal cancer; colon cancer; lung cancer; neorac cancer; hepatic cancer; melanoma; malignant lymphoma; tongue cancer; oesophagus cancer; breast cancer; uterus cancer; pharynx cancer; brain tumour; malignant myoma; ss.
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                                                                                                              36.4%; Score 8; DB 1; Length 11; 100.0%; Pred. No. 6.2e+02; tive 0; Mismatches 0; Indels
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                                                                            Sequence 11 BP; 1 A; 4 C; 4 G; 2 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                991/c
AAX34991 standard; DNA; 12 BP.
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                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Geiser TG;
                                                                                                                                                                               GCCAGGAG 735
                                                                                               Query Match
Best Local Similarity
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                                                                                                                                                                                                              11 GCCAGGAG 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Synthetic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Triplex formation; DNA detection; triple helix; identification; bacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                          Oligo:nucleotide contg. human protein kinase A gene sequence - useful as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                      Antisense oligonucleotide targeted to protein kinase A-RI-alpha gene.
                                                                                                                 Human protein kinase A-RI-alpha gene; antisense oligonucleotide; carcinostatic; leukemia; large intestinal cancer; rectal cancer; colon cancer; lung cancer; cancer; hepatic cancer; melanoma; malignant lymphoma; tongue cancer; oesophagus cancer; breast cancer; uterus cancer; pharynx cancer; brain tumour; malignant myoma; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 12 BP; 6 A; 0 C; 5 G; 1 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 7; Page 16; 24pp; Japanese.
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           ВР
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          AAX34986 standard; DNA; 12
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                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                             (POKK ) POLA CHEM IND INC
                                                                                                                                                                                                                                                                                                                                                                                         Geiser TG;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               oncogene; virus; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               carcinostatic agent.
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Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                           Isuchiya M,
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                                      AAX34986;
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0; Gaps

36.4%; Score 8; DB 1; Length 12; 100.0%; Pred. No. 6.4e+02; ative 0; Mismatches 0; Indels

Conservative

Local Similarity

Query Match Best Local S Matches 8

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8 8

AGGAGAAA 2

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This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and merabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC009989, ABF00010-ABF9989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but the wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Oligonucleotide primer SEQ ID NO 333883 for detecting SNP TSC0037810.
                                                                                                    oligonucleotides, useful for diagnosis and cell typing, ied to detect single-nucleotide polymorphisms and cytosine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; SEQ ID NO 333883; 29pp + Sequence Listing; German.
                                                                                                                                                                                    Claim 1; SEQ ID NO 274736; 29pp + Sequence Listing; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             36.4%; Score 8; DB 1; Length 12; 100.0%; Pred. No. 6.4e+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Set of oligonucleotides, useful for diagnosis and cell designed to detect single-nucleotide polymorphisms and methylation status.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 12 BP; 2 A; 4 C; 0 G; 6 T; 0 U; 0 Other;
                      Berlin K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Berlin K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABI33910 standard; DNA; 12 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 100.
Matches 8, Conservative
                    Olek A, Piepenbrock C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Olek A, Piepenbrock C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (EPIG-) EPIGENOMICS AG
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                                                         WPI; 2001-657177/75.
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                                                                                                                                              methylation status.
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                                                                                                    Set of
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ABI33910/c
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                                                                                                                                                                                                                                                                                        Assay of genetic sequences based on triplex formation from double stranded analyte - and hybrid of anchor and reporter sequences, with reporter released if triplex formation occurs, used e.g. to identify bacteria.
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                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Col 13-14; 168pp; English.
                                                                                                                                                                (PROF-) PROFILE DIAGNOSTIC SCI INC.
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Best Local Similarity 10v...
8; Conservative
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                                                                                                                                                                                                          Wang C;
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                                                                                22-DEC-1993;
                                                                                                                      29-OCT-1992;
                                                                                                                                                                                                          Hepburn AG,
US5861244-A.
                                        19-JAN-1999
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC9989, ABF00010-ABF9989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC9989, ABF00010-ABF9989, ABH0010-ABH99989 and ABI0010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at fire wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 12 BP; 3 A; 3 C; 0 G; 6 T; 0 U; 0 Other;
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Matches 8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                     0; Indels
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36.4%; Score 8; DB 1; Lei
100.0%; Pred. No. 6.4e+02;
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   Query Match
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ABIS5796 standard; DNA; 12 BP.

Sequence 12 BP; 7 A; 0 C; 3 G; 2 T; 0 U; 0 Other;

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, ardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99899, ABF00010-ABF99989, ABH00010-ABH99999 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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designed to detect single-nucleotide polymorphisms and cytosine
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tive 0; Mismatches
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                                                                                                               SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                             Oligonucleotide primer SEQ ID NO 355769 for detecting SNP TSC0049804.
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ABI55796;
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Homo sapiens

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligomucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC9989, ABF00010-ABF9989, ABH00010-ABH99989 and ABI00010-ABH82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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Set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status.
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                                                                                                                                                       Claim 1; SEQ ID NO 379637; 29pp + Sequence Listing; German.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
             represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences
-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
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                                                                                                                          Query Match
Best Local Similarity 100..
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les 8; Conserv
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                                                    Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                     This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC09989, ABC0010-ABE9989, ABC0010-ABE9989 and ABI0010-ABE9989 and ABI0010-ABE9989 and ABI0010-ABE9989 and ABI0010-ABE9073 data for this patent did not form par of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                  SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Oligonucleotide primer SEQ ID NO 319093 for detecting SNP TSC0029068.
                                                                                                                             Oligonucleotide primer SEQ ID NO 285914 for detecting SNP TSC0012507.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                             ABH85921 standard; DNA; 12
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Best Local Similarity 100.
Matches 8; Conservative
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                                                                                                                                                                                                                                                                                                           (EPIG-) EPIGENOMICS AG
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SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; 8s; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Oligonucleotide primer SEQ ID NO 276821 for detecting SNP TSC0004297.
                                                                                                                                       Set of oligonucleotides, useful for diagnosis and cell typing, idesigned to detect single-nucleotide polymorphisms and cytosine methylation status.
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                                                                     Berlin K;
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                                                                   Piepenbrock C,
                                   (EPIG-) EPIGENOMICS AG
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           This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC9989, ABF0010-ABF9989, ABH0010-ABF9989 and ABI0010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from MIPO at
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, ardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABT00010-ABI82073 the preparent the oligomers described in the invantion. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                          SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                     Oligonucleotide primer SEQ ID NO 281108 for detecting SNP TSC0009446.
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ABH81115 standard; DNA; 12
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                                                                                                                                                                                                                                                                                                                                                                                   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                                                                                                                                                                                  Oligonucleotide primer SEQ ID NO 300224 for detecting SNP TSC0018914.
                                                                        Gaps
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36.4%; Score 8; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 6.4e+02;
Matches 8; Conservative 0; Mismatches 0; Indels
Sequence 12 BP; 5 A; 0 C; 6 G; 1 T; 0 U; 0 Other;
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Matches 8; Conservative
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                               h 36.4%; Score 8; DB 1; Length 12; Similarity 100.0%; Pred. No. 6.4e+02; 8; Conservative 0; Mismatches 0; Indels
Seguence 12 BP; 7 A; 0 C; 3 G; 2 T; 0 U; 0 Other;
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RESULT 935

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This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genemic DNA. The oligonuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from MIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nuclectide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                        Set of oligonuclectides, useful for diagnosis and cell typing, i designed to detect single-nuclectide polymorphisms and cytosine methylation status.
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                                                                                                                                           Claim 1; SEQ ID NO 356916; 29pp + Sequence Listing; German.
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               WPI; 2001-657177/75.
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                                                                                                                                                                                                                                                                                                                                  Set of oligonucleotides, useful for diagnosis and cell typing, idesigned to detect single-nucleotide polymorphisms and cytosine methylation status.
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range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cartiovascular and metabolic disorders. The coligomers are also used for detecting cell type differentiation. ABC0010-ABC99889, ABF00010-ABF99889, ABF00010-ABF99889, ABF00010-ABF99889 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                          SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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Best Local Similarity
731 AGGAGAAA
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36.4%; Score 8; DB 1; Length 12; 100.0%; Pred. No. 6.4e+02;

Query Match Best Local Similarity

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06-APR-2001; 2001WO-IB000713
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ABI71127/c
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                                                       SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                            Oligonucleotide primer SEQ ID NO 334468 for detecting SNP TSC0038169.
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligomucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99999, ABF00010-ABF99999, ABH00010-ABH99999 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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Best Local Similarity 100..
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                                                                     Piepenbrock C,
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                                                 This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC9989, ABF00010-ABF9989, ABM0010-ABH99989 and ABI00010-ABH82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but ftp.wipo.int/pub/published_pct_sequences
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                           Claim 1; SEQ ID NO 371100; 29pp + Sequence Listing; German.
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                                                                                                                                Sequence 12 BP; 1 A; 6 C; 0 G; 5 T; 0 U; 0 Other
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Pred. No. 6.4e+02;
0; Mismatches 0;
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Best Local Similarity 100.0%;
Matches 8; Conservative 0
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, contral nervous system, artdiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF9989, ABH00010-ABH99989 and ABI00010-ABI82073 data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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                                                                                                                                                                                                                                                             Oligonucleotide primer SEQ ID NO 304059 for detecting SNP TSC0020766.
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peptide nucleic acid, cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00016-ABC99989, ABC0010-ABP9989 ABH0010-ABH99989 and ABI0010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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New human alanine transaminase polypeptide (ALT2) and gene, useful for detecting injury, damage or disease involving a tissue that contains the ALT2 in an animal, or in diagnosing conditions associated with altered
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                                                                                                                                Human; alanine transaminase; ALT2; diagnosis; injury; ds.
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                                                                                        Human ALT2 gene intron11/exon12 junction DNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF99899, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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                                                                                                                                                                                                                                                                                                                                                                           SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                                                                                                                                                                           Oligonucleotide primer SEQ ID NO 280828 for detecting SNP TSC0009139.
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100.0%; Pred. No. 6.4
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The invention relates to a composition comprising an aryl-hydrocarbon receptor interacting protein-like 1 (AIPL) sequence within the Leber congenital amaurosis 4 (LCA4) region of chromosome 17pl3, which is a wild type or a mutant AIPL1 sequence. The aryl-hydrocarbon receptor interacting protein-like 1 (AIPL1) polynucleotides and polypeptides are useful for diagnosing or treating retinal diseases associated with AIPL1 mutations, for example, Leber congenital amaurosis, juvenile retinitis pigmentosa, dominant cone-rod dystrophy or other inherited or acquired retinopathies. The AIPL1 polynucleotides and polypeptides are also useful for determining if a cell or sample has an AIPL1 mutation or if an animal has a retinal disease or has a propensity to pass a retinal disease to component the methods are useful for screening of compounds that especifically bind to the mutated polypeptides, which can be used to treat resistant diseases that are associated with the mutations. Sequences ACD40383-ACD40433 represent human AIPL1 CDNA fragments of the invention
                                                                                                                                                                             New aryl-hydrocarbon receptor interacting protein-like 1 (AIPL1) polynucleotides and proteins, useful for diagnosing or treating retinal diseases associated with AIPL1 mutations, e.g. Leber congenital
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36.4%; Score 8; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 6.4e+02;
Matches 8; Conservative 0; Mismatches 0; Indels
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                                        (SOHO/) SOHOCKI M M. (DAIG/) DAIGER S P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to human alanine transaminase polypeptide (ALT2) and gene. The invention is useful for diagnosing or detecting injury, damage or disease involving a tissue that contains the ALT2 polypeptide in an animal, in diagnosing conditions associated with altered levels of ALT2 and/or ALT1 in bodily fluids. The present sequence is human ALT2 gene intron/exon junction DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New human alanine transaminase polypeptide (ALT2) and gene, useful for detecting injury, damage or disease involving a tissue that contains the ALT2 in an animal, or in diagnosing conditions associated with altered levels of ALT2.
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                                                                                                                                                                                                                                This invention describes a novel non-MRL healer mouse (M) having at least one quantitative trait locus selected from those given in the specification, exhibiting an enhanced healing response to a wound compared to mice (m) without the locus. The invention describes a novel method of identifying a gene involved in enhanced wound healing by identifying DA microsatellite markers which can distinguish healer mice from non-healer mice and identifying microsatellite markers which segregate with enhanced wound healing in progeny of the mice, where a chromosomal locus containing at least one enhanced wound healing gene is identified. A method of treating a wound; sepecially central and peripheral nerve wound. The methods of the invention are useful for restoring function after nerve injury in a mammal. (M) is useful as a mammalian model of enhanced wound healing, useful for identifying genes and gene products involved in enhanced wound healing, and to provide methods for wound healing. Asiafsleyl-121936 represent murine SAGE tags from CSTBL/6 and MRL mice which are used to illustrate the method of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                               New mammalian model for enhanced wound healing - useful for identifying enhanced wound healing genes.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    35.5%; Score 7.8; DB 1; Length 11; 81.8%; Pred. No. 6.6e+02; tive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 11 BP; 0 A; 3 C; 3 G; 5 T; 0 U; 0 Other;
                                                                                                                                                                               Claim 13; Page 56; 136pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAX54601 standard; DNA; 11 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  05-JUL-1999 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         732 GGAGAAACAGA 742
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WPI; 1999-494533/41.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            invention
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The specification describes antisense oligonucleotides (AAX52869-X55271)

directed against at least 2 mRNAs selected from target genes, coding and
non-coding regions of RNAs corresponding to target genes, gene initiation
codons, genomic flanking regions, intron-exon borders, the 5'-end, the 3'
end and the juxta-section between coding and non-coding regions and all
segments of RNAs encoding proteins associated with one or more diseases,
conditions or mixtures. The artisense oligonucleotides may be derived
from sequences AAX55272-74. These multiple target oligonucleotides
cofficially AAX5100-271) can be used for the antisense treatment of
diseases and conditions. Typical diseases and conditions are those
associated with impaired respiration and inflammation, including lung
diseases, pulmonary vasoconstriction, inflammation, respiratory
distress syndrome, pain, cystic fibrosis, pulmonary hypertension,
disease (COPD), and cancers such as leukemias, lymphomas, carcinomas e.g.
colon cancer, breast cancer, lung cancer, melanoma, hepatic metastases,
as all types of cancers which may metastasize or have metastasized
to the lungs, including breast and prostate cancer
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                                                                   New antisense oligonucleotides used in treatment of, e.g. pulmonary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match

35.5%; Score 7.8; DB 1; Length 11;

Best Local Similarity 81.8%; Pred. No. 6.6e+02;

Matches 9; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 11 BP; 0 A; 4 C; 1 G; 6 T; 0 U; 0 Other;
                                                                                                                                                                                      Disclosure; Page 46; 120pp; English.
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WPI; 1999-229400/19.
                                                                                                                  vasoconstriction
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29-OCT-1992;
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                                     The present sequence represents a potential triple-helix forming region. It can be used to demonstrate the assay of the invention. The assay comprises adding a sample containing double-stranded DNA test sequences, e.g. containing the present sequence, to an aqueous medium containing at least one complex of anchor DNA, attached to a solid support, and reporter DNA, where either a part of the anchor DNA or reporter DNA is designed to form a triple-strand structure with part of the test sequence. Triplex formation results in displacement of the reporter DNA which is detected as an indication of the presence of the DNA test sequence. The method is used to detect DNA sequences, particularly for identification of bacteria (DN detecting genes for ribosomal RNA) in clinical samples, but also detection of oncogenes and Hepatitis B virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        phosphorothicate; impaired respiration; inflammation; allergy; allergic disease; bronchoconstriction; inhibitor; antinflammatory; antiallergic; antiathmatic; cytostatic; analgesic; impaired airway; lung disease; ischaemic condition; pulmonary vasoconstriction; asthma; respiratory distress syndrome; pain; cystic fibrosis; emphyseme; pulmonary hyperiension; chronic obstructive pulmonary disease; COPD;
                                                                                                                                                                                                                                                                                                                                                                                                   0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; adenosine receptor; low adenosine antisense oligonucleotide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New antisense oligonucleotides useful for treating e.g. pulmonary vasoconstruction, inflammation, allergies, asthma, hypertension, bronchitis, emphysema, respiratory distress syndrome, ischemia or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human adenosine receptor related polynucleotide SEQ ID NO:1737.
                                                                                                                                                                                                                                                                                                                                                       35.5%; Score 7.8; DB 1; Length 11; 81.8%; Pred. No. 6.6e+02; ive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.
                                                                                                                                                                                                                                                                                                               Sequence 11 BP; 6 A; 0 C; 5 G; 0 T; 0 U; 0 Other;
Disclosure; Col 17-18; 168pp; English.
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Best Local Similarity 81.80
Local 9, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                         731 AGGAGAAACAG 741
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      03-AUG-1999;
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useful for the treatment of diseases associated with inflammation, coffects affiliat the lungs of a subject. They can be used for treating e.g. ischaemic conditions, pulmonary vasoconstriction, allergies, asthma, impeded respiration, respiratory distress syndrome, pain, cystic. C.fibrosis, pulmonary hypertension, emphysema, chronic obstructive pulmonary hypertension, emphysema, chronic obstructive concers which may metastasise to the lungs, including breate and prostate cancer. The reduction of the adenosine content of the construction and inflammation. AAA3313 to AAA3312 represent the release of deoxyadenosine which activates adenosine receptors causing bronchoconstriction and inflammation. AAA3313 to AAA3312 represent the invention, which correspond to SEQ ID NO:1 to 2815, and then the last 185 sequences are also called SEQ ID NO:1 to 2815, and then the last 185 sequences are also called SEQ ID NO:1 to 185, but the sequences differ from the previously named sequences. SEQ ID NO:1 to 2815, and then the last 185 sequences given in the disclosure of the present invention. N. B. Sequences given in the disclosure of the present invention. N. B. C. Up with their corresponding SEQ ID NO: sequences given in the sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Low adenosine (A) content antisense oligonuclectides which do not trigger adenosine receptors during metabolism, useful e.g. for treating cancers and respiratory obstructions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Low adenosine antisense oligonucleotide, phosphorothioate, allergy, human, airway disorder, bronchoconstriction, lung inflammation, surfactant depletion; respiratory, bronchodialeor; antinflammatory, immunosuppressive, antiasthmatic; analgesic; hypotensive, cytostatic; respiratory obstruction; pulmonary obstruction; impeded respiration, surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS; respiratory distress syndrome; pain; cystic fibrosis, allergic rhinitis; pulmonary hypertension; emplysema; pulmonary transplantation rejection; chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human eosinophil derived neurotoxin polynucleotide fragment #1737.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 7.8; DB 1; Length 11;
Pred. No. 6.6e+02;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 11 BP; 0 A; 4 C; 1 G; 6 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAF20170 standard; DNA; 11 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99US-0127958P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24-MAR-2000; 2000WO-US008020.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     35.5%;
81.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (UYEC-) UNIV EAST CAROLINA. (NYCE/) NYCE J W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14-MAR-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      731 AGGAGAAACAG 741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11 AGCAGAAAGAG 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2000-679539/66.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200062736-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  06-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26-OCT-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cancer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAF20170;
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                                                                                                                                                                                                                                                                                                                                                                                                        listing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 959
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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Query Match
Best Local Similarity 81.6-
has 9; Conservative
qq
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The present sequence is that of a fragment of HS501, a DNA probe located at the 5' end of the promoter region of a rice alpha-amylase gene, OSAmy-b. It covers nucleotides -108 to -118 of the gene and has a sequence is milar to that of the animal core enhancer. Rice aleurons was found to contain proteins that interacted with this HS501 DNA fragment. The invention relates to the use of an alpha-amylase gene promoter and signal invention relates to the use of an alpha-amylase gene promoter and signal cangenic plants and transgenic plant seeds. A transgenic monocot is obtained by: transforming an immature embryo with DNA comprising a plant cangina-amylase promoter that is induced under a sugar-depleted or sugar-free condition, a signal peptide sequence, and an exogenous sequence condition, a signal peptide sequence, and an exogenous sequence condition a gene product; regenerating the transformed plant; and growing the transgenic plant, which expresses the gene product under sugar-depleted or sugar-free conditions. The transgenic plants and their products are useful in brewing and to produce glucose from starch
                                                                                                               Producing a transgenic monocot plant comprising a transgene under control of an alpha amylase promoter and signal peptide sequences, provides transgenic plants particularly cereals for the brewing industry.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 11 BP; 0 A; 2 C; 3 G; 6 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                          Example 1; Col 20; 44pp; English.
                                     WPI; 2001-647191/74.
g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             activating proteins, and trainshivers, trainstitution interests, calculations and antibody receptors, cytokines and chemokines, endogenously produced specific and non-specific enzymes, binding proteins, adensine molecules and their receptors, cytokine and chemokine receptors, adenseine receptors, bradykinin receptors, central nervous system (CNS) and peripheral nervous and non-nervous system receptors, CNS and peripheral nervous and non-nervous system peptide transmitters, defensins, growth factors, vasoactive peptides and receptors, binding proteins and malignancy associated proteins. The anticlusing respiratory obstruction (especially pulmonary obstruction and/or bronchoconstriction) and/or lung inflammation, allergy(ies) and/or surfactant hypproduction which are associated with a disease or condition selected from pulmonary vasoconstriction, inflammation, allergies, asthma, impeded respiration, respiratory distress syndrome (RDS), pain, cystic fibrosis (CR), allergic thinisis (CR), pulmonary disease (COPP), pulmonary transplantation rejection, pulmonary infections, pronchitis,
                                                                                                                    The present invention describes low adenosine (A) content antisense oligonucleotides and compositions (I) comprising them. In the antisense oligonucleotides the A is replaced by a 'Universal' or alternative base. (I) can have respiratory, bronchodilator, antiinflammatory, analgesic, immunosuppressive, antiasthmatic, hypotensive and cytostatic activities. The antisense oligonucleotides and (I) can be used to down-regulate the expression and or activity of target polypoptides associated with lung/respiratory disorders and malignancies, such as stimulating and activating peptide factors and transmitters, transcription factors,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        pulmonary transplantation rejection, pulmonary infections, bronchitis, and/or cancer. AAF18434 to AAF21543 represent human polynucleotide fragments and antisense oligonucleotides used in the exemplification of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 11 BP; 0 A; 4 C; 1 G; 6 T; 0 U; 0 Other;
                                              Claim 14; Page 142; 1592pp; English.
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Human; skin ageing; skin stress; EST; expressed sequence tag; ss.
Match 11; Match 15.5%; Score 7.8; DB 1; Length 11; Local Similarity 81.8%; Pred. No. 6.6e+02; see 9; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                              Human skin stress/ageing related EST SEQ ID NO 1044.
                                                                                                                             ABQ87289 standard; cDNA; 11 BP
                                                                                                                                                                                                                                                                                                          20-DEC-2001; 2001WO-EP015178.
                                                                                                                                                                                                                                                                                                                                 03-JAN-2001; 2001DE-01000121
                                                                                                                                                                         10-SEP-2002 (first entry)
                                               734 AGAAACAGAAC 744
                                                                     11 AGAAACGCAAC 1
                                                                                                                                                                                                                                                                                                                                                        (HENK ) HENKEL KGAA
                                                                                                                                                                                                                                                               40200253773-A2
                                                                                                                                                                                                                                           Homo sapiens.
                                                                                                                                                                                                                                                                                      11-JUL-2002.
                                                                                                                                                    ABQ87289;
    Query Match
                                                                                                        961
                           Matches
                                                                                                      RESULT 96
ABQ87289/
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                                                                                                                                                                                                                                                                                                            Alpha-amylase; promoter; rice; transgenic plant; angiosperm; monocot;
                                                                                                                     Gaps
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                                                                                             35.5%; Score 7.8; DB 1; Length 11; 81.8%; Pred. No. 6.6e+02;
                                                                                                                   2; Indels
                                                                                                                                                                                                                                                                                        Rice alpha-amylase gene promoter probe fragment.
                                                                                                                   0; Mismatches
                                                                                                                                           731 AGGAGAAACAG 741
                                                                                                                                                                11 AGCAGAAAGAG 1
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The invention relates to identifying (M1) genes in vitro that, in humans or animals, are important for skin ageing and/or skin stress by serial analysis of gene expression between mixtures of transcribed and

Claim 8; Page 80; 325pp; German.

gene

Identifying genes involved in skin stress and aging, useful e.g. in screening for cosmetic or therapeutic agents, based on differential expression.

Conradt M, Hofmann K;

Petersohn D,

WPI; 2002-528865/56.

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Gaps

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optionally translated, genetically encoded factors (A) obtained from young and aged Stin, to identify that genes that show strong differential expression. (A) comprises protein or mRNAs or their fragments. (MI) is useful for: identifying markers of skin ageing and/or stress; determining skin ageing and/or stress; and identifying or determining the effects of pharmaceutical or cosmetic agents for control of skin ageing. The present sequence is one of a group of human skin ageing/stress related expressed sequence tags (ABQ86246-ABQ87680) of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to identifying (MI) genes in vitro that, in humans or animals, are important for skin ageing and/or skin stress by serial analysis of gene expression between mixtures of transcribed and optionally translated, genetically encoded factors (A) obtained from young and aged skin, to identify that genes that show strong differential expression. (A) comprises protein or mRNAs or their fragments. (MI) is useful for: identifying markers of skin ageing and/or stress; determining skin ageing and/or stress; and identifying or determining the effects of pharmaceutical or cosmetic agents for control of skin ageing. The present sequence is one of a group of human skin ageing/stress related expressed sequence tags (ABQ86246-ABQ87680) of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Identifying genes involved in skin stress and aging, useful e.g. in screening for cosmetic or therapeutic agents, based on differential gene
                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; skin ageing; skin stress; EST; expressed sequence tag; ss.
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                                                                                                                                                                                                      35.5%; Score 7.8; DB 1; Length 11; 81.8%; Pred. No. 6.6e+02; rive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    35.5%; Score 7.8; DB 1; Length 11; 81.8%; Pred. No. 6.6e+02; tive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human skin stress/ageing related EST SEQ ID NO 297
                                                                                                                                                                     Sequence 11 BP; 1 A; 5 C; 1 G; 4 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 11 BP; 2 A; 3 C; 2 G; 4 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hofmann K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 8; Page 49; 325pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                   BP.
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                                                                                                                                                                                                                                                                                                                                                                                                               ABQ86542 standard; cDNA; 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                Conservative
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                                                                                                                                                                                                                                                                                  732 GGAGAAACAGA 742
                                                                                                                                                                                                                                                                                                                    11 GGGGATACAGA 1
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                                                                                                                                                                                    Query Match
Best Local Similarity
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Best Local Similarity
Local 9; Conserve
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200253773-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Petersohn D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10-SEP-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABQ86542;
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8X33333553X8
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In vitro identification of skin-expressed genes, useful for determining homeostasis and identifying cosmetic or pharmaceutical agents against

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Hofmann

Petersohn D, Conradt M,

(HENK) HENKEL KGAA

WPI; 2002-590638/63.

e.g. skin cancer.

20-DEC-2001; 2001WO-EP015179. 03-JAN-2001; 2001DE-01000127

WO200253774-A2.

11-JUL-2002

Homo sapiens.

Human, skin, dermatological, vulnerary, antipsoriatic, antiseborrhaeic, immunosuppressive, antiinflammatory, cytostatic, SAGE, neurodermatitis, psoriasis, dermatitis, skin cancer, EST, expressed sequence tag, ss.

BP.

entry)

(first

21-OCT-2002

ABV63070;

Human skin EST 856

ABV63070 standard; cDNA; 11

ABV63070

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                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to in vitro identification (M1) of genes expressed in the skin of humans or animals by subjecting a mixture of genetically encoded factors from skin, to serial analysis of gene expression ($AGE) so as to identify skin-expressed genes and quantify their expression. (M1) is useful for identifying genes involved in skin homeostasis; to determine skin homeostasis and to test agent (A) that maintains or promotes skin homeostasis or that can be used for treating skin disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma; ichthyosis atopic dermatitis; acne, seborthea; lupus erythematosus; rosaces; melanoma; basal cell carcinoma; and carcinoma or starcoma of the skin. The present sequence is that of a human expressed sequence tag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 11 BP; 7 A; 1 C; 3 G; 0 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 49; 1345pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABV64588 standard; cDNA; 11 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          35.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 81.8
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               735 GAAACAGAACA 745
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 GAAACAGGAAA 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (EST) of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human skin EST
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ABV64588/C
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AC ABV645
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DT 21-OCT
DT 21-OCT
DE HUMAN
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Conservative 727 TGCCAGGAGAA 737

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The invention relates to in vitro identification (M1) of genes expressed in the skin of humans or animals by subjecting a mixture of genetically encoded factors from skin, to serial analysis of gene expression (SAGE) so as to identify skin-expressed genes and quantify their expression.

(M1) is useful for identifying genes involved in skin homeostasis; to determine skin homeostasis and to test agent (A) that maintains or promotes skin homeostasis or that can be used for treating skin disorders, specifically neurodermatitis, sumburn; psoriasis; scleroderma; ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus; rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the skin. The present sequence is that of a human expressed sequence tag (EST) of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human, skin, dermatological, vulnerary, antipsoriatic, antiseborrhaeic, immunosuppressive, antiinflammatory, cytostatic, SAGE, neurodermatitis, psoriasis, dermatitis, skin cancer, EST, expressed sequence tag, ss.
            Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic; immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis; psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
                                                                                                                                                                                                                                                                                                                                                 In vitro identification of skin-expressed genes, useful for determining homeostasis and identifying cosmetic or pharmaceutical agents against
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 11 BP; 2 A; 4 C; 1 G; 4 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Page 91; 1345pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20-DEC-2001; 2001WO-EP015179.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 81.8
Matches 9; Conservative
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                                                                                                                                                                                                                                                                                   Conradt
                                                                                                                                                                                                                                                                                                                   WPI; 2002-590638/63.
                                                                                                                                                                                                                                                 (HENK ) HENKEL KGAA
                                                                                                                                                                                                                                                                                                                                                                                     e.g. skin cancer.
                                                                                                                                                                                                                                                                                   Petersohn D,
                                                                                 Homo sapiens
                                                                                                                                                 11-JUL-2002
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Hofmann K;

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The invention relates to in vitro identification (M1) of genes expressed in the skin of humans or animals by subjecting a mixture of genetically encoded factors from skin, to serial analysis of gene expression (SAGE) so as to identify skin-expressed genes and quantify their expression. (M1) is useful for identifying genes involved in skin homeostasis; to promotes skin homeostasis and to test agent (A) that maintains or promotes skin homeostasis or that can be used for treating skin disorders, specifically neurodermatitis; sunburn, psoriasis; scleroderma; ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus; rosacea, melanoma; basal cell carcinoma; and carcinoma or sarcoma of the skin. The present sequence is that of a human expressed sequence tag (EST) of the invention
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                                                                                                                                                                                                                                                      In vitro identification of skin-expressed genes, useful for determining homeostasis and identifying cosmetic or pharmaceutical agents against
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic; immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis; psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 11 BP; 2 A; 3 C; 2 G; 4 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 172; 1345pp; German
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03-JAN-2001; 2001DE-01000127.
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35.5%; Score 7.8; DB 1; Length 11; 81.8%; Pred. No. 6.6e+02; rive 0; Mismatches 2; Indels

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Disclosure; Page 182; 1345pp; German

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                             The invention relates to in vitro identification (M1) of genes expressed in the skin of humans or animals by subjecting a mixture of genetically encoded factors from Skin, to serial analysis of gene expression (SAGE) so as to identify skin-expressed genes and quantify their expression.

(M1) is useful for identifying genes involved in skin homeostasis; to determine skin homeostasis and to test agent (A) that maintains or promotes skin homeostasis or that can be used for treating skin disorders, specifically neurodermatitis; sunburn; psoriasis, scleroderma; ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus; rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the skin. The present sequence is that of a human expressed sequence tag.
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(MI) is useful for identifying genes and quantify their expression.

(MI) is useful for identifying genes involved in skin homeostasis; to determine skin homeostasis and to test agent (A) that maintains or promotes skin homeostasis or that can be used for treating skin disorders, specifically neurodermatitis; sunburn; psoriasis, scleroderma; ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus; rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the skin. The present sequence is that of a human expressed sequence tag
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35.5%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 6.6e+02;
Matches 9; Conservative 0; Mismatches 2; Indels
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Human, skin, dermatological, v immunosuppressive, antinflamm kW immunosuppressive, and an
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                                            Length 11;
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81.8%; Pred. No. 6.6e+02;
iive 0; Mismatches 2; Indels
            Sequence 11 BP; 0 A; 2 C; 1 G; 8 T; 0 U; 0 Other;
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                                                             Best Local Similarity 81.8
Matches 9; Conservative
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les 9; Conservative
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RESULT 969

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Conradt M, Hofmann K;
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les 9; Conserv
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ABV65783 standard; cDNA; 11 BP
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The invention relates to in vitro identification (M1) of genes expressed in the skin of humans or animals by subjecting a mixture of genetically encoded factors from skin, to serial analysis of gene expression (\$AGE) so as to identify skin-expressed genes and quantify their expression. (M1) is useful for identifying genes involved in skin homeostasis; to determine skin homeostasis and to test agent (A) that maintains or promotes skin homeostasis or that can be used for treating skin disorders, specifically neurodermatitis; sumburn; psoriasis; scleroderma; ichthyosis; atopic dermatitis; acnes; sebornhea; lupus expressed scleroderma; rosacea, melanoma; basal cell carcinoma, and carcinoma or sarcoma of the skin. The present sequence is that of a human expressed sequence tag In vitro identification of skin-expressed genes, useful for determining homeostasis and identifying cosmetic or pharmaceutical agents against e.g. skin cancer. Disclosure; Page 226; 1345pp; German. skin. The present seque (EST) of the invention

Sequence 11 BP; 1 A; 3 C; 2 G; 5 T; 0 U; 0 Other; Query Match

35.5%; Score 7.8; DB 1; Length 11; 81.8%; Pred. No. 6.6e+02; ive 0; Mismatches 2; Indels 9; Conservative 733 GAGAACAGAA 743 Local Similarity Best Loc Matches δ

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ABV63496 standard; cDNA; 11 ABV63496;

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(first entry) Human skin EST 1282, 21-OCT-2002

Human, skin, dermatological, vulnerary, antipsoriatic, antiseborrhaeic, immunosuppressive, antiinflammatory, cytostatic, SAGE, neurodermatitis, psoriasis, dermatitis, skin cancer, EST, expressed sequence tag, ss.

Homo sapiens

WO200253774-A2.

11-JUL-2002.

20-DEC-2001; 2001WO-EP015179

03-JAN-2001; 2001DE-01000127

(HENK) HENKEL KGAA.

WPI; 2002-590638/63.

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Hofmann

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Petersohn D, Conradt

In vitro identification of skin-expressed genes, useful for determining homeostasis and identifying cosmetic or pharmaceutical agents against e.g. skin cancer.

Disclosure; Page 60; 1345pp; German.

The invention relates to in vitro identification (MI) of genes expressed in the skin of humans or animals by subjecting a mixture of genetically encoded factors from skin, to serial analysis of gene expression (SAGE) so as to identify skin-expressed genes and quantify their expression.

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(M1) is useful for identifying genes involved in skin homeostasis; to determine skin homeostasis and to test agent (A) that maintains or promotes skin homeostasis or that can be used for treating skin disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma; ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus; rosacea, melanoma; basal cell carcinoma; and carcinoma or sarcoma of the skin. The present sequence is that of a human expressed sequence tag (EST) of the invention
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Pred. No. 6.6e+02;
0; Mismatches 2; Indels
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81.8%;
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Best Local Similarity
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9; Conservative

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RESULT 97 ABV69104

ABV69104 standard; cDNA; 11 BP.

ABV69104;

(first entry) 21-OCT-2002

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Gaps .; 0 Human skin EST 6890

Human, skin, dermatological, vulnerary, antipsoriatic, antiseborrhaeic, immunosuppressive, antiinflammatory, cytostatic, SAGE, neurodermatitis, psoriasis, dermatitis, skin cancer, EST, expressed sequence tag, ss.

Homo sapiens.

WO200253774-A2

11-JUL-2002.

20-DEC-2001; 2001WO-EP015179.

03-JAN-2001; 2001DE-01000127.

(HENK) HENKEL KGAA.

Hofmann Σ Conradt Petersohn D,

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WPI; 2002-590638/63.

In vitro identification of skin-expressed genes, useful for determining homeostasis and identifying cosmetic or pharmaceutical agents against e.g. skin cancer.

Disclosure; Page 216; 1345pp; German.

The invention relates to in vitro identification (M1) of genes expressed in the skin of humans or animals by subjecting a mixture of genetically encoded factors from skin, to serial analysis of gene expression (SAGE) so as to identify kin-expressed genes and quantify their expression. (M1) is useful for identifying genes involved in skin homeostasis, to promotes skin homeostasis and to test agent (A) that maintains or promotes skin homeostasis or that can be used for treating skin disorders, specifically neurodermatitis; sunburn; psoriasis, scleroderma; ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus; rosace; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the skin. The present sequence is that of a human expressed sequence tag (EST) of the invention

Sequence 11 BP; 3 A; 2 C; 5 G; 1 T; 0 U; 0 Other;

35.5%; Score 7.8; DB 1; 81.8%; Pred. No. 6.6e+02; Query Match Best Local Similarity schultz1-727.rng

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21-OCT-2002 (first entry)
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                                              Human skin EST 2284
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(M1) is useful for identifying genes involved in skin homeostasis, to promotes skin homeostasis and to test agent (A) that maintains or promotes skin homeostasis or that can be used for treating skin disorders, specifically neurodermatitis; sunburn, psoriasis, scleroderma; ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus; rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the skin. The present sequence is that of a human expressed sequence tag
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Pred. No. 6.6e+02;
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  Mismatches
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81.8%;
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Best Local Similarity 81.8.
Local Similarity 81.8.
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  9; Conservative
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     Matches
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The ABY6
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ABV64498 standard; cDNA; 11 BP.

ABV64498 RESULT 975
ABV64498
ID ABV6449
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733 GAGAACAGAA 743

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Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic; immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis; psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
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ABV70542/c
ID ABV70542 standard; cDNA; 11
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Best Local Similarity 81.0
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Gaps

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Length 11;

Score 7.8; DB 1; Length 11 Pred. No. 6.6e+02; 0; Mismatches 2; Indels

35.5%;

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The invention relates to in vitro identification (MI) of genes expressed in the skin of humans or animals by subjecting a mixture of genetically encoded factors from skin, to serial analysis of gene expression (SAGE) so as to identify skin-expressed genes and quantify their expression. (MI) is useful for identifying genes involved in skin homeostasis; to promotes skin homeostasis and to test agent (A) that maintains or promotes skin homeostasis or that can be used for treating skin disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma; ichthyosisis atopic dermatitis; acnes; seborthea; lupus erythematosus; rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the skin. The present sequence is that of a human expressed sequence tag
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                                    Disclosure; Page 64; 1345pp; German.
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Best Local Similarity 81.8
Matches 9; Conservative
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e.g. skin cancer.
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81.8%;
                     20-DEC-2001; 2001WO-EP015179
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                                                   03-JAN-2001; 2001DE-01000127
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The invention relates to in vitro identification (MI) of genes expressed in the skin of humans or animals by subjecting a mixture of genetically encoded factors from skin, to serial analysis of gene expression ($AGE) so as to identify skin-expressed genes and quantify their expression. (MI) is useful for identifying genes involved in skin homeostasis; to determine skin homeostasis and to test agent (A) that maintains or promotes skin homeostasis or that can be used for treating skin disorders, specifically neurodermatitis; sunburn, psoriaais, scleroderma; ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
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733 GAGAAACAGAA 743
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Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic; immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis; psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
                                                             ABV72009 standard; cDNA; 11 BP.
                                                                                                                21-OCT-2002 (first entry)
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rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the skin. The present sequence is that of a human expressed sequence tag (EST) of the invention
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                                                                                        Length 11;
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                                                             Sequence 11 BP; 0 A; 1 C; 3 G; 7 T; 0 U; 0 Other;
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81.8%;
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                                                                           Query Match
Best Local Similarity 81.8.
Local 9; Conservative
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Best Local Similarity 81.8
Matches 9; Conservative
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Pred. No. 6.6e+02;
0; Mismatches 2; Indels
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                                                                                                                                                          Hofmann K;
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81.8%;
20-DEC-2001; 2001WO-EP015179.
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Best Local Similarity
Matches 9; Conserv
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ABV66736
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immunosuppressive, antiinflammatory; cytostatic; SAGE; neurodermatitis; psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
                                                                                                                                                                                                                                                                                                       In vitro identification of skin-expressed genes, useful for determining homeostasis and identifying cosmetic or pharmaceutical agents against
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Best Local Similarity 81.87
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                                               Homo sapiens.
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immunosuppressive, antiinflammatory, cytostatic, SAGE, neurodermatitis,
psoriasis, dermatitis, skin cancer, EST, expressed sequence tag, ss.
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Pred, No. 6.6e+02;
Pred. Tribales 2; Indels
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                                                            Hofmann
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81.8%;
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Best Local Similarity 81.8-
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(M1) is useful for identifying genes involved in skin homeostasis; to determine skin homeostasis and to test agent (A) that maintains or promotes skin homeostasis or that can be used for treating skin disorders, specifically neurodermatitis; sumburn; psoriasis; scleroderma;
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81.8%;
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The invention relates to in vitro identification (M1) of genes expressed in the skin of humans or animals by subjecting a mixture of genetically encoded factors from skin, to serial analysis of gene expression (SAGE) so as to identify skin-expressed genes and quantify their expression. (M1) is useful for identifying genes involved in skin homeostasis; to promotes skin homeostasis and to test agent (h) that maintains or promotes skin homeostasis or that can be used for treating skin disorders, specifically neurodermatitis; sunburn, psoriasis; scleroderma; ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus; rosacea, melanoma; basal cell carcinoma; and carcinoma or sarcoma of the skin. The present sequence is that of a human expressed sequence tag (EST) of the invention
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ABV66108/c
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ABV66108 standard; cDNA; 11 BP.

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The invention relates to in vitro identification (M1) of genes expressed in the skin of humans or animals by subjecting a mixture of genetically encoded factors from skin, to serial analysis of gene expression ($AGE$) so as to identify skin-expressed genes and quantify their expression. (M1) is useful for identifying genes involved in skin homeostasis; to promotes skin homeostasis and to test agent (A) that maintains or promotes skin homeostasis or that can be used for treating skin disorders, specifically neurodermatitis; sunburn, psoriasis, scleroderma; ichthyosis; atopic dermatitis; acne; seborrhes; lupus erythematosus; rosaces; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the skin. The present sequence is that of a human expressed sequence tag (EST) of the invention
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In vitro identification of skin-expressed genes, useful for determining homeostasis and identifying cosmetic or pharmaceutical agents against
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            e.g. skin cancer.
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The invention relates to in vitro identification (M1) of genes expressed in the skin of humans or animals by subjecting a mixture of genetically encoded factors from skin, to serial analysis of gene expression (SAGE) so as to identify skin-expressed genes and quantify their expression. (M1) is useful for identifying genes involved in skin homeostasis; to determine skin homeostasis and to test agent (A) that maintains or promotes skin homeostasis or that can be used for treating skin disorders, specifically neurodermatitis, sunburn; psoriasis; scleroderma; ichthyosis; atopic dermatitis; acne; sebornhea; lupus erythematosus; rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the skin. The present sequence is that of a human expressed sequence tag
In vitro identification of skin-expressed genes, useful for determining homeostasis and identifying cosmetic or pharmaceutical agents against
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(EST) of the invention
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11 AGGAGGACCAG

(first entry) Human skin EST 5888. Human, skin, dermatological, vulnerary, antipsoriatic, antiseborrhaeic, immunosuppressive, antiinflammatory, cytostatic, SAGE, neurodermatitis, psoriasis, dermatitis, skin cancer, EST, expressed sequence tag, ss.

20-DEC-2001; 2001WO-EP015179

03-JAN-2001; 2001DE-01000127

Hofmann K; Σ

Disclosure; Page 188; 1345pp; German.

The invention relates to in vitro identification (M1) of genes expressed in the skin of humans or animals by subjecting a mixture of genetically encoded factors from skin, to serial analysis of gene expression (SAGE) so as to identify skin-expressed genes and quantify their expression. (M1) is useful for identifying genes involved in skin homeostasis, to determine skin homeostasis and to test agent (A) that maintains or

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Query Match 35.5%; Score 7.8; DB 1; Length 11; Best Local Similarity 81.8%; Pred. No. 6.6e+02; Matches 9; Conservative 0; Mismatches 2; Indels

Sequence 11 BP; 7 A; 3 C; 0 G; 1 T; 0 U; 0 Other;

0 disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma; ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus; rosces, melanoma; basal cell carcinoma; and carcinoma or sarcoma of the skin. The present sequence is that of a human expressed sequence tag (EST) of the invention The invention relates to in vitro identification (M1) of genes expressed in the skin of humans or animals by subjecting a mixture of genetically encoded factors from skin, to serial analysis of gene expression (SAGE) so as to identify skin-expressed genes and quantify their expression. (M1) is useful for identifying genes involved in skin homeostasis; to promotes skin homeostasis and to test agent (A) that maintains or promotes skin homeostasis or that can be used for treating skin disorders, specifically neurodermatitis; sunburn, psoriasis, scleroderma; ichthyosis; atopic dermatitis; acne, seborrhea; lupus erythematosus; rosacea, melanoma; basal cell carcinoma; and carcinoma or sarcoma of the skin. The present sequence is that of a human expressed sequence tag (EST) of the invention In vitro identification of skin-expressed genes, useful for determining homeostasis and identifying cosmetic or pharmaceutical agents against Human; skin; dermatological; vulnerary; antipsoriátic; antiseborrhaeic; immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis; psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss. Gaps can be used for treating skin .; Score 7.8; DB 1; Length 11; Pred. No. 6.6e+02;); Mismatches 2; Indels Seguence 11 BP; 5 A; 3 C; 3 G; 0 T; 0 U; 0 Other; Disclosure; Page 205; 1345pp; German. Hofmann K; ., BP. 35.5%; 81.8%; 20-DEC-2001; 2001WO-EP015179. 03-JAN-2001; 2001DE-01000127 ABV68680 standard; cDNA; 11 (first entry) Σ Query Match
Best Local Similarity 81.8
Matches 9; Conservative 730 CAGGAGAAACA 740 11 CAGCAGAAGCA Human skin EST 6466. (HENK) HENKEL KGAA WPI; 2002-590638/63 e.g. skin cancer. WO200253774-A2 Homo sapiens Petersohn D, 21-OCT-2002 11-JUL-2002. ABV68680; RESULT 99
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The invention relates to in vitro identification (M1) of genes expressed in the skin of humans or animals by subjecting a mixture of genetically encoded factors from skin, to serial analysis of gene expression (SAGE) so as to identify skin-expressed genes and quantify their expression.

(M1) is useful for identifying genes involved in skin homeostasis; to promotes skin homeostasis and to test agent (A) that maintains or promotes skin homeostasis or that can be used for treating skin disorders, specifically neurodermatitis; sunburn; psoriaeis, scleroderma; ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus; rosacea, melanoma; basal cell carcinoma; and carcinoma or sarcoma of the skin. The present sequence is that of a human expressed sequence tag
                                                                                                                                                                                                                                                                                                                                                             In vitro identification of skin-expressed genes, useful for determining homeostasis and identifying cosmetic or pharmaceutical agents against
                                Human, skin, dermatological, vulnerary, antipsoriatic, antiseborrhaeic, immunosuppressive, antiinflammatory, cytostatic, SAGE, neurodermatitis, psoriasis, dermatitis, skin cancer, EST, expressed sequence tag, ss.
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                                                                                                                                                                                               20-DEC-2001, 2001WO-EP015179.
                                                                                                                                                                                                                                03-JAN-2001; 2001DE-01000127.
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Best Local Similarity 81.8.
Final 9; Conservative
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                                                                                                                                                                                                                                                               (HENK ) HENKEL KGAA
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   Human skin EST 251
                                                                                                                                                                                                                                                                                                                                                                                               e.g. skin cancer.
                                                                                                                               WO200253774-A2
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(M1) is useful for identifying genes involved in skin homeostasis; to promotes skin homeostasis and to test agent (A) that maintains or promotes skin homeostasis or that can be used for treating skin disorders, specifically neurodermatitis; sunburn; psoriacis; scleroderma; ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus; rosacea; melanoma; basal cell carcinoma, and carcinoma or sarcoma of the skin. The present sequence is that of a human expressed sequence tag
                                                                                                                                                                                                                                         Human, skin, dermatological, vulnerary, antipsoriatic, antiseborrhaeic, immunosuppressive, antiinflammatory, cytostatic, SAGE, neurodermatitis, psoriasis, dermatitis, skin cancer, EST, expressed sequence tag, ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        In vitro identification of skin-expressed genes, useful for determining homeostasis and identifying cosmetic or pharmaceutical agents against
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                                                                                                              BP.
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81.8%;
                                                                                                            ABV69886 standard; cDNA; 11
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736 AAACAGAACAC 746
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Best Local Similarity
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ABV62465
ID ABV6241
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AC ABV6241
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DT 21-OCT
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immunosuppressive, antiinflammatory, cytostatic, SAGE, neurodermatitis,
psoriasis, dermatitis, skin cancer, EST, expressed sequence tag, ss.
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35.5%; Score 7.8; DB 1; Length 11; 81.8%; Pred. No. 6.6e+02; tive 0; Mismatches 2; Indels
                                                                                                                                     ABV65390 standard; cDNA; 11 BP
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The invention relates to in vitro identification (M1) of genes expressed in the skin of humans or animals by subjecting a mixture of genetically schooled from skin, to serial analysis of gene expression (SAGE) so as to identify skin-expressed genes and quantify their expression (M1) is useful for identifying genes involved in skin homeostasis, to determine skin homeostasis and to test agent (A) that maintains or promotes skin homeostasis or that can be used for treating skin promotes skin homeostasis or that can be used for treating skin ichthyosis, atopic dermatitis, and, subburn, psoriasis, scleroderma; ichthyosis, atopic dermatitis, acne, seborrhea; lupus erythematosus; rosacea; melanoma; basal call carcinoma, and carcinoma or sarcoma of the skin. The present sequence is that of a human expressed sequence tag

Claim 24; Page 265; 1345pp; German.

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Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic; immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis; psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        In vitro identification of skin-expressed genes, useful for determining homeostasis and identifying cosmetic or pharmaceutical agents against
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      03-JAN-2001; 2001DE-01000127
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(first entry)

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The invention relates to in vitro identification (M1) of genes expressed in the skin of humans or animals by subjecting a mixture of genetically encoded factors from skin, to serial analysis of gene expression (SAGE) so as to identify skin-expressed genes and quantify their expression.

(M1) is useful for identifying genes involved in skin homeostasis, to determine skin homeostasis and to test agent (A) that maintains or promotes skin homeostasis or that can be used for treating skin of promotes skin homeostasis or that can be used for treating skin to promote is a topic dermatitis, suchurn; psoriasis; scleroderma; ichthyosis; atopic dermatitis, acne; seborrhea; lupus erythematosus; rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the stand, of the present sequence is that of a human expressed sequence tag
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Pred. No. 6.6e+02;
0; Mismatches 2; Indels
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nes 9; Conservative
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(EST) of the invention
                                                                        Conradt
(HENK ) HENKEL KGAA
                                                                                                                                            WPI; 2002-590638/63
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                                                                        Petersohn D,
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35.5%; Score 7.8; DB 1; Length 11; 81.8%; Pred. No. 6.6e+02; tive 0; Mismatches 2; Indels

9; Conservative 735 GAAACAGAACA 745 1 GAAACAGGAAA 11

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Sequence 11 BP; 7 A; 1 C; 3 G; 0 T; 0 U; 0 Other;

of the invention

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The invention relates to in vitro identification (W1) of genes expressed in the skin of humans or animals by subjecting a mixture of genetically seconded factors from skin, to serial analysis of gene expression (SAGE) so as to identify skin-expressed genes and quantify their expression. (M1) is useful for identifying genes involved in skin homeostasis; to promotes skin homeostasis and to test agent (A) that maintains or promotes skin homeostasis or that can be used for treating skin disorders, specifically neurodermatitis; sunburn, psoriasis; scleroderma; inchthyosis; atopic dermatitis; acnow, seborrhea; lupus erythematosus; rosacca; melanoma; basal cell carcinoma, and carcinoma or sarcoma of the skin. The present sequence is that of a human expressed sequence tag
                                                                                                                                                                      Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic; immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis; psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                In vitro identification of skin-expressed genes, useful for determining homeostasis and identifying cosmetic or pharmaceutical agents against
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hofmann K;
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                                  ABV71042 standard; cDNA; 11 BP.
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                                                                                                        (first entry)
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                                                                                                                                            Human skin EST 8828
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                                                                                                        21-OCT-2002
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                                                                       ABV71042;
RESULT 995
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Hofmann K;

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                                                                                                                                                                                                                                                             Human; mouse, rat, TEM, tumour endothelial marker, NEM, PEM, cytostatic, normal endothelial marker; pan-endothelial marker; immunostimulant; antianglogenic; tumour; neoanglogenesis; vascularised tumour; polycystic kidney disease; diabetes; retinopathy; rheumatoid arthritis; psoriasis; ss.
                                                                    Gaps
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                                             Length 11;
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                      Sequence 11 BP; 6 A; 0 C; 5 G; 0 T; 0 U; 0 Other;
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                                           Score 7.8; DB 1;
Pred. No. 6.6e+02;
0; Mismatches 2.
                                                                                                                                                                                                                                        Human Pan-Endothelial Marker SEQ ID NO 49.
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                                                                                                                                                                     ABL91951 standard; cDNA; 11 BP.
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11-AUG-2000; 2000US-0224360P.
11-APR-2001; 2001US-0282850P.
                                            35.5%;
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                                Owery Match
Best Local Similarity 81.0.
9; Conservative
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(EST) of the invention
                                                                                        733 GAGAAACAGAA
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                                                                                                                                                                                                                                                                                                                                Homo sapiens
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The invention relates to a novel pharmaceutical composition, which has a first active agent comprising an oligonucleotide antisense to the intiation condon, coding region, 5' or 3' end genomic flanking regions, 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of junctions of genes encoding a polypeptide associated with lung and/or nasal airway dysfunction and a second active agent comprising an entiinflammatory steroid and ubjudinone. A composition of the invention has antiinflammatory, antiallergic, antiasthmatic, hypotensive, immunosuppressive, and cytostatic activity. The composition may have a use in antisense gene therapy. The composition may have a use in antisense gene therapy. The composition is useful for treating or preventing a respiratory, lung or malignant disease or condition, also for on thindiammatory steroid in a subject, for reducing levels of an antiinflammatory steroid in a subject, for reducing levels of denosine of the creducing sensitivity to adenosine, reducing levels of adenosine lung surfactant in a subject, a reaging levels of adenosine con lung surfactant in a subject, a reaging levels of using inflammation, lung allergies, or a respiratory disease or condition. In the patent is not represented in the printed entity of the patent is not represented in the printed entity of the patent is not represented in the printed entity of the patent is not represented in the printed entition.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human, antisense, lung dysfunction, nasal airway dysfunction, antinflammatory steroid; ubiquinone; antiinflammatory; antiallergic; antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy; antisense gene therapy; respiratory; lung; adenosine sensitivity; adenosine receptor; bronchodilation; bronchoconstriction; lung allergy; lung inflammation; respiratory disease; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human eosinophil derived neurotoxin antisense fragment no.1724.
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81.8%; Pred. No. 6.6e+02;
iive 0; Mismatches 2; Indels
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Tang L, Shahabuddin
                                                                                                                                                                                                                                                                                                      BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24-APR-2001; 2001US-0286137P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (EPIG-) EPIGENESIS PHARM INC.
                                                                                                                                                                                                                                                                                                 ABZ95864 standard; DNA; 11
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727 IGCCAGGAGAA 737
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Best Local Similarity
Matches 9; Conserv
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Miller S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ubiquinone
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Query Match 35.5%; Score 7.8; DB 1; Length 11; Best Local Similarity 81.8%; Pred. No. 6.6e+02; Matches 9; Conservative 0; Mismatches 2; Indels

Modified promoter associated DNA #6.

(first entry

23-JUL-2003

ACA61506;

ACA61506 standard; DNA; 11

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New purified human transmembrane protein, designated as tumor endothelial marker (TEM) 3, useful for detecting, diagnosing or treating tumors, polycystic kidney disease, diabetic retinopathy, rheumatoid arthritis or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention relates to a novel method for the isolation of endothelial cells (ECs), and the identification of genes expressed in normal and tumour ECs. Tumour endothelial marker (TEM), normal endothelial marker (TEM), normal normal and pan-endothelial marker (PEM) genes are identified in human ECs. The human EC marker proteins and the polynucleotide sequences encoding them are useful for detecting, diagnosing or treating tumours as well as polycystic kidney disease, diabetic retinopathy, rheumatoid arthritis, and psoriasis. They are also useful for inhibiting neoangiogenesis or tumour angiogenesis, for inducing an immune response to tumour andiothelial cells in a patient, or for identifying candidate drugs for treating tumours. ABX71828-ABX71899 represent DNA tags for human PEM, TEM or NEM genes
                                                                                                                                                                                                                                                                         Human; endothelial cell; EC; tumour endothelial cell; TEM; NEM; Tumour endothelial marker; normal endothelial marker; PEM; pan-endothelial marker; polycystic kidney disease; psoriasis; diabetic retinopathy; rheumatoid arthritis; tumour anglogenesis; necanglogenesis; immune response; cytostatic; antidiabetic; ophthalmological; antirheumatic; antiarthritic; antidiabetic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 7.8; DB 1; Length 11; Pred. No. 6.6e+02; 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kinzler KW, Vogelstein B;
                                                                                                                                                                                                                                         DNA tag used to identify human gene encoding PEM 49.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 11 BP; 2 A; 3 C; 4 G; 2 T; 0 U; 0 Other;
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                                                                                                                              BP.
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06-FEB-2002; 2002US-0354262P.
                                                                                                                              ABX71876 standard; DNA; 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (UYJO ) UNIV JOHNS HOPKINS
                                                                                                                                                                                                     12-MAR-2003 (first entry)
731 AGGAGAAACAG 741
                                 AGCAGAAAGAG 1
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Best Local Similarity
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ABX71876
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The invention describes a promoter which can function in a Bacillus genus microbe in which the ratio of adenine to cytosine in the sequence near the 3'-end of said promoter is 0.5 to 2 and the activity of the promoter is higher than that of a natural promoter. The promoter is useful in the preparation of a protein. This sequence represents a modified promoter
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                                                                                         Promoter; Bacillus genus microbe; protein production; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Promoter; Bacillus genus microbe; protein production; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 11 BP; 4 A; 1 C; 6 G; 0 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Modified promoter associated DNA #1.
                                                                                                                                                                                                                                                                                                                     Example 5; Page 8; 15pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACA61501 standard; DNA; 11 BP.
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                                                                                                                                                                                                                                   (SHOS ) SHOWA SANGYO CO.
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ses 9; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                       associated DNA
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ACA61501
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Conservative 727 TGCCAGGAGAA 737

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RESULT 99 ACA61506

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Length 12;

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Query Match
Best Local Similarity
Matches 9; Conserv
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modified_base
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                                                                                                                                                                            03-JAN-1996
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02-AUG-1994;
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                                                       The invention describes a promoter which can function in a Bacillus genus microbe in which the ratio of adenine to cytosine in the sequence near the 3'-end of said promoter is 0.5 to 2 and the activity of the promoter is higher than that of a natural promoter. The promoter is useful in the preparation of a protein. This sequence represents a modified promoter associated DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The inventors claim synthetic porcine preprorelaxin and prorelaxin and synthetic A, B and C peptide chains of prolaxin, and a gene for expression of porcine preprorelaxin or prorelaxin, and their sub- units (see AAN30186). They also claim a double-stranded DNA fragment for the expression of the signal peptide chain of porcine preprorelaxin comprising a coding strand and a complementary strand corresp. to a defined mRNA sequence (see AAN30187-N30194) which corresp. to the most homologous regions between the pig and rat cDNA sequences. A probe (AAAN30195) is also claimed. (Updated on 25-MAR-2003 to correct PF field.)
                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Genes and DNA transfer vectors for prorelaxin expression - useful in prodn. of porcine relaxin for veterinary and human use.
A modified promoter, an expression cassette, an expression vector, recombinant microbe, preparation of a protein.
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                                                                                                                                                                                                                                                                                                                                                                             Sequence of probe/primer which corresp. to bps 579-590 porcine
                                                                                                                                                              Query Match 35.5%; Score 7.8; DB 1; Length 11; Best Local Similarity 81.8%; Pred. No. 6.6e+02; Matches 9; Conservative 0; Mismatches 2; Indels
                                                                                                                                       Sequence 11 BP; 4 A; 2 C; 4 G; 1 T; 0 U; 0 Other;
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                                 Example 5; Page 8; 15pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Niall HD,
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                                                                                                                                                                                                                                                                                              BP.
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                                                                                                                                                                                                                                                                                            AAN30191 standard; DNA; 12
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                                                                                                                                                                                                            731 AGGAGAAACAG 741
                                                                                                                                                                                                                                  1 AGGAGTACCAG 11
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                                                                                                                                                                                                                                                                                                                                          (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                      Sus scrofa domestica.
                                                                                                                                                                                                                                                                                                                                                                                                              Relaxin; hormone; ds
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                                                                                                                                                                                                                                                                                                                                                                                        preprorelaxin cDNA.
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25-MAY-1992
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AAN30191
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tiling strategy, immobilised nucleic acid probe array, mitochondrial DNA, D-loop region; biological chip; hybridisation fingerprint; interrogation position; ss.
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/note= "3'-end of probe is covalently attached to chip
surface"
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Lipshutz RJ, Lobban PE, Miyada CG, Morris MS, Shah N, Sheldon EL;
                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                             2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human mitochondrial D-loop region DNA probe 12-15.
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Score 7.8; DB 1;
Pred. No. 6.8e+02;
0; Mismatches 2:
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Pred. No. 6.8e+02;
0; Mismatches 2
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94US-00284064.
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ilarity 81.8%;
Conservative
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Best Local Similarity 81.00,
Best Local Similarity 61.00,
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                                                                                                                     735 GAAACAGAACA 745
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14-SEP-1995;
Synthetic
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                                                                                                                                                                                                                                                                                                                                                                                    APTII906-41 are antisense oligonucleotides that are selectively hybridisable with a gene or the transcription products for sub-units of isoprenyl protein transferases, pref. farnesyl protein transferase or a gerany gerany protein transferase. Oligonucleotides contg. these antisense sequences or their derive, are useful in human or veterinary medicine for treatment of abnormal and/or uncontrolled cell proliferation, e.g. in cases of cardiovascular disease, cancer, viral infections or dermatology. Inhibiting prenylation prevents proteins from binding to active sites on cell membranes, so prevents transduction of extracellular cell signals and thus cell proliferation
                                                                                                                     isoprenyl protein transferase; farnesyl; geranyl geranyl; prenylation; inhibition; abnormal; uncontrolled; cell proliferation; cancer; cardiovascular disease; treatment; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Translation rate; heterologous protein; hydrophobicity; human; 1150RF; transmembrane domain; insertion; vaccine; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                         Anti-sense oligo-nucleotide(s) hybridising to isoprenyl protein transferase genes - or their transcripts, for treating abnormal or uncontrolled cell proliferation e.g. cancer.
                                                                                                   Antisense DNA to inhibit isoprenyl protein transferase expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Seguence 12 BP; 5 A; 1 C; 5 G; 1 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 7.8; DB 1;
Pred. No. 6.8e+02;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Translation rate controlling sequence AN.EKEK.
                                                                                                                                                                                                                                                                 (SCRC ) SCRAS SOC CONSEILS RECH APPL SCI.
                                                                                                                                                                                                                                                                                                                                                                    Claim 2; Page 12; 27pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAV05933 standard; DNA; 12 BP.
                                         AAT11908 standard; DNA; 12 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        35.5%;
81.8%;
                                                                                                                                                                                                                           95GB-00013246
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              731 AGGAGAAACAG 741
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                                                                                                                                                                                                                                                                                       Colote S, Pirotzky E;
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les 9; Conserv
                                                                                                                                                                                                                           29-JUN-1995;
                                                                                                                                                                                                                                              29-JUN-1994;
                                                                                13-JUL-1996
                                                                                                                                                                                   3B2290791-A.
                                                                                                                                                                Synthetic.
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                                                              AAT11908;
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                                 AAT11908
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This oligonucleotide comprises a sequence that is used to control the rate of translation of a protein in a heterologous organism. The sequence is based on regions of amino acid hydrophobicity in the amino acid sequence of the human 115RF protein and is adapted for controlling the rate of protein translation in Aspergillus nidulans. The rate control sequences are found downstream of regions encoding transmembrane domains (TMD) and at a distance of 50-85 codons from these regions. The control region increases production and assembly yield of the heterologous protein and improves correct insertion into the membrane. The translation delay imposed by the sequence favours formation of the protein with its native 3-dimensional structure. The control sequence can be used to generate constitute for the expression of heterologous proteins especially
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nucleic acid encoding protein with hydrophobic or trans-membrane domain includes downstream of this domain a region that slows down translation, improves product and assembly yield and correct incorporation into the membrane, e.g. for use in vaccines.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INF-alpha mRNA series 1 (5' untranslated cap region) oligonucleotide 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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0
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Pred. No. 6.8e+02;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 12 BP; 10 A; 0 C; 2 G; 0 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                     (COMS ) COMMISSARIAT ENERGIE ATOMIQUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Fig 5; 73pp; French.
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Local Similarity 81.8%;
Local Similarity 81.8%;
Les 9; Conservative (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           735 GAAACAGAACA 745
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 GAAAAAGAAAA 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1997-489636/45.
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Homo sapiens.
                                                                                                                                                                                                                                                                        26-MAR-1996;
                                                                                                                                                                                                    25-MAR-1997;
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                                                                                                                                    02-OCT-1997
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                                                                                                                                                                                                                                                                                                                                                                                                      Kepes F;
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AAT63016/c
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95GB-000188647.

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98US-00019387
  05-FEB-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gorski JA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAV16650;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic
                                             Meyer RB,
                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 1007
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Matches
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                                                                                                                              oligonucleotides of series 1,AAT63014-21, have specific anti-mRNA sequences to the 5' untranslated cap region of tumour necrosis factor (TNF)-alpha mRNA. These Oligonucleotides are an example of a new chimeric oligonucleotide library, used to identify an antisense binding site in a target mRNA (in this case TNF-alpha). The library comprises a set of distinct chimeric oligonucleotides capable of hybridising to mRNA to form a duplex, the nucleotide sequences of which each have a common length of 7-20 bases. All of the nucleotides of the common length which are present as subsequences in the target mRNA are present in the library. Each as subsequences omprises a recognition region recognisable by a duplex-cutting RNAse, and a flanking region of chemically modified nucleotides which binds to the mRNA sufficiently tightly to stabilise the duplex for the RNAse. Each oligonucleotide is protected against cutlents antisense compounds against specific mRNA targets. The continents of the second of the second of the second of the second of effective antisense compounds against specific mRNA targets. The antisense compounds against the reapeutic agents, and as
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CCR-5 gene, CRR-5; chemokine receptor; triple-stranded complex; therapy; co-receptor prevention; human immunodeficiency virus resistance; HIV; macrophage entry inhibition; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /*tag= a
/note= "ClAmb-NH-(CH2)6-0-pG nucleotide, where ClAmb is
                                                                          Chimeric oligo:nucleotide library - for use in identifying anti-sense binding sites in target messenger RNA.
                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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/note= "Gp-O-(CH2)6-OH modified nucleotide"
                                                                                                                                                                                                                                                                                                                                                              Sequence 12 BP; 0 A; 4 C; 2 G; 6 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CCR-5 gene targeting sequence TFO1.
                                                                                                             Example 2; Page 27; 44pp; English.
                                                                                                                                                                                                                                                                                                                      drug target validation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAV55018 standard; DNA; 12 BP.
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          (BRAX-) BRAX GENOMICS LTD
                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                           734 AGAAACAGAAC 744
                                                                                                                                                                                                                                                                                                                                                                                                                                 12 AGGAAGAGAAC 2
                                                    WPI; 1997-202228/18.
                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
Matches 9; Conserv
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modified_base
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                                Schmidt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 1006
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a triple-stranded complex with part of the gene for CCR-5. CCR-5 is a chemofathe receptor, also known as CRR-5. The oligonucleocide, when modified by attachment of alkylating (cross-linking) agents, modify the CCR-5 gene, preventing its product from acting as a co-receptor for human immunodeficiency virus (HIV), and rendering cells resistant to this virus. They can be used to prevent entry of HIV into macrophages or therapeutically to prevent viral spread in infected subjects. The acid delivery, e.g. transfection, co-precipitation, liposome-mediated transfer etc. The sequences have a longer lasting effect than antisense
                                                                                                                                                                                                         Oligo:nucleotide(s) that form triplex(es) with part of chemokine receptor CCR-5 gene - are modified with crosslinking agents to alter gene so that cells are rendered resistant to human immunodeficiency virus.
                                                                                                                                                                                                                                                                                                                                                                                                                              This sequence represents an oligonucleotide of the invention, that forms a triple-stranded complex with part of the gene for CCR-5. CCR-5 is a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sequences directed to mRNA, and may produce heritable modifications in the gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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HLA-DR beta consensus sequence; allelic polymorphism;
HLA-DR beta-allelic polymorphism; probe; bone marrow; transplant; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 7.8; DB 1; Length 12;
Pred. No. 6.8e+02;
0; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                          Claim 7; Page 23; 33pp; English.
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Similarity 81.8%;
9; Conservative (
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(EPOC-) EPOCH PHARM INC
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                                                                Kutyavin IV;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 GGAGAAGAAGA 11
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probes AAV16647-64 are used to identify differences in the DR region of human major histocompatibility complex (HLA-DR). The specification describes a method for HLA-typing, which includes an oligonucleotide probe which undergoes sequence-specific hybridisation with an HLA-DR beta consensus sequence at positions 61-64. The probe contains a labelling substance other than a nucleotide sequence, which facilitates detection of the probe. The HLA sequence of a subject is PCR amplified, and a probe that recognises an allelic polymorphism at a selected HLA locus is contacted with the amplified product. This first probe recognises a HLA-DR beta to probe mallelic polymorphism. A second different) probe is brought into contact with a second sample of the amplified DNA in a separate reaction, and hybridisation detected. The probes and primers are used for HLA typing, e.g. for tissue, especially bone marrow, transplants
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New Antioxidant Response Element (ARE), useful for identifying drugs and transcription factors for increasing transcription of mRNA, useful for treatment of atherosclerosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Antioxidant responsive element; ARE; low density lipoprotein; LDL; high density lipoprotein; HDL; apolipoprotein; apo AI; atherosclerosis; heart disease; transcription; ss.
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Col 29; 20pp; English
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an ARE). UV cross-linking studies using an apoAl-ARE probe isolated two polypeptides of 100 and 115 kDa. These compounds are useful for treatment of a human or animal with atherosclerosis. ARE's can also be used in DNA constructs when operably linked to heterologous protein coding sequences to effect the transcription of those heterologous sequences
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Pred. No. 6.8e+02;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                  35.5%; Score 7.8; DB 1; Length 12; 81.8%; Pred. No. 6.8e+02; tive 0; Mismatches 2; Indels
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Matches 9; Conserv
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Triple-helix forming region; Triplex formation; DNA detection; identification; bacteria; oncogene; virus; ds.
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                                               Escherichia coli.
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20-MAY-1999
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                                                                                                                                                                                                                                                                                                                                                                                        Assay of genetic sequences based on triplex formation from double stranded analyte - and hybrid of anchor and reporter sequences, with reporter released if triplex formation occurs, used e.g. to identify
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                                                                                                                                                                Triple-helix forming region; Triplex formation; DNA detection; identification; bacteria; oncogene; virus; ds.
                                                                                                                                         Triple helix forming nucleotides1066-1077 of the p53 gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     35.5%; Score 7.8; DB 1; Length 12; 81.8%; Pred. No. 6.8e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Triple helix forming nucleotides 212-223 of 23S rRNA gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 12 BP; 7 A; 0 C; 5 G; 0 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Col 25-26; 168pp; English.
                                                                                                                                                                                                                                                                                                                      (PROF-) PROFILE DIAGNOSTIC SCI
                                                                    AAX14964 standard; DNA; 12 BP
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                                                                                                                                                                                                                                                                        93US-00173489.
                                                                                                                                                                                                                                                                                              92US-00968436.
                                                                                                                   (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     733 GAGAACAGAA 743
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|||| | ||||
1 GAGATAGAGAA 11
                                                                                                                                                                                                                                                                                                                                              Hepburn AG, Wang C;
                                                                                                                                                                                                                                                                                                                                                                   WPI; 1999-130384/11.
                                                                                                                   24-MAR-1999
                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                        22-DEC-1993;
                                                                                                                                                                                                                                                                                              29-OCT-1992;
                                                                                                                                                                                                                         US5861244-A.
                                                                                                                                                                                                                                                 19-JAN-1999
                                                                                            AAX14964;
                                                                                                                                                                                                                                                                                                                                                                                                                             bacteria.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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AAX14828
ID AAX14828
AC AAX14828
XX
DT 24-MAR-:
DT 24-MAR-:
DE Triple }
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The present sequence represents a potential triple-helix forming region. It can be used to demonstrate the assay of the invention. The assay comprises adding a sample containing double-stranded DNA test sequences, e.g. containing the present sequence, to an aqueous medium containing at least one complex of anchor DNA, attached to a solid support, and reporter DNA, where either a part of the anchor DNA or reporter DNA is designed to form a triple-strand structure with part of the test sequence. Triplex formation results in displacement of the reporter DNA which is detected as an indication of the presence of the DNA test sequence. The method is used to detect DNA sequences, particularly for identification of bacteria (By detecting genes for ribosomal RNA) in clinical samples, but also detection of oncogenes and Hepatitis B virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                             Assay of genetic sequences based on triplex formation from double stranded analyte - and hybrid of anchor and reporter sequences, with reporter released if triplex formation occurs, used e.g. to identify
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Probe, nucleic acid determination; sequence determination;
triple stranded binding complex; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 12 BP; 8 A; 0 C; 4 G; 0 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Col 21-22; 168pp; English.
(PROF-) PROFILE DIAGNOSTIC SCI INC.
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The invention relates to systems, methods and reagents for cell-based screening or detection of compounds which affect particular biological functions. The methods of the invention utilise fluorescent biodetector alteration in the cellular distribution of at least the fluorescent calteration in the cellular distribution of at least the fluorescent control moiety. In one embodiment, the biosensors comprise heat shock proteins control moiety in one embodiment, the biosensors comprise heat shock proteins control protein (GFP), or derivatives thereof). Such biosensors are located in protein (GFP), or derivatives thereof). Such biosensors are located in the cytoplasm, but on stress activation translocate to the mucleus. In the cytoplasm, but on stress activation translocate to the mucleus. In the cytoplasm, but on stress activation translocate to the mucleus. In the cytoplasm, but on stress activation signal which is cleaved by the protease biodetector fusion proteins compared by the protease of material so may be from heterologues sources. Due to the or components may be from heterologues sources. Due to the or components may be from heterologues sources. Due to the consistion signal, the biodetector protein is localised to a particular localisation signal, the biodetector protein is localised to a particular components of the fluorescent protein is cleaved from the localisation sequence, and is free to migrate to other locations within the cell. The presence of a second localisation signal attached to the fluorescent protein to be directed to a different cellular compounds which modulate these change in distribution of the fluorescent protein can be detected using language may be used for the screening of compounds which modulate these campities and to screen compounds which modulate these appropriatives. Biosensors containing a recognition site for caspase, for the activities and to screen compounds which modulate cappaid quantity while biosensors containing a recognition paray capaget of a paper of fact collecti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; vascular endothelial growth factor; VEGF; phosphorothioate; antisense oligomuclectide; inhibition; cytostatic; angiogenic; gene therapy; abnormal vascular permeability; cell proliferation; cell permeation; angiogenesis; neovascularisation; tumour cell growth;
                    Automated cell-based characterization of toxin by contacting cells containing luminescent reporter molecules with test substance and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            35.5%; Score 7.8; DB 1; Length 12; 81.8%; Pred. No. 6.8e+02; tive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VEGF derived short antisense oligonucleotide SEQ ID NO:21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 12 BP; 6 A; 1 C; 3 G; 2 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    biosensor fusion proteins of the invention
                                                                                                                                  Example 11; Fig 29B; 336pp; English
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Guery Match

Best Local Similarity 81.00.
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                                                                                analyzing optically.
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                                                                                                                                                                                                                                                                                                                                                                                                   This sequence represents a probe analyte used to test the method of the invention. The method is for the determination of a nucleic acid A, and comprises formation of a triple stranded binding complex (1) between A and two different nucleic acid binding molecules B and C, the formation of (1) detected by inclusion of B or C. (1) is more thermostable than a complex between A and two Bs or two identical Cs. The nucleic acid binding molecules B and C are useful as probes for specifically determining a nucleic acid, useful in diagnostics. Short Hoogsteen binding oligomer B is stabilised by a longer Watson-Crick molecule C, preventing the need for a long homopurine tract in A, allowing the high discriminative power of short Hoogsteen binding probes without loss of specificity. (Updated on 20-MAR-2003 to correct PA field.)
                                                                                                                                                                                                                                          Determining nucleic acids by formation of a triple stranded binding complex - using two separate probe molecules which bind to the nucleic acid via Watson-Crick and Hoogsteen base pairing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 35.5%; Score 7.8; DB 1; Length 12; Best Local Similarity, 81.8%; Pred. No. 6.8e+02; Matches 9; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 12 BP; 5 A; 3 C; 2 G; 2 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                             Example 1; Page 14; 28pp; English
                                                      (BOEF ) BOEHRINGER MANNHEIM GMBH. (HOFF ) ROCHE DIAGNOSTICS GMBH.
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     22-AUG-1997; 97EP-00114512
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     729 CCAGGAGAAC 739
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (CELL-) CELLOMICS INC
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P-PSDB; AAB22892.
                                                                                                                                                                                              WPI; 1999-134650/12.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cleavage site;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26-FEB-1999;
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                                                                                                                                          Naesby M;
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Mon Oct 18 14:40:07 2004
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The present sequence is that of DNA encoding the substrate recognition sequence (see AAY79594) of caspase-6. The DNA is used in a claimed consequence (see AAY79594) of caspase-6. The DNA is used in a claimed consequence (see AAA27568-76) encoding at case AA2275627-43) comprises: (1) a sequence (see AAA27568-76) encoding at least 1 detectable signal polypeptide; (2) a sequence (see AAA27577-511) consequence; and (3) a sequence (see AAA27561-26) that encodes at least 1 protease recognition site, sunch as the present caractant target sequence. An expression vector, a genetically engineered constraint a recombinant protease biosensor are also claimed. A claimed method for identifying compounds that modify protease activity in a cell involves contacting a host cell that possesses the recombinant protease biosensor with a test compound, and determining the protease contacting a host cell, that possesses the recombinant confounds that modify protease biosensor are changes in the distribution of the protease biosensor are contained with modification of protease activity in a host cell include the recombinant nucleic acid, or the recombinant protease biosensor, or the vector, or the host cell. The protease biosensor is useful in high content screens to detect in vivo activation of enzymatic activity, and content screens to detect in vivo activation of enzymatic activity, and content screens to detect in vivo activation of enzymatic activity on the content of enzymatic activity and content screens to detect in vivo activation of enzymatic activity and content screens to detect in vivo activation of enzymatic activity on the content of activity based on cleavage of a known recognition
                                                                                                       Recombinant nucleic acid encoding a protease biosensor useful for fluorescence based cell and molecular biochemical assays for drug discovery comprising three operably linked nucleic acid sequences.
                  Olson K, Burroughs-Tencza S;
                                                                                                                                                                            Claim 6; Fig 29B; 218pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAA88229 standard; DNA; 12 BP.
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Best Local Similarity 81.8
Matches 9; Conservative
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                  Guiliano KA, Bright G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 GTAGAATAGA 11
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                                                      2000-365644/31.
                                                                     P-PSDB; AAY79594
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                                                                                                                                                                                                                                                                                                                                                                                                    The present invention describes oligonucleotides (I) of 10-15 residues corresponding to a part of a vascular endothelial growth factor (VEGF) comprising 1 of 6 sequences given in AAAO6692 to AAAO6697. AAAO6698 to AAAO6783 represent VEGF antisene oligonucleotides used in the exemplification of the present invention. The antisense oligonucleotides can contain phosphorothicate linkages. Oligonucleotides from the present invention have expostatic and analysident activities, and can be used in gene therapy. The oligonucleotides are useful for inhibiting the expression of VEGF, e.g. for the treatment of diseases associated with anglogenesis, neovascularisation, tumour cell growth and/or metastasis. AAAO6784 represents a human VEGF nucleotide sequence from which the oligonucleotides are derived
                                                                                                                                                                                                                                                                                                   Novel oligonucleotides corresponding to a part of a vascular endothelial growth factor, useful for treating e.g. tumor cell growth and/or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 81.8%; Pred. No. 6.8e+02;
Matches 9; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA encoding caspase-6 substrate recognition sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 12 BP; 6 A; 2 C; 4 G; 0 T; 0 U; 0 Other;
                                                                                                                                                                                                                                 Woessner RD;
                                                                                                                                                                                             DEUT GMBH.
                                                                                                                                                                                                                               Ulhmann E, Peyman A, Bitonti AJ,
                                                                                                                                                                                                                                                                                                                                                                        Example 1; Page 16; 73pp; English.
                                                                                                                                                                                             (HMRI ) HOECHST MARION ROUSSEL
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99US-0136078P.
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                                                                                                                                                                                                                                                                   WPI; 2000-258586/23
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 Homo sapiens
Synthetic.
                                                                                                                                                           07-AUG-1998;
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26-MAY-1999;
                                                                                                                          37-AUG-1998;
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                                                  EP979869-A1.
                                                                                      16-FEB-2000
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                                                                                                                                                                                                                                                                                                                                          metastasis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   pp32 upstream consensus sequence for an active steroid receptor #1.
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0
                                                             35.5%; Score 7.8; DB 1; Length 12; 81.8%; Pred. No. 6.8e+02; rive 0; Mismatches 2; Indels
Sequence 12 BP; 6 A; 1 C; 3 G; 2 T; 0 U; 0 Other;
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                                                                                                                                                                               The present invention describes a method (M1) for treating malignant cells comprising restoration of pp32 function. Also described are: (1) a method (M2) of screening to determine whether a compound is an inducer of pp32 expression comprising measuring pp32 expression by cells cultured in the presence and absence of the compound; and (2) a method (M3) of screening to determine whether a compound is an inducer of pp32 function comprising measuring protein phosphatase activity in cells cultured in the presence and absence of the compound. The methods are useful for treating cancer and for identifying agents which may be used to treat cancer. Human pp32 is a phosphoprotein which may be used to treat chromosome 15q22.3-q23. The present sequence represents a consensus sequence for an active steroid receptor found in the upstream sequence of
                                                         Treatment of cancer comprising restoration of pp32 function in malignant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PCR primer; amplification; microarray; genotyping; mutational analysis; cytosine methylation pattern; ss.
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sequence for an active steroid receptor found in the upstrear
pp32, which is used in an example from the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                35.5%; Score 7.8; DB 1; Length 12; 81.8%; Pred. No. 6.8e+02; tive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Seguence 12 BP; 0 A; 2 C; 0 G; 10 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Complex PCR amplification type 2 primer #3.
                                                                                                                                      Example 3; Page 41; 90pp; English.
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12-OCT-2000; 2000DE-01051714
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Best Local Similarity 81...
Best Local 9; Conservative
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ઠે 엄 This invention describes a novel controllable performance method of complex polymerase chain reaction (PCR) amplifications. Firstly, PCR is carried out with at least 50 different primers (P1) of one type, complementary to one strand of sample DNA, and with a primer (or library of primers) of a second type (P2) complementary to the other strand of

Controlling performance of complex polymerase chain reaction amplification, useful e.g. for genotyping, using a set of many specific primers and non-specific counter-strand primers.

Example 2; Page 18; 26pp; German.

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the DNA, with P2 carrying a marker (M1). Amplicons are hybridized either to an array of oligonucleotides (ON) that hybridize to the primer used complements of the primer used complementary to the primers used in PCR, and then the lengths of amplicons bound to the array are determined using a second marker (M2), different from M1, that is correlated with the length of the relevant DNA fragments. Signals from M1 and M2 are quantified at relevant DNA the ON array. The method is used in whole genomic amplification for genotyping, mutational analysis or related applications, e.g. determining the cytosine methylation pattern of DNA. The method makes possible
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This invention describes a novel method for identifying major histocompatibility complex (MHC)-restricted antigens. A gene or CDNA bank is constructed from the cells or organism under test, then incorporated into a retroviral genome or, as additional RNA, into a modified influenza virus that has increased transcription, replication and/or expression rate, relative to the wild type, so as to produce viral particles (VP). VP are used to infect immortalized autologous cells that express MHC class I and/or II molecules on the surface, so that proteins encoded by the gene bank inserts are expressed and their cleavage products exposed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Identifying major histocompatibility complex-restricted antigens, useful potentially in antitumor vaccines, by forming DNA bank in virus and testing for I cell stimulation.
                                                                                                                                                                                                                                      determination of the number and length of many different amplicons, something that is almost impossible when using two non-specific primers, as in the conventional method. AAH20756-AAH20823 represent the PCR primers used to illustrate the method of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Major histocompatibility complex restricted antigen; antitumor vaccine; MMC-restricted antigen; T cell-restricted antigen; antigen identification; promoter; ss.
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                                                                                                                                                                                                                                                                                                                                                               Sequence 12 BP; 8 A; 4 C; 0 G; 0 T; 0 U; 0 Other;
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99DE-01051543.
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26-OCT-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAF61471;
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on the cell surface. These cells are co-cultured with T cells which are stimulated if the autologous cells express a T cell-restricted antigen. Clones that express antigens are isolated and the antigens sequenced. The products of the invention can be used for identifying antigens for microbial antigens. The method does not require knowledge of the restricted MHC molecule, allows unlimited proliferation of target cells and can identify, simultaneously, both Class I and II antigens. The transfer, with high level expression of the inserted gene, providing high sensitivity and simple detection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                     Score 7.8; DB 1; Length 12;
Pred. No. 6.8e+02;
0; Mismatches 2; Indels
                                                                                                                                                                                                                       Sequence 12 BP; 0 A; 5 C; 2 G; 0 T; 5 U; 0 Other;
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Best Local Similarity B1...
9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Oligonuclectide primer SEQ ID NO 294707 for detecting SNP TSC0016233.
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   Length 12;
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Score 7.8; DB 1; Length 12
Pred. No. 6.8e+02;
0; Mismatches 2; Indels
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81.8%; Pred. No. 6.8e+02;
tive 0; Mismatches 2; Indels
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   35.5%;
81.8%;
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Query Match
Best Local Similarity 81.8
Matches 9; Conservative
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tes 9; Conserv
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ID ABH6989
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Sequence 12 BP; 2 A; 5 C; 0 G; 5 T; 0 U; 0 Other;

WO200177384-A2.

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genemic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC9989, ABF00010-ABF9989, ABH00010-ABH99899 and ABI00010-ABH82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                  SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                               Oligonucleotide primer SEQ ID NO 269876 for detecting SNP TSC0001913.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; SEQ ID NO 269876; 29pp + Sequence Listing; German.
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Berlin K;

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This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABF82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but the wipo int/pub/published_pct_sequences
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nuclectide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABH99989 and ABI00010-ABH82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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    Set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status.
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                                                                                             Claim 1; SEQ ID NO 322294; 29pp + Sequence Listing; German.
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oligomers are also used for detecting cell type differentiation. ABC00010-ABC9989, ABF0010-ABF99889, ABH00110-ABH99989 and ABI0010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at fip.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SNP, single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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ftp.wipo.int/pub/published_pct_sequences
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Oligonucleotide primer SEQ ID NO 275513 for detecting SNP TSC0003914.
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Matches 9; Conservative
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                                                                                                                                                                                                                                                           SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                                                            Oligonucleotide primer SEQ ID NO 300210 for detecting SNP TSC0018905.
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35.5%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 6.8e+02;
Matches 9; Conservative 0; Mismatches 2; Indels
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                                                                                                                       ABI00237 standard; DNA; 12 BP
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RESULT 1027

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18-OCT-2001

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RESULT 1026

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC9989, ABF00010-ABF9989, ABH0010-ABH99999 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from MIPO at
SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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Claim 1; SEQ ID NO 279099; 29pp + Sequence Listing; German.
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                                                                                                                                                                                                                                                                       1 GAAAAACAAAA 11
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Best Local Similarity
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                                                                                                                                                                      This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, contral nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABH99989 and ABI00010-ABH82073 tepresent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but the was obtained in electronic format from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                            oet or oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status.
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35.5%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 6.8e+02;
Matches 9; Conservative 0; Mismatches 2; Indels
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                                                         Berlin K;
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            07-APR-2000; 2000DE-01019173.
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                                                                               WPI; 2001-657177/75.
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically prereated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic formmat from WIPO at
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     35.5%; Score 7.8; DB 1; Length 12; 81.8%; Pred. No. 6.8e+02; ive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 12 BP; 10 A; 1 C; 1 G; 0 T; 0 U; 0 Other;
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RESULT 1032
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                                                                                                                                                                                                                                                                                                      SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                              Gaps
                                                                                                                                                                                                                                                                               Oligonucleotide primer SEQ ID NO 330051 for detecting SNP TSC0035297.
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Pred. No. 6.8e+02;
0; Mismatches 2; Indels
                                                     Length 12;
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35.5%; Score 7.8; DB 1; Length 12
Best Local Similarity 81.8%; Pred. No. 6.8e+02;
Matches 9; Conservative 0; Mismatches 2; Indels
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                          Sequence 12 BP; 1 A; 0 C; 2 G; 9 T; 0 U; 0 Other;
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ABI30078 standard; DNA; 12 BP.
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81.8%;
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Best Local Similarity 81.8
Matches 9; Conservative
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                                                                                                                                                                                                                                  SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                                                                        Oligonucleotide primer SEQ ID NO 307730 for detecting SNP TSC0022657.
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ABI07757 standard; DNA; 12
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                                                                                                                     22-FEB-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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             Homo sapiens.
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligomucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, ardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but the was obtained in electronic format from WFPO at
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                                                                                           Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single-nucleotide polymorphisms and cytosine
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                                                                                                                                                                                       Claim 1; SEQ ID NO 284255; 29pp + Sequence Listing; German.
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Piepenbrock C,
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range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC09989, ABF00010-ABF99889, ABF00010-ABH99889 and ABI00010-ABH82073 represent the oligomers described in the invention. NOTE: The sequence was obtained in electronic format from WIPO at fire printed specification, but ftp.wipo.int/pub/published_pct_sequences
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   oligonuclectides are used for diagnosis and/or prognosis of cancer and a
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XX MO200177384-A2.

XX WO200177384-A2.

XX SW WO200177384-A2.

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                                                                                                                                                                                                                                                                                                 SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                                                                                               Oligonucleotide primer SEQ ID NO 368968 for detecting SNP TSC0057362.
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designed to detect single-nucleotide polymorphisms and cytosine
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Pred. No. 6.8e+02;
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81.8%;
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ABI69973
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ABI69973;

35.5%; Score 7.8; DB 1; Length 12;

Query Match

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABF82073 tepresent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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                                                                                                        SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                               Oligonucleotide primer SEQ ID NO 369946 for detecting SNP TSC0057901.
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Set of oligonucleotides, useful for diagnosis and cell typing, is

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, entral nervous system, ardiovascular and metholic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF99989, ABF00010-ABF99989 and ABI00010-ABF82073
                                                                                                 This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligomucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF9989, ABF00010-ABF9989, ABF00010-ABF9989, ABF00010-ABF9989, and ABI00010-ABF99989 and ABI00010-ABF90013 represent the oligomers described in the invention. NOTE: The sequence was obtained in electronic format from WIPO at the printed specification, but the wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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designed to detect single-nucleotide polymorphisms and cytosine methylation status.
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                                                                Claim 1; SEQ ID NO 357949; 29pp + Sequence Listing;
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Matches 9; Conservative 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                            SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                        Oligonucleotide primer SEQ ID NO 366962 for detecting SNP ISC0005306.
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Best Local Similarity
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                                                                                                                                                                                           Homo sapiens.
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                                                                            ABI66989
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                                 RESULT 1043
ABI66989
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC9989, ABF00010-ABF99989, ABH00010-ABH99999 and ABI00010-ABF82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status.
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Set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status.
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Best Local Similarity 81.8.
Local 9; Conservative
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                   Piepenbrock C,
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                                                   designed to detect methylation status.
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ABH94122/c
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Claim 1; SEQ ID NO 294115; 29pp + Sequence Listing; German.

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC09080, ABC00100-ABE09089, ABH00010-ABH99999 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABF82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at fix.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC9989, ABF00010-ABF9989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but type was obtained in electronic format from WIPO at
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, ardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABF82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                                                  SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                                           Oligonucleotide primer SEQ ID NO 271142 for detecting SNP TSC0002409.
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ABH71165 standard; DNA; 12 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                  Score 7.8; DB 1; Length 12; Pred. No. 6.8e+02;
                                                                                                2; Indels
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       Sequence 12 BP; 6 A; 4 C; 0 G; 2 T; 0 U; 0 Other;
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81.8%;
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                                                                                                Conservative
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                          WPI; 2001-657177/75.
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Gaps

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RESULT 1049 ABH71165

Matches

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schultz1-727.rng

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosite methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                   Set of oligonucleotides, useful for diagnosis and cell typing, idesigned to detect single-nucleotide polymorphisms and cytosine methylation status.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        / Match 12; Score 7.8; DB 1; Length 12; Local Similarity 81.8%; Pred. No. 6.8e+02; les 9; Conservative 0; Mismatches 2; Indels
                                                                                                                      Claim 1; SEQ ID NO 323559; 29pp + Sequence Listing; German
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WPI; 2001-657177/75.
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                                                                                                                                                                                                                                                                                                                                                                                                                                   This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC9989, ABC0010-ABF9989, ABH0010-ABF9989 and ABI0010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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                                                                                                                                                                                                                                                                                                            Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single-nucleotide polymorphisms and cytosine methylation status.
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Best Local Similarity 81.0
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central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABR00010-ABR99989, ABR00010-ABR99989, ABR00010-ABR99989 and ABI00010-ABR182073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at figurial form the printed specification, but ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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ABI02156 standard; DNA; 12 BP.
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, ardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                                                                                                                               SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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Matches 9, Conservative
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                                  11 AAACCTAACAC 1
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ABI35801
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Query Match 35.5%; Score 7.8; DB 1; Length 12; Best Local Similarity 81.8%; Pred. No. 6.8e+02; Matches 9; Conservative 0; Mismatches 2; Indels

Page 468

schultz1-727.rng

06-APR-2001; 2001WO-IB000713

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SND; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
         Oligonucleotide primer SEQ ID NO 335774 for detecting SNP TSC0039007.
                                                                                                                                                                                                                                                             Set of oligonucleotides, useful for diagnosis and cell typing, i
designed to detect single-nucleotide polymorphisms and cytosine
                                                                                                                                                                                                                                                                                                         Claim 1; SEQ ID NO 335774; 29pp + Sequence Listing; German.
                                                                                                                                                06-APR-2001; 2001WO-IB000713.
                                                                                                                                                                     07-APR-2000; 2000DE-01019173
                                                                                                                                                                                                                 Olek A, Piepenbrock C,
                                                                                                                                                                                           (EPIG-) EPIGENOMICS AG
                                                                                                                                                                                                                                       WPI; 2001-657177/75
                                                                                                                                                                                                                                                                          designed to detect methylation status.
                                                                                                   WO200177384-A2.
                                                                              Homo sapiens.
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× Berlin This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and oytosine methylation status in chemically pretreated genomic DNA. The oligomucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC09989, ABC0010-ABE99899 and ABI00010-ABE82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but typ.wipo.int/pub/published_pct_sequences ö Gaps . 0 35.5%; Score 7.8; DB 1; Length 12; 81.8%; Pred. No. 6.8e+02; tive 0; Mismatches 2; Indels Seguence 12 BP; 8 A; 3 C; 1 G; 0 T; 0 U; 0 Other; Query Match
Best Local Similarity 81.0

738 ACAGAACACCG 748 ACAAAAAACCG 11 ð

22-FEB-2002 (first entry)

ABI45744;

ABI12030 standard; DNA; 12 ABI12030,

BP.

22-FEB-2002 (first entry)

Oligonucleotide primer SEQ ID NO 312003 for detecting SNP TSC0024799.

SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.

Homo sapiens.

WO200177384-A2.

18-OCT-2001

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This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, ardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABH82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but thous, int/pub/published_pct_sequences
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                                                                                                                                                                                             Set of oligonucleotides, useful for diagnosis and cell typing, idesigned to detect single-nucleotide polymorphisms and cytosine methylation status.
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                                                                                                                    Berlin K;
                                    07-APR-2000; 2000DE-01019173
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SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic. Oligonucleotide primer SEQ ID NO 345717 for detecting SNP TSC0044157 Set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status. Berlin K; 06-APR-2001; 2001WO-IB000713. 07-APR-2000; 2000DE-01019173 Piepenbrock C, (EPIG-) EPIGENOMICS AG WPI; 2001-657177/75. WO200177384-A2. Homo sapiens 18-OCT-2001 olek A,

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                                                                                             This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, contral nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABF82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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designed to detect single-nucleotide polymorphisms and cytosine
methylation status.
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                                 Claim 1; SEQ ID NO 345717; 29pp + Sequence Listing; German.
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Best Local Similarity 81.8*; Pred. No. 6.8e+02;
Matches 9; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 12 BP; 1 A; 1 C; 1 G; 9 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                              SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                    Length 12;
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                                                   Sequence 12 BP; 8 A; 3 C; 0 G; 1 T; 0 U; 0 Other;
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                                                                                Score 7.8; DB 1;
Pred. No. 6.8e+02;
0; Mismatches 2;
was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences
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                                                                                    35.5%;
81.8%;
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Best Local Similarity 81.8
Matches 9; Conservative
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Best Local Similarity
Matches 9; Conserv
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central nervous system; gastrointestinal; respiratory; immune; metabolic.
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Matches 9; Conservative
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                                               Homo sapiens.
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                                                                                                                                                                                                              Oligonucleotide primer SEQ ID NO 360812 for detecting SNP TSC0052304.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            was obtained in electronic format from WI
ftp.wipo.int/pub/published_pct_sequences
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                                                                      ABI60839 standard; DNA; 12 BP
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ABI18875 standard; DNA; 12
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Best Local Similarity 81.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Olek A, Piepenbrock C,
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                                                                                                                   ABI60839
            RESULT 1060
ABIG0839
LD ABIG083
XX ABIG083
XX ABIG083
XX ABIG083
XX SNP; S
KW SNP; S
KW SNP; S
KW CEDTA
XX COLFE
XX COLF
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ABI18875/ XX AC. ABI11 XX DT 22-FI XX XX DE Olige XW SNP; KW PEPC.

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Set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status.
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                                                                                                                                                                                       This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genemic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF9989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Oligonucleotide primer SEQ ID NO 296368 for detecting SNP TSC0017049.
                                                                                    Set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status.
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                                                                                                                                                        Claim 1; SEQ ID NO 269788; 29pp + Sequence Listing; German
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                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 12 BP; 6 A; 5 C; 1 G; 0 T; 0 U; 0 Other;
                  Berlin K;
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Best Local Similarity 81.5-
Best Local 9; Conservative
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                Piepenbrock C,
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ABH96375/c
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and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010 -ABC9989, ABF0010-ABF9989 and ABI0010-ABF182073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but the was obtained in electronic format from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Oligonucleotide primer SEQ ID NO 271555 for detecting SNP TSC0002547.
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligomucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC9989, ABF00010-ABF99989, ABF00010-ABF99989, ABF00010-ABF99989, ABF00010-ABF99989 and ABI00010-ABF8073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                              SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                             Oligonucleotide primer SEQ ID NO 275630 for detecting SNP TSC0003950.
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                                                            22-FEB-2002 (first entry)
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Matches 9; Conservative
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     ABH75639;
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     BXSXEXEXEXPXSXE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                            Gaps
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Score 7.8; DB 1; Length 12;
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0; Mismatches 2; Indels
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     35.5%;
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                                                            Conservative
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Query Match
Best Local Similarity
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ABH98926/C
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AC ABH98927
DT 22-FEB-:
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SNP; Sil
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SN
SNP; Sil
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Gaps

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WO200177384-A2

Homo sapiens.

ABH75639 standard; DNA; 12 BP.

ABH75639/c ID ABH75 XX

RESULT 1066

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Homo sapiens.
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                                                                                                                                                                                            This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretraeted genomic DNA. The oligonuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, contral nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABH82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Oligonucleotide primer SEQ ID NO 277094 for detecting SNP TSC0004382.
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                                                                                                                                  Set of oligonucleotides, useful for diagnosis and cell typing, : designed to detect single-nucleotide polymorphisms and cytosine
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                                                                                                                                                                           Claim 1; SEQ ID NO 275702; 29pp + Sequence Listing; German.
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ABH77101 standard; DNA; 12
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Set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status.
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                                                                                                                                                                                Claim 1; SEQ ID NO 277094; 29pp + Sequence Listing; German.
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Local Similarity 81.8%; Pred. No. 6.8e+02;
es 9; Conservative 0; Mismatches 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the Oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                                                          Gaps
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Pred. No. 6.8e+02;
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Best Local Similarity 81.8
Matches 9; Conservative
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Best Local Similarity
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This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99899, ABF00010-ABF99989, ABF00010-ABF99989, ABF00010-ABF99989, ABF00010-ABF99989 and ABI00010-ABF82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at the printed specification, but ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                       SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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ABI29767 standard; DNA; 12
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Best Local Similarity 81.0.
Best Local 9; Conservative
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABE99989, ABF00010-ABE99989, ABF00010-ABE99989 and ABI00010-ABE82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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  07-APR-2000; 2000DE-01019173.
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              SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99389, ABF00010-ABF99389, ABF00010-ABF99389, ABF00010-ABF99389 and ABI00010-ABF82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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           This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
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Matches 9; Conservative 0; Mismatches 2; Indels
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Best Local Similarity 81.8%; Pred. No. 6.8e+02;
Matches 9; Conservative 0; Mismatches 2; Indels
                                                                   Query Match 35.5%; Score 7.8; DB 1; Length 12; Best Local Similarity 81.8%; Pred. No. 6.8e+02; Matches 9; Conservative 0; Mismatches 2; Indels
Sequence 12 BP; 0 A; 1 C; 3 G; 8 T; 0 U; 0 Other;
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RESULT 1077

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                                                                                                                      SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                             Oligonucleotide primer SEQ ID NO 286849 for detecting SNP TSC0012849.
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This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, coingomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABH82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but the was obtained in electronic format from WIPD at
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                                                                                                                                                                    Claim 1; SEQ ID NO 286850; 29pp + Sequence Listing; German.
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Pred. No. 6.8e+02;
0; Mismatches 2; Indels
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81.8%;
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Olek A, Piepenbrock C,
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Best Local Similarity
Matches 9; Conserv
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This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a
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Best Local Similarity 81.0
                                                                                      Set of oligonucleotides, designed to detect singlemethylation status.
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AAA ABH91152
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, contral nervous system, cardiovascular and metabolic disorders. The coligomers are also used for detecting cell type differentiation. ABC00010-ABC99899, ABF00010-ABF99899, ABH00010-ABF99899, ABH00010-ABF99899, ABH00010-ABF89899 and ABI00010-ABF82073 represent the oligomers described in the invention. NoTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from NIPO at
range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABE9989, ABF00010-ABE9989, ABH0010-ABE9989 and ABI00010-ABE9989 and ABI00010-ABE90010-ABE9989, and the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPD at ftp.wipo.int/pub/published_pct_sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                    35.5%; Score 7.8; DB 1; Length 12; 81.8%; Pred. No. 6.8e+02; tive 0; Mismatches 2; Indels
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                                                                                                                            tides, useful for diagnosis and cell typing, i single-nucleotide polymorphisms and cytosine
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35.5%; Score 7.8; DB 1; Length 12; 81.8%; Pred. No. 6.8e+02;

Query Match Best Local Similarity

Seguence 12 BP; 2 A; 0 C; 3 G; 7 T; 0 U; 0 Other;

ftp.wipo.int/pub/published_pct_sequences

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This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) cligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF9989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                        SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                        Oligonucleotide primer SEQ ID NO 267240 for detecting SNP TSC0000063.
                                                                                                                                                                                                                                                                                                                                                                                                                                    Set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; SEQ ID NO 267240; 29pp + Sequence Listing; German.
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     22-FEB-2002 (first entry)
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                                                                                                                                                                                                                                                                                                   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
     Gaps
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Best Local Similarity
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Matches
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                                                           Match 35.5%; Score 7.8; DB 1; Length 12; Local Similarity 81.8%; Pred. No. 6.8e+02; tes 9; Conservative 0; Mismatches 2; Indels
                                 Sequence 12 BP; 0 A; 0 C; 3 G; 9 T; 0 U; 0 Other;
ftp.wipo.int/pub/published_pct_sequences
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Gaps

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ABH67263 standard; DNA; 12 BP

RESULT 1083

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736 AAACAGAACAC 746

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07-APR-2000; 2000DE-01019173.
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                     Olek A, Piepenbrock C,
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               (EPIG-) EPIGENOMICS AG
                                                                                                 WPI; 2001-657177/75.
                            WPI; 2001-657177/75
                                     designed to detect methylation status.
                                                                                                                                                                                    WO200177384-A2.
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Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single-nucleotide polymorphisms and cytosine

Berlin K;

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06-APR-2001; 2001WO-IB000713.
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  methylation status.
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designed to detect single-nucleotide polymorphisms and cytosine
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretraeted genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic discorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC09989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABF82073 represent the oligomers described in the invention. NOTE: The sequence
                                     This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF9989, ABF00010-ABF9989, ABF00010-ABF9989, ABF00010-ABF9989 and ABI00010-ABF8073 represent the oligomers described in the invention. NoTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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Claim 1; SEQ ID NO 367431; 29pp + Sequence Listing; German.
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Best Local Similarity 81.8%; Pred. No. 6.8e+02;
Matches 9; Conservative 0; Mismatches 2; Indels
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data for this patent did not form part of the printed specification, but

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                                                                                                                                                                                                                                                                                                                      SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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35.5%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 6.8e+02;
Matches 9; Conservative 0; Mismatches 2; Indels
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                                                 Sequence 12 BP; 1 A; 0 C; 6 G; 5 T; 0 U; 0 Other;
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              was obtained in electronic format from WIPO at
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and oytosine methylation status in chemically prerreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomer are also used for detecting cell type doliferentiation. ABC0010-ABC9989, ABF00010-ABF99989, ABF00010-ABF99989, ABF00010-ABF99989 and ABI00010-ABF82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but the wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                            SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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ABI57057 standard; DNA; 12
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This invention describes novel oligonuclectide primers or peptide nucleic
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peptide nucleic acid, cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABH82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at fire.wipo.int/pub/published_pct_sequences
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Berlin K;
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Piepenbrock C,
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretracted genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC9989, ABF00010-ABF9989, ABH00010-ABF9989, and ABI00010-ABF82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Oligonucleotide primer SEQ ID NO 377307 for detecting SNP TSC0062255.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               of oligonucleotides, useful for diagnosis and cell typing, : igned to detect single-nucleotide polymorphisms and cytosine
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                                                                                                                                                                                                                                                                                35.5%; Score 7.8; DB 1; Length 12; 81.8%; Pred. No. 6.8e+02; tive 0; Mismatches 2; Indels
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Best Local Similarity 81.8%,

Best Local Similarity 7.7%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Oligonucleotide primer SEQ ID NO 317430 for detecting SNP TSC0028004.
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   Length 12;
                                                                          2; Indels
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Score 7.8; DB 1;
Pred. No. 6.8e+02;
0; Mismatches 2;
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ID ABH94174 standard; DNA; 12 BP.
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81.8%;
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   Query Match
Best Local Similarity 81.8
Matches 9; Conservative
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                                                                                                                                                                                                                                                                                                                       RESULT 1093
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Page 484

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genemic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF9989, ABH00010-ABH99899 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but the wipo.int/pub/published_pct_sequences
                                                                                                                           SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                         Oligonucleotide primer SEQ ID NO 294167 for detecting SNP TSC0015981.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single-nucleotide polymorphisms and cytosine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; SEQ ID NO 294167; 29pp + Sequence Listing; German.
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                                                     (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                             (EPIG-) EPIGENOMICS AG
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Best Local Similarity
'Local 9; Conserve
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            designed to detect methylation status.
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                 ABH94174
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and oytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF99989, ABH0010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence was obtained in electronic formmat from WIPD at the printed specification, but the wipo.int/pub/published_pct_sequences

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Set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status.

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Berlin

Piepenbrock C,

olek A,

WPI; 2001-657177/75

(EPIG-) EPIGENOMICS

06-APR-2001; 2001WO-IB000713. 07-APR-2000; 2000DE-01019173.

WO200177384-A2

18-OCT-2001

Claim 1; SEQ ID NO 296939; 29pp + Sequence Listing; German.

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SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                                         Oligonucleotide primer SEQ ID NO 299360 for detecting SNP TSC0018537.
                                 Gaps
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35.5%; Score 7.8; DB 1; Length 12
81.8%; Pred. No. 6.8e+02;
wiemalches 2; Indels
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ABH99367 standard; DNA; 12 BP.
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Best Local Similarity 81.0.
                                                         736 AAACAGAACAC 746
                                                                             2 AAACACAAAAC 12
                                                                                                                                                                                                                                                                                                                                                                                                                Piepenbrock C,
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Conservative 733 GAGAAACAGAA 743

GAGAGAAAGAA 1

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WPI; 2001-657177/75.

SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.

Homo sapiens

Oligonucleotide primer SEQ ID NO 296939 for detecting SNP TSC0017352.

BP

ABH96946 standard; DNA; 12

RESULT 1095 **ABH96946** 22-FEB-2002 (first entry)

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Length 12;

Seguence 12 BP; 9 A; 3 C; 0 G; 0 T; 0 U; 0 Other;

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PMA) oligoners for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, cardiovascular and metabolic disorders. The oligoners are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF9989, ABF00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but twipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNN. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Oligonucleotide primer SEQ ID NO 325340 for detecting SNP TSC0032513.
                of oligonuclectides, useful for diagnosis and cell typing, is igned to detect single-nuclectide polymorphisms and cytosine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             set or oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status.
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                                                                                         Claim 1; SEQ ID NO 299360; 29pp + Sequence Listing; German.
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                                                                                                                                                                                                                                                                                                                                                                                 Sequence 12 BP; 1 A; 0 C; 2 G; 9 T; 0 U; 0 Other;
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Best Local Similarity 81...
9, Conservative
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                                                      methylation status
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oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF99889, ABH0010-ABH99999 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at flow but pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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llarity 81.8%; Pred. No. 6.8e+02;
Conservative 0; Mismatches 2; Indels
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735 GAAACAGAACA 745

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Oligonucleotide primer SEQ ID NO 303807 for detecting SNP TSC0020650

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF9989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                          SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                         Oligonucleotide primer SEQ ID NO 301735 for detecting SNP TSC0019628.
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                   ABI01762 standard; DNA; 12
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligomucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC9989, ABF00010-ABF99999, ABH00010-ABH99999 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but the was obtained in electronic format from WIPD at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                            SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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06-APR-2001; 2001WO-IB000713.

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This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99899, ABF00010-ABF99989, ABH00010-ABF99989 and ABI00010-ABF80013 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, contral nervous system, ardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from NIPO at
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                                This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleicide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from MIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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Claim 1; SEQ ID NO 305954; 29pp + Sequence Listing; German.
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acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligomucleotides are used for diagnosis and/or prognosis of cancer and range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABE09989, ABF00010-ABE99989, ABH0010-ABH99989 and ABI00010-ABE82073 cata for this patent did not form part of the printed specification, but was obtained in electronic format from WIPD at the printed specification, but fire wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                            SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                                                                                                Oligonucleotide primer SEQ ID NO 332558 for detecting SNP TSC0036990
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                                                                                             Match 35.5%; Score 7.8; DB 1; Length 12; Local Similarity 81.8%; Pred. No. 6.8e+02; les 9; Conservative 0; Mismatches 2; Indels
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, ardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99999, ABF00010-ABF9989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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                                                                                  Set of oligonucleotides, useful for diagnosis and cell typing, idesigned to detect single-nucleotide polymorphisms and cytosine methylation status.
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oligonuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The coligomers are also used for detecting cell type differentiation. ABC00010-ABC9989, ABF00010-ABF99899, ABH00010-ABH99989 and ABI00010-ABH82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but the was obtained in electronic format from WIPO at
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Oligonucleotide primer SEQ ID NO 285344 for detecting SNP TSC0012249.
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ID ABH89351 standard; DNA; 12 BP
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ABH89351/C

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ABH89351;
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ABH89351;
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Z2-FEB-2002 (first entry)
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SNP; single nucleotide polymo
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WO20017384-A2.
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WO200177384-A2.
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WPI; 2001-657177/75.
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Claim 1; SEQ ID NO 285344; 29
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Claim 1; SEQ ID NO 285344; 20
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Cange of diseases including i
Central nervous system, cardi
Contral nervous system, card
Contral nervous system
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Best Local Similarity 81.8
Matches 9; Conservative
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                                                                                                                                                                                                                                                                                                                          SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                                                                                                                         Oligonucleotide primer SEQ ID NO 335449 for detecting SNP TSC0038833.
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                   Indels
Pred. No. 6.8e+02;
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ID ABH89723 standard; DNA; 12 BP.
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Best Local Similarity 81.8
Matches 9; Conservative
                                                     734 AGAAACAGAAC 744
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                                                                                          11 ACAAACATAAC
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Matches
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically prereated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC9989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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designed to detect single-nucleotide polymorphisms and cytosine
                                                                                                                                                                                                                                                                                                                                                                   Claim 1; SEQ ID NO 341275; 29pp + Sequence Listing; German.
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                                            06-APR-2001; 2001WO-IB000713.
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Best Local Similarity 81.85,
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                                                                                                                                                          central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                         SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
                                                             Oligonucleotide primer SEQ ID NO 289716 for detecting SNP TSC0014062.
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                   22-FEB-2002 (first entry)
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Set of oligonucleotides, useful for diagnosis and cell typing, is

WPI; 2001-657177/75.

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Homo sapiens

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABH82073
                                                                                                                                                                    This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99999, ABF00010-ABF99989 and ABI00010-ABF82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form par of the printed specification, but was obtained in electronic format from WIPO at
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designed to detect single-nucleotide polymorphisms and cytosine methylation status.
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designed to detect single-nucleotide polymorphisms and cytosine
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                                                                                                          Claim 1; SEQ ID NO 346679; 29pp + Sequence Listing; German
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81.8%; Pred. No. 6.8e+02;
ative 0; Mismatches 2; Indels
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ABI49128 standard; DNA; 12
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represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                       SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                             Oligonucleotide primer SEQ ID NO 352117 for detecting SNP TSC0047677.
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SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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               Olek A, Piepenbrock C,
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretraeted genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99389, ABF00010-ABF99899, ABF00010-ABF99989 and ABI00010-ABF82073 represent the oligomers described in the invention. NOTE: The sequence was obtained in electronic format from WIPO at the printed specification, but the wipo.int/pub/published_pct_sequences
This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF99899, ABF00010-ABF99989, ABF00010-ABF99999 and ABI00010-ABF82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                                                                                                                                                                                                                                             Sequence 12 BP; 1 A; 5 C; 0 G; 6 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                          This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, contral nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC9989, ABF00010-ABF9989, ABH00010-ABH99989 and ABI00010-ABI82073 targresent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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                                                                                                                                                                                            Set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status.
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                                                                                                                                                                                                                                                                                                 Claim 1; SEQ ID NO 355037; 29pp + Sequence Listing; German
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                                                                                            Berlin K;
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, ardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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                                                                                                                                                                                 SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                       Oligonucleotide primer SEQ ID NO 268597 for detecting SNP TSC0001243.
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ftp.wipo.int/pub/published_pct_sequences
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  ABH68620 standard; DNA; 12 BP.
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designed to detect single-nucleotide polymorphisms and cytosine
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                                             35.5%; Score 7.8; DB 1; Length 12; 81.8%; Pred. No. 6.8e+02;
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Sequence 12 BP; 10 A; 2 C; 0 G; 0 T; 0 U; 0 Other;
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Homo sapiens

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acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99899, ABF00010-ABF9989, ABF00010-ABF9989, ABF00010-ABF9989 and ABI00010-ABF82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but ftp.wipo.int/pub/published_pct_sequences
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Best Local Similarity
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35.5%; Score 7.8; DB 1; Length 12; 81.8%; Pred. No. 6.8e+02; Live 0; Mismatches 2; Indels

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99999, ABF00010-ABF9989, ABH00010-ABH99989 and ABT00010-ABI82073 targement the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Oligonucleotide primer SEQ ID NO 295498 for detecting SNP TSC0016614.
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                        Set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status.
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                                                                                                 Claim 1; SEQ ID NO 319191; 29pp + Sequence Listing; German.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 AGGAGAGTAG 11
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WPI; 2001-657177/75.
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PMA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory,

Claim 1; SEQ ID NO 295498; 29pp + Sequence Listing; German.

737 AACAGAACACC 747

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central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF9989, ABF00010-ABF99899 and ABI00100-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this parent did not form part of the printed specification, but was obtained in electronic format from WIPO at finted specification, but fitp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                                                                                         35.5%; Score 7.8; DB 1; Length 12; 81.8%; Pred. No. 6.8e+02; rive 0; Mismatches 2; Indels
                                                                                                                                                        Sequence 12 BP; 7 A; 4 C; 0 G; 1 T; 0 U; 0 Other;
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Best Local Similarity 81.0.
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                                                                                                                                                                                                                      SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                          Oligonucleotide primer SEQ ID NO 298289 for detecting SNP TSC0018011.
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35.5%; Score 7.8; DB 1; Length 12; llarity 81.8%; Pred. No. 6.8e+02; Conservative 0; Mismatches 2; Indels

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                                                                                                     methylation status.
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99889, ABF00010-ABF99889, ABF00010-ABF99899, ABF00010-ABF99899, and ABI00010-ABF82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at the printed specification, but ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF99989, ABH00010-ABF99989 and ABI00010-ABF82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form art of the printed specification, but the was obtained in electronic format from WIPO at
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                                                                                                         SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                        Oligonucleotide primer SEQ ID NO 298420 for detecting SNP TSC0018084.
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Set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status.

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ABH77615 standard; DNA; 12 BP.
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This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 terpresent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but the was obtained in electronic format from WIPO at
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                                                                                                                                                                         'Match 35.5%; Score 7.8; DB 1; Length 12; Local Similarity 81.8%; Pred. No. 6.8e+02; les 9; Conservative 0; Mismatches 2; Indels
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was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences
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                                                                                   This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nuclectide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, aradiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF99889, ABH00010-ABH99989 and ABI00010-ABF82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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                                                                                                                                                               Set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status.
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                                                                                                                                                                                                                                                                                                                                                                 Claim 1; SEQ ID NO 279498; 29pp + Sequence Listing; German.
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF99989 and ABI00010-ABF82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          invention describes novel oligonucleotide primers or peptide nucleic (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
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                                                                                  Set of oligonucleotides, useful for diagnosis and cell typing, : designed to detect single-nucleotide polymorphisms and cytosine
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                                                                                                                                                      Claim 1; SEQ ID NO 305113; 29pp + Sequence Listing; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   35.5%; Score 7.8; DB 1; Length 12; 81.8%; Pred. No. 6.8e+02; tive 0; Mismatches 2; Indels
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                  Berlin K;
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Best Local Similarity 81.0
For 9; Conservative
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                  Olek A, Piepenbrock C,
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                                                 WPI; 2001-657177/75.
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and cytosine methylation status in chemically pretreated genomic DNA. The oligomicleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABCC0010-ABC99989, ABF00010-ABF99989, ABF00010-ABF99989 and ABI00010-ABF82073 represent the oligomers described in the invention. NOTE: The sequence was obtained in electronic format from part of the printed specification, but ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic formmat from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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Best Local Similarity 81.8
Matches 9; Conservative
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                                                                                                                                                                                                                                    SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                           Gaps
                                                                                                                                                                                                              Oligonucleotide primer SEQ ID NO 282795 for detecting SNP TSC0011001.
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  Length 12;
Score 7.8; DB 1; Length 12
Pred. No. 6.8e+02;
0; Mismatches 2; Indels
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 Query Match 35.5%;
Best Local Similarity 81.8%;
Matches 9; Conservative C
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                                                                                                     SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                 Oligonucleotide primer SEQ ID NO 333223 for detecting SNP TSC0037427.
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Best Local Similarity 81.8
Matches 9; Conservative
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ABI09315/c
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WO200177384-A2

ABI33250 standard; DNA; 12 BP.

RESULT 1139 ABI33250/ ID ABI3

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les 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Oligonucleotide primer SEQ ID NO 313371 for detecting SNP TSC0025704.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
Set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status.
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                                                                                                                                                               Claim 1; SEQ ID NO 284738; 29pp + Sequence Listing; German.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
            represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
  -ABC99989, ABF00010-ABF99989, ABH00010-ABH999889 and ABI00010-ABI82073
                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Oligonucleotide primer SEQ ID NO 288736 for detecting SNP TSC0013650.
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                                                                                                                                                    h Similarity 81.8%; Score 7.8; DB 1; Length 12; Similarity 81.8%; Pred. No. 6.8e+02; 9; Conservative 0; Mismatches 2; Indels
                                                                                                                Sequence 12 BP; 2 A; 0 C; 4 G; 6 T; 0 U; 0 Other;
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Best Local Similarity
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ABH88743/c
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABE99989, ABF00010-ABE99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but twipo.int/pub/published_pct_sequences
                                                                                                                                                   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                     Oligonucleotide primer SEQ ID NO 289342 for detecting SNP TSC0013898.
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              ABH89349 standard; DNA; 12 BP.
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Matches 9; Conservative
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ABI15497/
ABH89345
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35.5%; Score 7.8; DB 1; Length 12; llarity 81.8%; Pred. No. 6.8e+02; Conservative 0; Mismatches 2; Indels

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             SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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35.5%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 6.8e+02;
Matches 9; Conservative 0; Mismatches 2; Indels
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, ardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABF82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but the was obtained in electronic format from WIPO at

Sequence 12 BP; 2 A; 0 C; 2 G; 8 T; 0 U; 0 Other;

oet or oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status.

Berlin K;

Olek A, Piepenbrock C,

WPI; 2001-657177/75.

(EPIG-) EPIGENOMICS AG

07-APR-2000; 2000DE-01019173.

Claim 1; SEQ ID NO 348340; 29pp + Sequence Listing; German.

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SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                                                                          Oligonucleotide primer SEQ ID NO 350600 for detecting SNP TSC0046773.
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Query Match 35.5%; Score 7.8; DB 1; Length 12; Best Local Similarity 81.8%; Pred. No. 6.8e+02; Matches 9; Conservative 0; Mismatches 2; Indels
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically prereated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic discorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF99899 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                          acid (PNA) oligomers for detecting single nuclectide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNN. The oligonuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF9989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                             invention describes novel oligonucleotide primers or peptide nucleic
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AB168739 Standard; DNA; 12 BP
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SNP; single nucleotide polymon
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SNP; single nucleotide polymon
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Homo sapiens.
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Homo sapiens.
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NO200177384-A2.
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CEPIG-) EPIGENOMICS AG.
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Best Local Similarity 81.8%;
Matches 9; Conservative 0
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                                                                                                                                                                                                                                                                                                                                                           SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                               35.5%; Score 7.8; DB 1; Length 12; 81.8%; Pred. No. 6.8e+02; tive 0; Mismatches 2; Indels
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Sequence 12 BP; 3 A; 4 C; 0 G; 5 T; 0 U; 0 Other;
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, ardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99999, ABF00010-ABF99999, ABH00010-ABF99999 and ABI00010-ABF82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic formmat from WIPO at
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                                                                                                                                                                                               SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                                                        Oligonucleotide primer SEQ ID NO 372229 for detecting SNP TSC000966.
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                 ABI72256 standard; DNA; 12 BP.
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AB172256
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AB172256
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RESULT 1151

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Best Loca Matches

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06-APR-2001; 2001WO-IB000713
                                                                                                                    Olek A, Piepenbrock C,
 WPI; 2001-657177/75
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                                                                         ABH94151
                                                                 RESULT 1153
ABH94151
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, contrain nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC9989, ABF00010-ABF9989, ABH00010-ABH99999 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from MIPO at
      73
Set of oligonucleotides, useful for diagnosis and cell typing, : designed to detect single-nucleotide polymorphisms and cytosine
                                                                                                                                                                                                                               Claim 1; SEQ ID NO 268837; 29pp + Sequence Listing; German.
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            35.5%; Score 7.8; DB 1; Length 12; 81.8%; Pred. No. 6.8e+02; ive 0; Mismatches 2; Indels
Query Match
Best Local Similarity 81.0
For 9; Conservative
                                                                         732 GGAGAAACAGA 742
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2 GGAAAAAGAGA 12

ABH94151 standard; DNA; 12 BP. 22-FEB-2002

Oligonucleotide primer SEQ ID NO 294144 for detecting SNP TSC0015973. (first entry)

SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.

Homo sapiens

18-OCT-2001

07-APR-2000; 2000DE-01019173

(EPIG-) EPIGENOMICS

Berlin

Set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status.

This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, contral nervous system, ardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at

Score 7.8; DB 1; Length 12; Pred. No. 6.8e+02;

35.5%;

Best Local Similarity

Query Match

Sequence 12 BP; 0 A; 2 C; 2 G; 8 T; 0 U; 0 Other;

was obtained in electronic format from WI ftp.wipo.int/pub/published_pct_sequences

Claim 1; SEQ ID NO 294614; 29pp + Sequence Listing; German.

Claim 1; SEQ ID NO 294144; 29pp + Sequence Listing; German.

This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a

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range of diseases including immune system, gastrointestinal, respiratory, central nervous system. Cardiovascular and metabolic disorders. The coligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF99989, ABF00010-ABF99989, ABF00010-ABF99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                        SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                                                            35.5%; Score 7.8; DB 1; Length 12; 81.8%; Pred. No. 6.8e+02; Artive 0; Mismatches 2; Indels
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                                                                                                                                                                                                                       737 AACAGAACACC 747
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                                                                                                                                                           Query Match
Best Local Similarity
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22-FEB-2002 (first entry)
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                                                                                                                                                                                    SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                  Oligonucleotide primer SEQ ID NO 294752 for detecting SNP TSC0016258.
  Gaps
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larity 81.8%; Pred. No. 6.8e+02;
Conservative 0; Mismatches 2; Indels
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 9; Conservative
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                     733 GAGAAACAGAA
                                           12 GAAAAACCGAA
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Matches 9; Conserv
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                                                                          SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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Oligonucleotide primer SEQ ID NO 321146 for detecting SNP TSC0030082.
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Matches 9; Conservative
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Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single-nucleotide polymorphisms and cytosine
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Best Local Similarity 81.0
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                                   WPI; 2001-657177/75.
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Berlin

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF99989, ABH00010-ABF99989 and ABI00010-ABF82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                 Claim 1; SEQ ID NO 322055; 29pp + Sequence Listing; German.
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 12 BP; 1 A; 0 C; 3 G; 8 T; 0 U; 0 Other;
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methylation status.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC9989, ABF00010-ABF9989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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                                                                                                                                                                                                                                                              set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status.
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Pred. No. 6.8e+02;
0; Mismatches 2; Indels
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81.8%;
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                                                                                                                                                                                   Piepenbrock C,
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BP.

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SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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designed to detect single-nucleotide polymorphisms and cytosine
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                                                                                                ABH73280 standard; DNA; 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               designed to detect methylation status.
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                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
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                                                                                                                                                   ABH73280;
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                                                   RESULT 1161
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
the printed specification, but
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                                                                                                                                              35.5%; Score 7.8; DB 1; Length 12; llarity 81.8%; Pred. No. 6.8e+02; Conservative 0; Mismatches 2; Indels
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                                                                                                Sequence 12 BP; 7 A; 0 C; 5 G; 0 T; 0 U; 0 Other;
data for this patent did not form part of the pass obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences
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Best Local Similarity 81.8
Matches 9; Conservative
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF99899, ABH00010-ABH99899 and ABI00010-ABI82073 targement the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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Best Local Similarity 81.8%; Pred. No. 6.8e+02;
Matches 9; Conservative 0; Mismatches 2; Indels
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ftp.wipo.int/pub/published_pct_sequences
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, entrain nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABH99999 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but the was obtained in electronic format from WIPO at
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                                                                                                                                                                        Set of oligonucleotides, useful for diagnosis and cell typing, idesigned to detect single-nucleotide polymorphisms and cytosine
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Pred. No. 6.8e+02;
0; Mismatches 2; Indels
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Best Local Similarity 81.8%;
Matches 9; Conservative C
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                                                         Piepenbrock C,
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(EPIG-) EPIGENOMICS AG
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peptide nucleic acid, cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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Pred. No. 6.8e+02;
0; Mismatches 2; Indels
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Best Local Similarity 81.8%;
Matches 9; Conservative 0
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acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABC0010-ABE9989, AHH0010-ABH99899 and ABI0010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this parent did not form part of the printed specification, but ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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81.8%; Pred. No. 6.8e+02;
iive 0; Mismatches 2;
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                                                                                                                                                                                                                                                                                                                                                  SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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Best Local Similarity 81.8%; Pred. No. 6.8e+02;
Matches 9; Conservative 0; Mismatches 2; Indels
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ID ABI25571 standard; DNA; 12
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WO200177384-A2

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SND; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                Oligonucleotide primer SEQ ID NO 325544 for detecting SNP TSC0032598
                                                                                                                                                                                                                                                                     set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status.
                                                                                                                                                                                                                                                                                                                        Claim 1; SEQ ID NO 325544; 29pp + Sequence Listing; German.
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                              22-FEB-2002 (first entry)
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Berlin

This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, contral nervous system, ardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 tapeseen the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ö Gaps Sequence 12 BP; 1 A; 0 C; 4 G; 7 T; 0 U; 0 Other; ftp.wipo.int/pub/published_pct_sequences Query Match

; 0 35.5%; Score 7.8; DB 1; Length 12; 81.8%; Pred. No. 6.8e+02; ative 0; Mismatches 2; Indels Local Similarity 81.8 les 9; Conservative Best Loc Matches

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ABH75743 standard; DNA; 12 BP. ABH75743; RESULT 1168

22-FEB-2002 (first entry)

Oligonucleotide primer SEQ ID NO 275736 for detecting SNP TSC0003981.

SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.

Homo sapiens

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This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and oytosine methylation status in chemically pretreated genemic DNA. The coligonuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC0005989, ABF00010-ABF99899, ABH00010-ABF99899 and ABI00010-ABF82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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ABI01324 standard; DNA; 12 BP. ABI01324; RESULT 1169

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SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic. Oligonucleotide primer SEQ ID NO 301297 for detecting SNP TSC0019438. 22-FEB-2002 (first entry)

Homo sapiens

WO200177384-A2,

18-OCT-2001

16-APR-2001; 2001WO-IB000713.

07-APR-2000; 2000DE-01019173

(EPIG-) EPIGENOMICS AG

Berlin K; Piepenbrock C, olek A,

WPI; 2001-657177/75.

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acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligomerloctides are used for disagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC099899, ABF00010-ABF9989, ABF00010-ABF9989 and ABI0010-ABF82073 capta for this parent did not form par of the printed specification, but was obtained in electronic format from WIPO at fire, wipo.int/pub/published_pct_sequences
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                     Set of oligonucleotides, useful for diagnosis and cell typing, idesigned to detect single-nucleotide polymorphisms and cytosine methylation status.
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35.5%; Score 7.8; DB 1; Length 12; 81.8%; Pred. No. 6.8e+02; ive 0; Mismatches 2; Indels
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Oligonuclectide primer SEQ ID NO 302416 for detecting SNP TSC0019990. ABI02443 standard; DNA; 12 BP. (first entry) 22-FEB-2002 ABI02443; RESULT 1170

SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.

Homo sapiens.

18-OCT-2001.

WO200177384-A2.

06-APR-2001; 2001WO-IB000713.

07-APR-2000; 2000DE-01019173

(EPIG-) EPIGENOMICS AG

Berlin K; Olek A, Piepenbrock C, WPI; 2001-657177/75. Claim 1; SEQ ID NO 302416; 29pp + Sequence Listing; German.

Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single-nucleotide polymorphisms and cytosine methylation status.

This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, respiratory, range of diseases including immune system, gastrointestinal, res central nervous system, cardiovascular and metabolic disorders.

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oligomers are also used for detecting cell type differentiation. ABC00010
-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pot_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                                                                            Score 7.8; DB 1; Length 12
Pred. No. 6.8e+02;
0; Mismatches 2; Indels
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Matches 9; Conservative
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Oligonucleotide primer SEQ ID NO 306291 for detecting SNP TSC0021928
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ABI29661 standard; DNA; 12
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Best Local Similarity 81.8
Matches 9; Conservative
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    736 AAACAGAACAC 746
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                                              AAACGTAACAC 11
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA). Oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99999 and ABI00010-ABI82073 trepresent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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Best Local Similarity 81.8%; Pred. No. 6.8e+02;
Matches 9; Conservative 0; Mismatches 2; Indels
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This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) eligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretraeted genomic DNA. The eligonuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, aradiovascular and metabolic disorders. The eligoners are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but typo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                      Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single-nucleotide polymorphisms and cytosine methylation status.
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Mon Oct 18 14:40:07 2004
                                                                                                                                   07-APR-2000; 2000DE-01019173
                                                                                                                                                                                                                      Olek A, Piepenbrock C,
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35.5%; Score 7.8; DB 1; Length 12; 81.8%; Pred. No. 6.8e+02; ive 0; Mismatches 2; Indels Ouery Match
Best Local Similarity 81.87
Conservative
9, Conservative 734 AGAAACAGAAC 744 2 ATAAACAAAAC 12 ò

ABH82668 standard; DNA; 12 BP 22-FEB-2002 (first entry) ABH82668; RESULT 1175

Oligonucleotide primer SEQ ID NO 282661 for detecting SNP TSC0010937.

SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.

Homo sapiens.

WO200177384-A2

06-APR-2001; 2001WO-IB000713 18-OCT-2001.

07-APR-2000; 2000DE-01019173.

(EPIG-) EPIGENOMICS AG

Berlin K; Olek A, Piepenbrock C,

WPI; 2001-657177/75.

Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single-nucleotide polymorphisms and cytosine methylation status.

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, contral nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC9989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI32073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but the was obtained in electronic format from WIPO at
Claim 1; SEQ ID NO 282661; 29pp + Sequence Listing; German.
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Sequence 12 BP; 7 A; 2 C; 0 G; 3 T; 0 U; 0 Other;

·, Query Match 35.5%; Score 7.8; DB 1; Length 12; Best Local Similarity 81.8%; Pred. No. 6.8e+02; Matches 9; Conservative 0; Mismatches 2; Indels

736 AAACAGAACAC 746 AAACATAATAC 12

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1176 RESULT 11 ABI09948/

ABI09948 standard; DNA; 12 BP. 22-FEB-2002 (first entry) ABI09948;

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0; Gaps

Oligonucleotide primer SEQ ID NO 309921 for detecting SNP TSC0023735.

SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.

Homo sapiens.

WO200177384-A2.

18-OCT-2001.

06-APR-2001; 2001WO-IB000713.

07-APR-2000; 2000DE-01019173.

(EPIG-) EPIGENOMICS AG.

Berlin K; Olek A, Piepenbrock C,

WPI; 2001-657177/75.

Set of oligonucleotides, useful for diagnosis and cell typing, idesigned to detect single-nucleotide polymorphisms and cytosine methylation status.

Claim 1; SEQ ID NO 309921; 29pp + Sequence Listing; German.

This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligomucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC9989, ABF00010-ABF9989, ABH00010-ABH99989 and ABI00010-ABF82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at

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This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF9989, ABF00010-ABF9989 and ABI00010-ABF3073 represent the oligomers described in the invention. NOTE: The sequence was obtained in electronic format from WIPO at the printed specification, but the wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                    SNP, single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                               Oligonucleotide primer SEQ ID NO 337350 for detecting SNP TSC0039831.
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ABI13567 standard; DNA; 12 BP.
                                      ABI37377 standard; DNA; 12 BP.
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RESULT 1178
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; 8S; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                           Sequence 12 BP; 0 A; 0 C; 4 G; 8 T; 0 U; 0 Other;
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                                                                                      35.5%;
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RESULT 1
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Match 35.5%; Score 7.8; DB 1; Local Similarity 81.8%; Pred. No. 6.8e+02; les 9; Conservative 0; Mismatches 2;
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This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nuclectide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0910-ABC9989, ABF00010-ABF9989, ABH00010-ABH99899 and ABI00010-ABI82073 data for this patent did not form part of the printed specification, but fitp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                          Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single-nucleotide polymorphisms and cytosine methylation status.
                                                                                                                                                                                                                                                                                                                        Claim 1; SEQ ID NO 313540; 29pp + Sequence Listing; German.
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, ardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABH82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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                                                        bet or oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status.
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Query Match

Sequence 12 BP; 0 A; 1 C; 1 G; 10 T; 0 U; 0 Other;

This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF99989, ABH00010-ABF99989 and ABI00010-ABF82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at

ABI50150

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oligonuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central inervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99899, ABF00010-ABF99899, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at fire. The printed specification, but fire.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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               81.8%;
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Best Local Similarity 81.0
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This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010 +ABC99989, ABF00010-ABF9989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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Pred. No. 6.8e+02;
0; Mismatches 2; Indels
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                                                                                                    SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                             Oligonucleotide primer SEQ ID NO 350123 for detecting SNP TSC0046517.
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH999989 and ABI00010-ABI82073 tepresent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from NIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC000010-ABC99989, ABF00010-ABF99989 and ABI00010-ABI82073
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designed to detect single-nucleotide polymorphisms and cytosine methylation status.
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                                                                  SEQ ID NO 354059; 29pp + Sequence Listing; German
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                                                                                                                                                                                                                                                                                                   was obtained in electronic format from W. ftp.wipo.int/pub/published_pct_sequences
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represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Oligonucleotide primer SEQ ID NO 358512 for detecting SNP TSC0051167.
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                                                                                                                                      35.5%; Score 7.8; DB 1; Length 12; llarity 81.8%; Pred. No. 6.8e+02; Conservative 0; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                      SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                                                                                              Oligonuclectide primer SEQ ID NO 372475 for detecting SNP TSC0059414.
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Best Local Similarity 81.00,
                                                                                                               ABI72502 standard; DNA; 12
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABF99989 and ABI00010-ABF82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic formmat from WIPO at
SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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Query Match RESULT 1193 Best Loca Matches ò g This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a renge of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF9989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at Set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status. Claim 1; SEQ ID NO 375427; 29pp + Sequence Listing; German. Sequence 12 BP; 9 A; 0 C; 2 G; 1 T; 0 U; 0 Other; ftp.wipo.int/pub/published_pct_sequences Berlin K; Piepenbrock C, (EPIG-) EPIGENOMICS AG WPI; 2001-657177/75

Gaps ; 0 35.5%; Score 7.8; DB 1; Length 12; illarity 81.8%; Pred. No. 6.8e+02; Conservative 0; Mismatches 2; Indels Best Local Similarity Matches 9, Conserv

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733 GAGAAACAGAA 743 GAGAAATAAAA 12 ABI75528 standard; DNA; 12 (first entry)

Oligonucleotide primer SEQ ID NO 375501 for detecting SNP TSC0061294

SNP, single nucleotide polymorphism, human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.

Homo sapiens

WO200177384-A2

06-APR-2001; 2001WO-IB000713.

07-APR-2000; 2000DE-01019173

(EPIG-) EPIGENOMICS AG.

Berlin K; Olek A, Piepenbrock C,

typing, is cytosine oligonucleotides, useful for diagnosis and cell of to detect single-nucleotide polymorphisms and methylation status.

This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genemic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99889, ABF00010-ABF99899, ABH00010-ABH99989 and ABI00010-ABF82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic formmat from WIPO at

Claim 1; SEQ ID NO 375501; 29pp + Sequence Listing; German.

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99899, ABF00010-ABF99899, ABH00010-ABH99989 and ABI00010-ABF82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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|AB162507 standard; DNA; 12 BP.
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, oardiovascular and metabolic discorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99899, ABC0010-ABE9989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but two botained in electronic format from WIPO at
                                                                                                                                    SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                         Oligonucleotide primer SEQ ID NO 365840 for detecting SNP TSC0055386.
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ABI65867 standard; DNA; 12 BP
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                                                                                                                                                                                                                                                                                                                                                                                  SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                                                                                                                                                                                 Oligonucleotide primer SEQ ID NO 377301 for detecting SNP TSC0062253.
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                             Query Match
Best Local Similarity 81.8%; Pred. No. 6.8e+02;
Matches 9; Conservative 0; Mismatches 2; Indels
BP; 0 A; 0 C; 3 G; 9 T; 0 U; 0 Other;
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35.5%; Score 7.8; DB 1; Length 12; 81.8%; Pred. No. 6.8e+02; ive 0; Mismatches 2; Indels
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RESULT 1195 ABI65867/c

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SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                       Set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status.
                                                                                                                                                                              Claim 1; SEQ ID NO 293359; 29pp + Sequence Listing; German.
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nes 9; Conservative
WPI; 2001-657177/75.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, ardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF9989, ABH00010-ABH99989 and ABI00010-ABI82073 data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                  set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; SEQ ID NO 366047; 29pp + Sequence Listing; German.
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                                                                                                                                                       06-APR-2001; 2001WO-IB000713.
                                                                                                                                                                                                                  37-APR-2000; 2000DE-01019173.
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736 AAACAGAACAC 746

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12 AAACAAAACTC

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                                                                                                                                                                                                          Oligonucleotide primer SEQ ID NO 268661 for detecting SNP TSC0001286.
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                                                                                          ABH68684 standard; DNA; 12 BP
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RESULT 1198
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ID 25 - |
ID 26 - |
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Berlin K;

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central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC9989, ABF00010-ABF9989, ABF00010-ABF9989, ABF00010-ABF9989, ABF00010-ABF9989 and ABI00010-ABF82073 represent the oligomers described in the invention. NoTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at thick pathology.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                                                                                                                                                                                                                                                         35.5%; Score 7.8; DB 1; Length 12; 81.8%; Pred. No. 6.8e+02; Live 0; Mismatches 2; Indels
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les 9; Conservative
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                                                                                                                                                                                                                                                                                                                      SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                                                                                      Oligonucleotide primer SEQ ID NO 322110 for detecting SNP TSC0030668.
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                                   ABI22137 standard; DNA; 12
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06-APR-2001; 2001WO-IB000713. 07-APR-2000; 2000DE-01019173.

(EPIG-) EPIGENOMICS

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SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
          Oligonucleotide primer SEQ ID NO 323079 for detecting SNP TSC0031211.
                                                                                                                                                                                                                                                    Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single-nucleotide polymorphisms and cytosine
                                                                                                                                                                                                                                                                                              Claim 1; SEQ ID NO 323079; 29pp + Sequence Listing; German.
                                                                                                                                         06-APR-2001; 2001WO-IB000713.
                                                                                                                                                                07-APR-2000; 2000DE-01019173
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                                                                                                                                                                                     (EPIG-) EPIGENOMICS AG
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                                                                                                                                                                                                                                                                          methylation status.
                                                                                              WO200177384-A2
                                                                            Homo sapiens
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but ftp.wipo.int/pub/published_pct_sequences Sequence 12 BP; 7 A; 4 C; 1 G; 0 T; 0 U; 0 Other;

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35.5%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 6.8e+02;
Matches 9; Conservative 0; Mismatches 2; Indels ે

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ABH98694;

22-FEB-2002 (first entry)

SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.

Homo sapiens

18-OCT-2001

Oligonucleotide primer SEQ ID NO 298687 for detecting SNP TSC0018236 ABH98694 standard; DNA; 12 BP 734 AGAAACAGAAC 744 AAAAACCGAAC 12

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC9989, ABF00010-ABF99989, ABF00010-ABF99989, and ABI00010-ABF82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but the was obtained in electronic format from WIPO at SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic. Oligonucleotide primer SEQ ID NO 275205 for detecting SNP TSC0003823. Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single-nucleotide polymorphisms and cytosine methylation status. Set of oligonucleotides, useful for diagnosis and cell typing, idesigned to detect single-nucleotide polymorphisms and cytosine methylation status. · 0 Claim 1; SEQ ID NO 298687; 29pp + Sequence Listing; German. 35.5%; Score 7.8; DB 1; Length 12; 81.8%; Pred. No. 6.8e+02; ative 0; Mismatches 2; Indels Sequence 12 BP; 1 A; 0 C; 3 G; B T; 0 U; 0 Other; Berlin K; Berlin K; ABH75214 standard; DNA; 12 BP 06-APR-2001; 2001WO-IB000713. 07-APR-2000; 2000DE-01019173 22-FEB-2002 (first entry) Conservative 736 AAACAGAACAC 746 Piepenbrock C, Piepenbrock C, 11 AAAAACAACAC 1 (EPIG-) EPIGENOMICS AG. WPI; 2001-657177/75. WPI; 2001-657177/75. Local Similarity es 9; Conserv WO200177384-A2. Homo sapiens 18-OCT-2001 Query Match olek A, olek A, Matches . 염

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers ealso used for detecting cell type differentiation. ABC0010-ABC99889, ABC0010-ABR99898 ABN0010-ABR99989 ABN0010-ABR99989 ABN0010-ABN99989 and ABI0010-ABN82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but ftp.wipo.int/pub/published_pct_sequences
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                          Claim 1; SEQ ID NO 275205; 29pp + Sequence Listing; German.
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Best Local 9; Conservative
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designed to detect single-nucleotide polymorphisms and cytosine
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was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences
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Thes 9; Conservative
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                                                                                                                                                           SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                      ABI06563 standard; DNA; 12 BP
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ABI08091 standard; DNA; 12
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central nervous system; gastrointestinal; respiratory; immune; metabolic
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                                     Homo sapiens.
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(EPIG-) EPIGENOMICS AG

SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;

Oligonucleotide primer SEQ ID NO 308064 for detecting SNP TSC0022861.

22-FEB-2002 (first entry)

AB108091,

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This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretracted genomic DNA. The oligonuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF9989, ABH00010-ABH99989 and ABI00010-ABH82073 tepsesm the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                             eet or oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status.
                                                                                                                                                                                                      Claim 1; SEQ ID NO 333900; 29pp + Sequence Listing; German.
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                        Berlin K;
                      Piepenbrock C,
                                                                  WPI; 2001-657177/75
                      Olek A,
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Query Match
35.5%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 6.8e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 737 AACAGAACACC 747 1 AACAAAACCCC 11 ò 셤

ABI37823 standard; DNA; 12 22-FEB-2002 ABI37823;

BP.

SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic. Oligonucleotide primer SEQ ID NO 337796 for detecting SNP TSC0040079. (first entry)

WO200177384-A2 Homo sapiens.

18-OCT-2001.

06-APR-2001; 2001WO-IB000713

07-APR-2000; 2000DE-01019173

(EPIG-) EPIGENOMICS AG.

Berlin K; Olek A, Piepenbrock C,

WPI; 2001-657177/75.

Set of oligonucleotides, useful for diagnosis and cell typing, idesigned to detect single-nucleotide polymorphisms and cytosine methylation status.

Claim 1; SEQ ID NO 337796; 29pp + Sequence Listing; German.

This invention describes novel oligonucleotide primers or peptide nucleic acid (FNA) oligomers for detecting single nucleotide polymorphisms (SNP)

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and cytosine methylation status in chemically pretreated genomic DNA. The cligonuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010 -ABC9989, ABF00010-ABF9989, ABF00010-ABH99999 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but ftp.wipo.int/pub/published_pct_sequences
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Sequence 12 BP; 1 A; 0 C; 4 G; 7 T; 0 U; 0 Other;

Gaps ö Score 7.8; DB 1; Length 12; Pred. No. 6.8e+02; 2; Indels 0; Mismatches 7 Match 35.5%; Local Similarity 81.8%; Local Similarity 91.8%; Query Match Best Loca Matches

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737 AACAGAACACC 747 N AACAAAACATC ઠે g

BP. ABI37865 standard; DNA; 12 RESULT

ABI37865

(first entry)

22-FEB-2002

Gaps

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Oligonucleotide primer SEQ ID NO 337838 for detecting SNP TSC0040099.

SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.

Homo sapiens.

WO200177384-A2

18-OCT-2001

06-APR-2001; 2001WO-IB000713.

07-APR-2000; 2000DE-01019173

(EPIG-) EPIGENOMICS AG.

Olek A, Piepenbrock C,

Berlin K;

WPI; 2001-657177/75.

Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single-nucleotide polymorphisms and cytosine methylation status.

Claim 1; SEQ ID NO 337838; 29pp + Sequence Listing; German.

This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligomucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABF82073 tepresent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from Wi ftp.wipo.int/pub/published_pct_sequences

Sequence 12 BP; 2 A; 0 C; 3 G; 7 T; 0 U; 0 Other;

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SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.

06-APR-2001; 2001WO-IB000713. 07-APR-2000; 2000DE-01019173

WO200177384-A2. Homo sapiens.

18-OCT-2001

(EPIG-) EPIGENOMICS AG

Oligonucleotide primer SEQ ID NO 340006 for detecting SNP TSC0041301.

(first entry)

22-FEB-2002

ABI40033;

Page 532

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                                     Length 12;
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Query Match Best Local Similarity 84... 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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to detect single-nucleotide polymorphisms and cytosine
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WO200177384-A2.

ABI40033 standard; DNA; 12 BP.

RESULT 1212
ABI40033
ID ABI4003:

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9; Conservative 737 AACAGAACACC 747

Local Similarity

Best Loc Matches

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Set of oligomucleotides, useful for diagnosis and cell typing, is designed to detect single-nucleotide polymorphisms and cytosine methylation status.
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Matches 9; Conservative
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                                        06-APR-2001; 2001WO-IB000713.
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                                            This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
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Claim 1; SEQ ID NO 342017; 29pp + Sequence Listing; German.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at the printed specification, the ftp.wipo.int/pub/published_pot_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Oligonucleotide primer SEQ ID NO 348458 for detecting SNP TSC0045601.
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Best Local Similarity 81.6-
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC09989, ABC0010-ABE09989, ABH0010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence was obtained in electronic formmat from WIPO at the printed specification, but the wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                             ABI48743 standard; DNA; 12
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Conservative

Local Similarity

Matches

Query Match

Oligonucleotide primer SEQ ID NO 356734 for detecting SNP TSC0050284.

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Gaps

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35.5%; Score 7.8; DB 1; Length 12; 81.8%; Pred. No. 6.8e+02; ative 0; Mismatches 2; Indels

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07-APR-2000; 2000DE-01019173.
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                       SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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Pred. No. 6.8e+02;
0; Mismatches 2; Indels
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Matches 9; Conservative
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                                                                                                                                   Homo sapiens.
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 tepresent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but typo.int/pub/published_pct_sequences
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                                                                                                            set or oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status.
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                                            Berlin K;
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Best Local Similarity 81.8
Matches 9; Conservative
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                                        Olek A, Piepenbrock C,
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(EPIG-) EPIGENOMICS AG
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Claim 1; SEQ ID NO 362076; 29pp + Sequence Listing; German.
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ABI62103 standard; DNA; 12 BP.
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Best Local Similarity 81.8
Matches 9; Conservative
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2 AAACACTACAC 12
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ABI 62103/c

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically prerreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99899, ABF00010-ABF9989, ABH00010-ABF9989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Oligonucleotide primer SEQ ID NO 365243 for detecting SNP TSC0054993.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Set of oligonucleotides, useful for diagnosis and cell typing, idesigned to detect single-nucleotide polymorphisms and cytosine methylation status.
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Pred. No. 6.8e+02;
0; Mismatches 2; Indels
                                             35.5%; Score 7.8; DB 1; Length 12; llarity 81.8%; Pred. No. 6.8e+02; Conservative 0; Mismatches 2; Indels
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Sequence 12 BP; 1 A; 0 C; 4 G; 7 T; 0 U; 0 Other;
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Matches 9; Conservative
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es 9; Conserv
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABE9989, ABF00010-ABE9989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from MIPO at
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acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligomers for detecting single nucleotide polymorphisms (SNP) oligomucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastronintestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC09989, ABC0010-ABE99989, ABR0010-ABE99989, ABR0010-ABE99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic formmat from WIPO at
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                                                                                                                                                                                                                                                                                                                                                                                Claim 1; SEQ ID NO 319017; 29pp + Sequence Listing; German.
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                                              WO200177384-A2.
             Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nuclectide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010 +ABC99989, ABF00010-ABF9989, ABH00010-ABH99989 and ABI00010-ABF82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                                   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                                  Oligonucleotide primer SEQ ID NO 317789 for detecting SNP TSC0028274.
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                              Gaps
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Score 7.8; DB 1; Length 12;
Pred. No. 6.8e+02;
0; Mismatches 2; Indels
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 Query Match
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Matches 9; Conservative
                                                    736 AAACAGAACAC 746
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Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single-nucleotide polymorphisms and cytosine methylation status.
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ö This invention describes novel oligonucleotide primars or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99899, ABF00010-ABF99899, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at fire,wipo.int/pub/published_pct_sequences Gaps ; Claim 1; SEQ ID NO 272831; 29pp + Sequence Listing; German. 35.5%; Score 7.8; DB 1; Length 12; 81.8%; Pred. No. 6.8e+02; tive 0; Mismatches 2; Indels Seguence 12 BP; 6 A; 6 C; 0 G; 0 T; 0 U; 0 Other; Similarity 81.8 9; Conservative 737 AACAGAACACC 747 AACCAAACACC 11

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SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic. Oligonuclectide primer SEQ ID NO 322943 for detecting SNP TSC0031137.

07-APR-2000; 2000DE-01019173

Set of oligonucleotides, useful for diagnosis and cell typing, idesigned to detect single-nucleotide polymorphisms and cytosine methylation status.

Claim 1; SEQ ID NO 322943; 29pp + Sequence Listing; German.

This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a

35.5%; 81.8%;

Query Match Best Local Similarity

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and merabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99899, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at fire.wipo.int/pub/published_pct_sequences
range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABE099899, ABE00010-ABE99989, ABE00010-ABE99989, ABE00010-ABE99989, ABE00010-ABE99989, ABE00010-ABE99989, and ABI00010-ABE99989, and ABI00010-ABE9073 represent the oligomers described in the invention. NOTE: The sequence was obtained in electronic form part of the printed specification, but the wipo.int/pub/published_pct_sequences
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC9989, ABF0010-ABF9989, ABH0010-ABH9989 and ABI00010-ABI32073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                     SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                     Oligonuclectide primer SEQ ID NO 275099 for detecting SNP TSC0003783
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                                                                                                                                                                                                                                                                                                SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                                                                                              Oligonucleotide primer SEQ ID NO 323965 for detecting SNP TSC0031691.
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 2; Indels
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                                                                                                                                                         ABI23992 standard; DNA; 12 BP.
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les 9; Conservative
                                 729 CCAGGAGAAAC 739
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                                                                   2 CCACGATAAAC 12
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Query Match 35.5%; Score 7.8; DB 1; Length 12; Best Local Similarity 81.8%; Pred. No. 6.8e+02; Matches 9; Conservative 0; Mismatches 2; Indels
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Set of oligonucleotides, useful for diagnosis and cell typing, i
designed to detect single-nucleotide polymorphisms and cytosine
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                                         Dlek A, Piepenbrock C,
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Berlin K;

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABE099899, ABF00010-ABE99989, ABR00010-ABE99989 and ABI00010-ABE32073 represent the oligomers described in the invention. NOTE: The sequence
                                                                                  This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, ardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI22073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic form at from MIPO at
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                                           Claim 1; SEQ ID NO 276855; 29pp + Sequence Listing; German.
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methylation status.
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les 9; Conserv
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                                                                                                                                                                                                                                                                           Set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status.
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SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                      Oligonucleotide primer SEQ ID NO 333587 for detecting SNP TSC0037618.
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                                                              ABI33614 standard; DNA; 12
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ABI33614
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                                                                                                                                                                                                                                                                                                                                                                            SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                 Oligonucleotide primer SEQ ID NO 283172 for detecting SNP TSC0011183.
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                                                                                      1 35.5%; Score 7.8; DB 1; Length 12; Similarity 81.8%; Pred. No. 6.8e+02; 9; Conservative 0; Mismatches 2; Indels
                                                         Sequence 12 BP; 9 A; 3 C; 0 G; 0 T; 0 U; 0 Other;
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, ardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF9989, ABH00010-ABH99989 and ABI00010-ABI32073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, ardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from NIPO at
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                               Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single-nucleotide polymorphisms and cytosine methylation status.
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                                                                                                                                                                                                 Claim 1; SEQ ID NO 335839; 29pp + Sequence Listing; German.
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(EPIG-) EPIGENOMICS AG.
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  peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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ABI35866 standard; DNA; 12
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35.5%;

Best_Local Similarity 81.8 Matches 9; Conservative

Query Match

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acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABH99989 and ABI00010-ABH82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABH99989 and ABI00010-ABH82073 tepresent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but they.wipo.int/pub/published_pct_sequences
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Sequence 12 BP; 2 A; 0 C; 3 G; 7 T; 0 U; 0 Other;

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, ardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invantion. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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Pred. No. 6.8e+02;
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligomucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC9989, ABF00010-ABF9989, ABH00010-ABH99899 and ABI00010-ABF82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but the was obtained in electronic format from WIPO at
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                                                                                                                SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                  Oligonucleotide primer SEQ ID NO 315650 for detecting SNP TSC0027020.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             designed to detect methylation status.
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, ardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 trepresent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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Best Local Similarity 81.8
Matches 9; Conservative
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                                                                                                                                                       Piepenbrock C,
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                                                                                                                                                                                        WPI; 2001-657177/75
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Gaps

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WPI; 2001-657177/75

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Set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status.

Claim 1; SEQ ID NO 348054; 29pp + Sequence Listing; German

oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF9989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences 88888888888

Sequence 12 BP; 9 A; 2 C; 1 G; 0 T; 0 U; 0 Other;

ö Gaps . 0

Query Match

736 AAACAGAACAC

This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligoners for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, contral nervous system, cardiovascular and metabolic disorders. The oligoners are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF9989, ABH00010-ABH99989 and ABI00010-ABI82073 tepresent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at

1 AAAAAAAACAC 11 ò

RESULT 1244 ABI51092

BP. ABI51092 standard; DNA; 12

Oligonucleotide primer SEQ ID NO 351065 for detecting SNP TSC0047060.

Homo sapiens.

WO200177384-A2

18-OCT-2001.

Claim 1; SEQ ID NO 351065; 29pp + Sequence Listing; German.

This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABE99989, ABF00010-ABE99989, ABH00010-ABE99989, and ABI00010-ABE3073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at

Gaps .. 0 35.5%; Score 7.8; DB 1; Length 12; 81.8%; Pred. No. 6.8e+02; cive 0; Mismatches 2; Indels Best Local Similarity 81.8 Matches 9; Conservative

This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The

Set of oligonucleotides, useful for diagnosis and cell typing, idesigned to detect single-nucleotide polymorphisms and cytosine methylation status.

Berlin K;

Olek A, Piepenbrock C,

WPI; 2001-657177/75.

(EPIG-) EPIGENOMICS AG

06-APR-2001; 2001WO-IB000713. 07-APR-2000; 2000DE-01019173

WO200177384-A2 Homo sapiens

18-OCT-2001,

Claim 1; SEQ ID NO 350284; 29pp + Sequence Listing; German.

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Query Match 35.5%; Score 7.8; DB 1; Length 12; Best Local Similarity 81.8%; Pred. No. 6.8e+02; Matches 9; Conservative 0; Mismatches 2; Indels

746

ABI51092;

22-FEB-2002 (first entry)

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Gaps

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35.5%; Score 7.8; DB 1; Length 12; 81.8%; Pred. No. 6.8e+02; cive 0; Mismatches 2; Indels

Local Similarity 81.8 737 AACAGAACACC 747

Query Match

1 AACACACCACC 11

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Sequence 12 BP; 6 A; 6 C; 0 G; 0 T; 0 U; 0 Other;

ftp.wipo.int/pub/published_pct_sequences

SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.

06-APR-2001; 2001WO-IB000713

0.7-APR-2000; 2000DE-01019173

(EPIG-) EPIGENOMICS

SNP, single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.

Oligonucleotide primer SEQ ID NO 350284 for detecting SNP TSC0046584.

(first entry)

22-FEB-2002

ABI50311;

ABI50311 standard; DNA; 12

Berlin K; Olek A, Piepenbrock C,

WPI; 2001-657177/75

Set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status.

Seguence 12 BP; 8 A; 3 C; 0 G; 1 T; 0 U; 0 Other;

Homo sapiens

ABI53202;

RESULT 1245

ਨੇ g 18-OCT-2001

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC9989, ABF00010-ABF99989, ABH00010-ABF99989, and ABI00010-ABF82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                         SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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Oligonucleotide primer SEQ ID NO 357031 for detecting SNP TSC0050442.
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ABI72935 standard; DNA; 12 BP.
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nes 9; Conservative
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                                                                                                                                                                                                                                                                                                                                              SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                                                                                                                                     Oligonucleotide primer SEQ ID NO 353175 for detecting SNP TSC0008584.
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                                                                                                                                                                ABIS3202 standard; DNA; 12 BP.
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    736 AAACAGAACAC 746
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                                2 AAAAATAACAC 12
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22-FEB-2002

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RESULT 1246
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Query Match

Matches

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC9989, ABF00010-ABF9989, ABH00010-ABH99989 and ABI00010-ABI82073 trepresent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from MIPO at
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                                                                                                                                                                                                                     claim 1; SEQ ID NO 372908; 29pp + Sequence Listing; German.
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Pred. No. 6.8e+02;
0; Mismatches 2; Indels
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Best Local Similarity 81.8%;
Matches 9; Conservative C
                07-APR-2000; 2000DE-01019173.
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                                                   (EPIG-) EPIGENOMICS AG
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This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, ardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABT00010-ABI82073 trepresent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from NIPO at
                              This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretraeted genomic DNA. The oligonuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Oligonucleotide primer SEQ ID NO 317839 for detecting SNP TSC0028286.
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Claim 1; SEQ ID NO 292395; 29pp + Sequence Listing; German.
                                                                                                                                                                                                                                                                                                                                                Match 12; Score 7.8; DB 1; Length 12; Local Similarity 81.8*; Pred. No. 6.8e+02; les 9; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                             Sequence 12 BP; 0 A; 1 C; 2 G; 9 T; 0 U; 0 Other;
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligomucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC9989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic formmat from WTPO at
                                                                                                                                                                                                                                                                                                                                                                                               SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                                                                                                                                                                                                Oligonucleotide primer SEQ ID NO 268523 for detecting SNP TSC0001198.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Set of oligonucleotides, useful for diagnosis and cell typing, idesigned to detect single-nucleotide polymorphisms and cytosine methylation status.
                                                                 35.5%; Score 7.8; DB 1; Length 12; 81.8%; Pred. No. 6.8e+02; cive 0; Mismatches 2; Indels
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                                    Sequence 12 BP; 1 A; 1 C; 2 G; 8 T; 0 U; 0 Other;
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ABH68546 standard; DNA; 12 BP.
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Best Local Similarity 81.0
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acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABE99989, ABF00010-ABE99989, ABF00010-ABE9989, ABF0001010-ABE9989, ABF000101010-ABE9989, ABF0001010-ABE9989, ABF0001010-ABE9098, ABF0001010-ABE9098, ABF0001010-ABE9989, ABF0001010-ABE9989, ABF0001010-ABE9989, ABF0001010-ABE9989, ABF0001010-ABE9989, ABF0001010-ABE9989, ABF0001010-ABE9989, ABF0001010-ABE9
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                                                                                                                                                                                                                                                                                          SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                                                                                                                                    Oligonucleotide primer SEQ ID NO 270546 for detecting SNP TSC0002178.
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                                                     ABH70569 standard; DNA; 12
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Matches 9; Conservative 0; Mismatches 2; Indels

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF99989, ABF00010-ABF99989, ABF00010-ABF99989 and ABI00010-ABF82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but twipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                   set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status.
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Best Local Similarity 81.8%; Pred. No. 6.8e+02;
Matches 9; Conservative 0; Mismatches 2; Indels
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Berlin K;
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Olek A, Piepenbrock C,
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                          range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting call type differentiation. ABC00010-ABC09989, ABF00010-ABF99889, ABF00010-ABH99989 and ABI0010-ABF820010 represent the oligomers described in the invention. NOTE: The sequence was obtained in electronic format from WIPO at the printed specification, but ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                  Score 7.8; DB 1; Length 12;
Pred. No. 6.8e+02;
0; Mismatches 2; Indels
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used for diagnosis and/or
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Best Local Similarity 81.8%;
Matches 9; Conservative C
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35.5%; Score 7.8; DB 1; Length 12;

Query Match

Sequence 12 BP; 2 A; 4 C; 0 G; 6 T; 0 U; 0 Other;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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81.8%; Pred. No. 6.8e+02;
cive 0; Mismatches 2; Indels
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                                   9; Conservative
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at [fp.wipo.int/pub/published_pot_sequences]
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                                                                                                                                                                                                                                                             oet or oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) eligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretraated genomic DNA. The eligonuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The eligomers are also used for detecting cell type differentiation. ABC0010-ABC99999, ABF00010-ABH99989 and ABI00010-ABH82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but fur wipo.int/pub/published_pct_sequences
                                                                                                          SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                              Oligonucleotide primer SEQ ID NO 274505 for detecting SNP TSC0003574.
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ABH75109 standard; DNA; 12
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Set of oligonucleotides, useful for diagnosis and cell typing, is

Berlin K;

Olek A, Piepenbrock C,

WPI; 2001-657177/75

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Query Match
35.5%; Score 7.8; DB 1;
Best Local Similarity 81.8%; Pred. No. 6.8e+02;
Matches 9; Conservative 0; Mismatches 2;
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represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences
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                                                                                                          This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nuclectide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC9989, ABF00010-ABF99999, ABH00010-ABH99999 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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         designed to detect single-nucleotide polymorphisms and cytosine methylation status.
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, ardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC9989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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Matches 9; Conservative 0; Mismatches 2; Indels
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                                                                                                                                                          SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                  Oligonucleotide primer SEQ ID NO 328638 for detecting SNP TSC0034432.
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SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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Berlin K;

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Sequence 12 BP; 6 A; 3 C; 1 G; 2 T; 0 U; 0 Other;
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ABIO7748/C

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(first entry)

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h 35.5%; Similarity 81.8%; 9; Conservative C

736 AAACAGAACAC 746 ATACATAACAC 11 Claim 1; SEQ ID NO 307721; 29pp + Sequence Listing; German.

Berlin K;

Piepenbrock C,

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, ardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABE99989, ABF00010-ABF99989, ABH00010-ABH99899 and ABI00010-ABI32073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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Pred. No. 6.8e+02;
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically prerreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC9989, ABF00010-ABF9989, ABF00010-ABF9989, ABF00010-ABF9989, ABF00010-ABF9989 and ABI00010-ABF82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but the wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                 SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                    Oligonucleotide primer SEQ ID NO 335676 for detecting SNP TSC0038955.
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     ABI35703 standard; DNA; 12 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                            Score 7.8; DB 1; Length 12;
Pred. No. 6.8e+02;
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Sequence 12 BP; 8 A; 3 C; 0 G; 1 T; 0 U; 0 Other;
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Matches
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Berlin K;

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                               Query Match 35.5%; Score 7.8; DB 1; Length 12; Best Local Similarity 81.8%; Pred. No. 6.8e+02; Matches 9; Conservative 0; Mismatches 2; Indels
Sequence 12 BP; 4 A; 0 C; 6 G; 2 T; 0 U; 0 Other;
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737 AACAGAACACC 747

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RESULT 1268 ABI35703

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06-APR-2001; 2001WO-IB000713
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cycosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABE9989, ABF00010-ABE9989, ABH00010-ABE9989 and ABI0010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from MIPO at
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                                      Set of oligonucleotides, useful for diagnosis and cell typing, designed to detect single-nucleotide polymorphisms and cytosine
                                                                                                                                     Claim 1; SEQ ID NO 311934; 29pp + Sequence Listing; German.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 1271
ABI14631/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nuclectide polymorphisms (SNP) and cytosine methylation status in chemically pretraeted genomic DNA. The oligonuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99999, ABC0010-ABF99989, ABM00110-ABH99989 and ABI00010-ABF82073 capresent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; Ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Oligonucleotide primer SEQ ID NO 311934 for detecting SNP TSC0024770.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                 set or oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status.
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81.8%;
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory,

Berlin K;

Piepenbrock C,

Claim 1; SEQ ID NO 314604; 29pp + Sequence Listing;

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732 GGAGAAACAGA 742

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GGAGAAAGAAA

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RESULT 1273

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central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010 ABC09989, ABR00010-ABF99989, ABR0010-ABF99989, ABR0010-ABF99989, ABR0010-ABF99989 and ABI00010-ABF8073 represent the oligomers described in the invention. NOTE: The sequence data for this parent did not form part of the printed specification, but ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Oligonucleotide primer SEQ ID NO 349210 for detecting SNP TSC0045997.
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                                                                                                                                                                                                                                                                                                                                                                            Query Match 35.5%; Score 7.8; DB 1; Length 12; Best Local Similarity 81.8%; Pred. No. 6.8e+02; Matches 9; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                  Sequence 12 BP; 1 A; 0 C; 5 G; 6 T; 0 U; 0 Other;
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AC ABI4923
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                                                                                                                                                   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                  Oligonucleotide primer SEQ ID NO 350261 for detecting SNP TSC0046575.
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81.8%; Pred. No. 6.8e+02;
iive 0; Mismatches 2; Indels
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              ABI50288 standard; DNA; 12
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ABI50288/
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35.5%; Score 7.8; DB 1; Length 12; llarity 81.8%; Pred. No. 6.8e+02; Conservative 0; Mismatches 2; Indels

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This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nuclectide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The coligomers are also used for detecting cell type differentiation. ABC00010-ABC99999, ABF00010-ABF99999 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from MIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                         SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
         Oligonucleotide primer SEQ ID NO 352121 for detecting SNP TSC0047678.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Oligonucleotide primer SEQ ID NO 373240 for detecting SNP TSC0059919.
                                                                                                                                                                                                                                                                                                                                                                                    Set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; SEQ ID NO 352121; 29pp + Sequence Listing; German.
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                                                                                                                                                                                                                                                                                        (EPIG-) EPIGENOMICS AG
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This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligoners for detecting single nuclectide polymorphisms (SNP) and oytosine methylation status in chemically pretreated genomic DNA. The oligonuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC09989, ABC0010-ABF99899, ABH00010-ABF9989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; 88; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Oligonucleotide primer SEQ ID NO 373922 for detecting SNP TSC0060388.
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                                                                                                                                                         Set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status.
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Best Local Similarity 81.8%; Pred. No. 6.8e+02;
Matches 9; Conservative 0; Mismatches 2; Indels
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06-APR-2001; 2001WO-IB000713.
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                                                                                                Piepenbrock C,
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                                                                (EPIG-) EPIGENOMICS
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Score 7.8, DB 1; Length 12; Pred. No. 6.8e+02; 0; Mismatches 2; Indels

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35.5%; 81.8%;

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Sequence 12 BP; 8 A; 0 C; 3 G; 1 T; 0 U; 0 Other;

was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences

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                                                             This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF9989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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                       Claim 1; SEQ ID NO 373922; 29pp + Sequence Listing; German.
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Best Local Similarity
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SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic. Oligonucleotide primer SEQ ID NO 377717 for detecting SNP TSC0062461. Berlin 07-APR-2000; 2000DE-01019173. 06-APR-2001; 2001WO-IB000713 Olek A, Piepenbrock C, (EPIG-) EPIGENOMICS AG. WPI; 2001-657177/75. WO200177384-A2. Homo sapiens 18-OCT-2001.

(first entry)

22-FEB-2002

ABI77744;

This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting call type differentiation. ABC0010-ABE79989, ABE70010-ABE79989 and ABI0010-ABE82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but Claim 1; SEQ ID NO 377717; 29pp + Sequence Listing; German.

Set of oligonucleotides, useful for diagnosis and cell typing, idesigned to detect single-nucleotide polymorphisms and cytosine methylation status.

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                                                                                                                                                                                                                                                                                                                                                                   peptide nucleic acid, cytosine methylation, cardiovascular, primer, ss, central nervous system, gastrointestinal, respiratory, immune, metabolic.
                                                                                                                                                                                                                                                                                                                                                  single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
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   Length 12;
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Query Match 35.5%; Score 7.8; DB 1; Length 12
Best Local Similarity 81.8%; Pred. No. 6.8e+02;
Matches 9; Conservative 0; Mismatches 2; Indels
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                                                                                                           2 GAAAGAGAAAA 12
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ABI77997
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This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
central nervous system; gastrointestinal; respiratory; immune; metabolic.
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Best Local Similarity 81.8%; Pred. No. 6.8e+02;
Matches 9; Conservative 0; Mismatches 2; Indels
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                                                                                                                                                                                                                                               SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic
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                                                                                                                                                                                                          Oligonucleotide primer SEQ ID NO 295102 for detecting SNP TSC0016434.
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This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nuclectide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The coligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABH99989 and ABI00010-ABH82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but the was obtained in electronic format from WIPO at
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                    Berlin K;
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                   Piepenbrock C,
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and cytosine methylation status in chemically pretreated genomic DNA. The oligomicleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABCC0010-ABC39989, ABF00010-ABF9989, ABF00010-ABF9998, ABF00010-ABF9998,
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Pred. No. 6.8e+02;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                    Sequence 12 BP; 2 A; 0 C; 3 G; 7 T; 0 U; 0 Other;
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Best Local Similarity 81.6-
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Gaps

Sequence 12 BP; 2 A; 0 C; 3 G; 7 T; 0 U; 0 Other;

was obtained in electronic format from Wl ftp.wipo.int/pub/published_pct_sequences

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SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                             Oligonucleotide primer SEQ ID NO 297933 for detecting SNP TSC0017835.
                                               22-FEB-2002 (first entry)
                                                                                                                                                                                                                                                                                                     WO200177384-A2.
                                                                                                                                                                                                                                                     Homo sapiens
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  ABH97940;
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ABH98624
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                            Oligonucleotide primer SEQ ID NO 322725 for detecting SNP TSC0031029.
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Pred. No. 6.8e+02;
0; Mismatches 2; Indels
     Length 12;
Score 7.8; DB 1; Length 12
Pred. No. 6.8e+02;
0; Mismatches 2; Indels
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A AB122752
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IX
C 12-FEB-2002 (first entry)
XX
C 12-FEB-2002 (first entry)
XX
SNP; single nuclectide polymony
XW
SNP; single nuclectide polymony
XW
SNP; single nuclectide polymony
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Homo sapiens.
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Homo sapiens.
XX
O -APR-2001, 2001WO-IB000713.
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O -APR-2001, 2001WO-IB000713.
XX
O -APR-2001, 201WO-IB000713.
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C 6-APR-2001, 201WO-IB000713.
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C 7 APR-2001, 201WO-IB000713.
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81.8%;
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ilarity 81.8%;
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Best Local Similarity
       Query Match
Best Local Similarity
Matches 9; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous. system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                                                                                                                                                                      Set of oligonucleotides, useful for diagnosis and cell typing; idesigned to detect single-nucleotide polymorphisms and cytosine methylation status.
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                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; SEQ ID NO 297933; 29pp + Sequence Listing; German.
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06-APR-2001; 2001WO-IB000713.
                                                   07-APR-2000; 2000DE-01019173.
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                                                                                                                                                                   Piepenbrock C,
                                                                                                            (EPIG-) EPIGENOMICS AG
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Best Local Similarity
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Conservative AAACAGAACAC 746

AACCAAAACAC

736 N

8 g ABH97940 standard; DNA; 12 BP.

RESULT 1285 ABH97940/c ID ABH9794(XX

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RESULT 1288
ABI24290/c
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                                                                                                                                                                                            Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single-nucleotide polymorphisms and cytosine methylation status.
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                                                                                                                                  Berlin K;
                                           06-APR-2001; 2001WO-IB000713.
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                                                                                                                                  Olek A, Piepenbrock C,
                                                                                                      (EPIG-) EPIGENOMICS AG
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              18-OCT-2001.
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                                             Gaps
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Query Match 35.5%; Score 7.8; DB 1; Length 12; Best Local Similarity 81.8%; Pred. No. 6.8e+02; Matches 9; Conservative 0; Mismatches 2; Indels
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SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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RESULT 1287
AB124220
XX
AC AB12422
AC AB12422
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DT 22-FEB-2
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PMA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABCO0010 Claim 1; SEQ ID NO 324263; 29pp + Sequence Listing; German.

Berlin

Piepenbrock C,

Olek A,

WPI; 2001-657177/75.

07-APR-2000; 2000DE-01019173. 06-APR-2001; 2001WO-IB000713

(EPIG-) EPIGENOMICS AG.

set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status.

Berlin K;

Olek A, Piepenbrock C,

WPI; 2001-657177/75.

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretraeted genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, ardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF9989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but the wibo.int/pub/published_pct_sequences
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Set of oligonuclectides, useful for diagnosis and cell typing, idesigned to detect single-nuclectide polymorphisms and cytosine methylation status.
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                                                                             Claim 1; SEQ ID NO 324193; 29pp + Sequence Listing; German.
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81.8%; Pred. No. 6.8e+02;
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Best Local Similarity 81.00.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
               -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part to of the printed specification, but was obtained in electronic format from WIPO at the printed specification ftp.wipo.int/pub/published_pot_sequences
                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Oligonucleotide primer SEQ ID NO 325088 for detecting SNP TSC0032385.
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llarity 81.8%; Pred. No. 6.8e+02;
Conservative 0; Mismatches 2; Indels
                                                                                                                                                                  35.5%; Score 7.8; DB 1; Length 12; 81.8%; Pred. No. 6.8e+02; cive 0; Mismatches 2; Indels
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Best Local Similarity 81...
9; Conservative
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                                                                                                                                                                   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Oligonucleotide primer SEQ ID NO 277024 for detecting SNP TSC0004361.
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                                                                                                                                   Oligonucleotide primer SEQ ID NO 301731 for detecting SNP TSC0019628
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                                 ABI01758 standard; DNA; 12
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This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, ardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99999, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from MIPO at
                                                                                                                                                                                 set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status.
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                       SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
Oligonucleotide primer SEQ ID NO 277609 for detecting SNP TSC0004523
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SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.

36-APR-2001; 2001WO-IB000713.

WO200177384-A2

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Homo sapiens

Oligonucleotide primer SEQ ID NO 277106 for detecting SNP TSC0004385.

22-FEB-2002

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABC0010-ABE9989, ABH0010-ABH9989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence was obtained in electronic format from MIPO at the printed specification, but typ.wipo.int/pub/published_pct_sequences
      This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABH82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99999, ABF00010-ABF99999, ABH00010-ABH99999 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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                                                                                 35.5%; Score 7.8; DB 1; Length 12; 81.8%; Pred. No. 6.8e+02; tive 0; Mismatches 2; Indels
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                  Sequence 12 BP; 2 A; 0 C; 3 G; 7 T; 0 U; 0 Other;
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ABIO 55124/2

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RESULT 1296

Berlin K;

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Set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status.
                                                                                                                                                                                                                                                                                   Claim 1; SEQ ID NO 309299; 29pp + Sequence Listing; German.
                                                                                06-APR-2001; 2001WO-IB000713.
                                                                                                             07-APR-2000; 2000DE-01019173
                                                                                                                                                                    Olek A, Piepenbrock C,
                                                                                                                                       (EPIG-) EPIGENOMICS AG
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Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                           SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                               Oligonucleotide primer SEQ ID NO 331734 for detecting SNP TSC0036439.
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Pred. No. 6.8e+02;
0; Mismatches 2; Indels
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81.8%;
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, ardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABH82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic formmat from WIPO at the printed specification, but ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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hes 9; Conservative
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Set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status.
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range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The coligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genemic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, ardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence was obtained in electronic formmat from WIPO at the printed specification, but the wipo.int/pub/published_pot_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                       Set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status:
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35.5%; Score 7.8; DB 1; Length 12; 81.8%; Pred. No. 6.8e+02;

Best Local Similarity

Query Match

This invention describes novel oligonucleotide primers or peptide nucleic acid (PRA) oligoners for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a

Berlin K;

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22-FEB-2002 (first entry)
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                                                                                                                                                                                      SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                   Oligonucleotide primer SEQ ID NO 288320 for detecting SNP TSC0013464.
 Gaps
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                                                                                                 ABH88327 standard; DNA; 12 BP.
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9; Conservative
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                     737 AACAGAACACC 747
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                                                                                                                                                                                                                                      Homo sapiens.
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ABI14362/C
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AC ABI1436:
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                                                                                       SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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Oligonucleotide primer SEQ ID NO 314335 for detecting SNP TSC0026287.
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ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                            set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status.
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                                                                                                              Berlin K;
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Best Local Similarity 81.0
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                                                                                                              Piepenbrock C,
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                                                                       This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, ardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABE99989, ABF00010-ABE99989, ABH00010-ABE99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                         Claim 1; SEQ ID NO 290385; 29pp + Sequence Listing; German.
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Pred. No. 6.8e+02;
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81.8%;
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Best Local Similarity 81.5-
Local Similarity 91.5-
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting call type differentiation. ABC00010-ABC99889, ABF00010-ABF9989, ABF00010-ABF89989, ABF00010-ABF82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                                                                                                                                              SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                                                                                                                                    Oligonucleotide primer SEQ ID NO 347885 for detecting SNP TSC0045323
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Best Local Similarity
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ABI47912
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SNP, single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences
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35.5%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 6.8e+02;
Matches 9; Conservative 0; Mismatches 2; Indels
                                                                                                                                           35.5%; Score 7.8; DB 1; Length 12; ilarity 81.8%; Pred. No. 6.8e+02; Conservative 0; Mismatches 2; Indels
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                                                                                                Sequence 12 BP; 1 A; 1 C; 2 G; 8 T; 0 U; 0 Other;
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Best Local Similarity
Local 9; Conserva
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, ardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABF82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but the wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Oligonucleotide primer SEQ ID NO 354264 for detecting SNP TSC0049006.
                                                                                                     Set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status.
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                                                                                                                                                                         Claim 1; SEQ ID NO 350939; 29pp + Sequence Listing; German.
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                                    Berlin K;
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Best Local Similarity 81.8
Matches 9; Conservative
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                                   Piepenbrock C,
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   (EPIG-) EPIGENOMICS AG
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acid; cytosine methylation; cardiovascular; primer; ss; system; gastrointestinal; respiratory; immune; metabolic.
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35.5%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 6.8e+02;
Matches 9; Conservative 0; Mismatches 2; Indels
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ABI50966 standard; DNA; 12
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 peptide nucleic
central nervous
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SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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Sequence 12 BP; 8 A; 3 C; 0 G; 1 T; 0 U; 0 Other;

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                                                                                                                                                                                                                                                                                                       SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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designed to detect single-nucleotide polymorphisms and cytosine
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99899, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABH82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                                                                                                                                              SNP, single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, ardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF9989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at

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ligonuclectides, useful for diagnosis and cell typing, it detect single-nuclectide polymorphisms and cytosine

Set of oligonucleotides,

methylation status.

WPI; 2001-657177/75

olek A,

Berlin K;

(EPIG-) EPIGENOMICS AG Piepenbrock

06-APR-2001; 2001WO-IB000713. 07-APR-2000; 2000DE-01019173

WO200177384-A2

18-OCT-2001

Claim 1; SEQ ID NO 358169; 29pp + Sequence Listing; German.

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SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                                                                                                       Oligonucleotide primer SEQ ID NO 358908 for detecting SNP TSC0051375.
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ABI58935/c
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35.5%; Score 7.8; DB 1; Length 12; 81.8%; Pred. No. 6.8e+02; Artive 0; Mismatches 2; Indels

9; Conservative 736 AAACAGAACAC 746

Matches

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Query Match Best Local Similarity

Sequence 12 BP; 8 A; 3 C; 0 G; 1 T; 0 U; 0 Other;

ftp.wipo.int/pub/published_pct_sequences

WPI; 2001-657177/75

SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.

Homo sapiens

Oligonucleotide primer SEQ ID NO 358169 for detecting SNP TSC0050979.

ABI58196 standard; DNA; 12 BP.

GAAACAATACA 2

12

22-FEB-2002 (first entry)

ABI58196,

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                                                                                                                          This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC9989, ABF00010-ABF9989, ABH00010-ABH99989 and ABI00010-ABI82073 trepresent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                  Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single-nucleotide polymorphisms and cytosine
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                                                                                            Claim 1; SEQ ID NO 358908; 29pp + Sequence Listing; German
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Post Local Similarity 81.0.
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                                                         methylation status.
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oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF99889, ABH0010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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Pred. No. 6.8e+02;
0; Mismatches 2; Indels
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81.8%; Pred. No. 6.8e+02;
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ftp.wipo.int/pub/published_pct_sequences
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llarity 81.8%;
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, ardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC9989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABF82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but the was obtained in electronic formmat from WIPO at
                               SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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Oligonucleotide primer SEQ ID NO 320124 for detecting SNP TSC0029574.
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                                                                                                                                                                                                                                                             SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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designed to detect single-nucleotide polymorphisms and cytosine
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                                                                                                                        ABH94123 standard; DNA; 12
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   736 AAACAGAACAC
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셤 ઠ ô This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, contral nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABE9989, ABF00010-ABE9989, ABH00010-ABH99989 and ABI00010-ABI82073 tepseson the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic. Oligonucleotide primer SEQ ID NO 298260 for detecting SNP TSC0017996. Gaps Set of oligonuclectides, useful for diagnosis and cell typing, is designed to detect single-nuclectide polymorphisms and cytosine methylation status. Set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status. ö Claim 1; SEQ ID NO 271141; 29pp + Sequence Listing; German. h 35.5%; Score 7.8; DB 1; Length 12; Similarity 81.8%; Pred. No. 6.8e+02; 9; Conservative 0; Mismatches 2; Indels Sequence 12 BP; 8 A; 4 C; 0 G; 0 T; 0 U; 0 Other; ftp.wipo.int/pub/published_pct_sequences Berlin K; Berlin K; ABH98267 standard; DNA; 12 BP. 06-APR-2001; 2001WO-IB000713. 07-APR-2000; 2000DE-01019173 07-APR-2000; 2000DE-01019173 (first entry) 736 AAACAGAACAC 746 ϋ 1 AAACAACACAC 11 Olek A, Piepenbrock C, (EPIG-) EPIGENOMICS AG (EPIG-) EPIGENOMICS AG WPI; 2001-657177/75 WPI; 2001-657177/75. Best Local Similarity Matches 9; Conserv WO200177384-A2 Homo sapiens 18-OCT-2001. 22-FEB-2002 ABH98267; Query Match Olek A, RESULT 1321
ABH98267
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, ardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF9989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent din ot form part of the printed specification, but was obtained in electronic format from WIPO at This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, cardiovascular and merabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABF82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but the was obtained in electronic format from WIPD at SND; single nuclectide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic. Gaps Oligonucleotide primer SEQ ID NO 275038 for detecting SNP TSC0003769. Set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status. . Claim 1; SEQ ID NO 298260; 29pp + Sequence Listing; German. Claim 1; SEQ ID NO 275038; 29pp + Sequence Listing; German. h 35.5%; Score 7.8; DB 1; Length 12; Similarity 81.8%; Pred. No. 6.8e+02; 9; Conservative 0; Mismatches 2; Indels Seguence 12 BP; 7 A; 3 C; 0 G; 2 T; 0 U; 0 Other; Berlin K; BP. 06-APR-2001; 2001WO-IB000713. 07-APR-2000; 2000DE-01019173 ABH75051 standard; DNA; 12 (first entry) 737 AACAGAACACC 747 Olek A, Piepenbrock C, AACATAATACC 11 (EPIG-) EPIGENOMICS AG. WPI; 2001-657177/75 Best Local Similarity WO200177384-A2. Homo sapiens. 18-OCT-2001. 22-FEB-2002 ABH75051; Query Match RESULT 1322 Matches

RESULT 1323

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligomucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, ardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABF82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but the wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                            SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                                                                                   Oligonucleotide primer SEQ ID NO 301526 for detecting SNP TSC0019537.
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designed to detect single-nucleotide polymorphisms and cytosine
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Matches 9; Conservative
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                                                                                         Match 15; Score 7.8; DB 1; Length 12; Local Similarity 81.8%; Pred. No. 6.8e+02; es 9; Conservative 0; Mismatches 2; Indels
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This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nuclectide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligomuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, contral nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABE99989, ABF00010-ABE99989, ABF00010-ABE99989 and ABI00010-ABE82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but two but hub/published_pot_sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardicoascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                Set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status.
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                                                                                                                                                                                                 Claim 1; SEQ ID NO 276696; 29pp + Sequence Listing; German.
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Berlin K;
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                          Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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designed to detect single-nucleotide polymorphisms and cytosine
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                             Local Similarity 81.8
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99889, ABF00010-ABF99989, ABH00010-ABF99989 and ABI00010-ABF82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic formmat from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                  Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single-nucleotide polymorphisms and cytosine
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                                                                                                                              SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                             Oligonucleotide primer SEQ ID NO 309298 for detecting SNP TSC0023469.
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                               (first entry)
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Best Local Similarity 81.0
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SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                          Oligonucleotide primer SEQ ID NO 311185 for detecting SNP TSC0024345.
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                                                                                                                                                                                                                                                                                            Set of oligonucleotides, useful for diagnosis and cell typing,
                                                                                                                                                                                                                                                    Berlin K;
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WO200177384-A2

Homo sapiens.

ABI35772;

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WO200177384-A2 Homo sapiens 18-OCT-2001 11 ABI11567; Query Match ઠે d

This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF99889 and ABI00010-ABF82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but fire wipo.int/pub/published_pct_sequences detect single-nucleotide polymorphisms and cytosine Claim 1; SEQ ID NO 311185; 29pp + Sequence Listing; German. / Match 12; Score 7.8; DB 1; Length 12; Local Similarity 81.8%; Pred. No. 6.8e+02; Local Si Conservative 0; Mismatches 2; Indels Sequence 12 BP; 0 A; 1 C; 3 G; 8 T; 0 U; 0 Other; designed to methylation

736 AAACAGAACAC 746 AAACGAAACAC 1 ABI11567 standard; DNA; 12 BP

22-FEB-2002 (first entry)

Oligonucleotide primer SEQ ID NO 311540 for detecting SNP TSC0024547.

SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.

06-APR-2001; 2001WO-IB000713.

07-APR-2000; 2000DE-01019173.

(EPIG-) EPIGENOMICS AG

Berlin K; Olek A, Piepenbrock C,

WPI; 2001-657177/75.

Set of oligonuclectides, useful for diagnosis and cell typing, idesigned to detect single-nuclectide polymorphisms and cytosine methylation status.

Claim 1; SEQ ID NO 311540; 29pp + Sequence Listing; German.

This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, aztdiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF99989, ABF00010-ABF99989 and ABI00010-ABF82073

ö represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at Gaps ; 0 Score 7.8; DB 1; Length 12; Pred. No. 6.8e+02; 0; Mismatches 2; Indels Sequence 12 BP; 2 A; 0 C; 4 G; 6 T; 0 U; 0 Other; ftp.wipo.int/pub/published_pct_sequences Match 35.5%; Local Similarity 81.8%; es 9; Conservative (736 AAACAGAACAC 746 11 AAACATAACCC 1 Query Match Best Local RESULT 1334 Matches 8888888 Š g

ABI13745 standard; DNA; 12 BP. (first entry) 22-FEB-2002 ABI13745;

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SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.

Oligonucleotide primer SEQ ID NO 313718 for detecting SNP TSC0025933.

Homo sapiens.

WO200177384-A2.

18-OCT-2001

06-APR-2001; 2001WO-IB000713.

07-APR-2000; 2000DE-01019173.

(EPIG-) EPIGENOMICS AG

Berlin K; Piepenbrock C, olek A,

WPI; 2001-657177/75.

Set of oligonucleotides, useful for diagnosis and cell typing, idesigned to detect single-nucleotide polymorphisms and cytosine methylation status

Claim 1; SEQ ID NO 313718; 29pp + Sequence Listing; German.

This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymcrphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC9989, ABF00010-ABF99989, ABF00010-ABF99989 and ABI00010-ABF82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but the was obtained in electronic format from WIPD at

Sequence 12 BP; 0 A; 0 C; 5 G; 7 T; 0 U; 0 Other;

Gaps ö h Similarity 81.8%; Score 7.8; DB 1; Length 12; Similarity 81.8%; Pred. No. 6.8e+02; 9; Conservative 0; Mismatches 2; Indels Query Match Best Local Similarity Matches 9; Conserv

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736 AAACAGAACAC 746

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Page 583

WO200177384-A2. WO200177384-A2 Homo sapiens 18-OCT-2001 18-OCT-2001 ABI16501; RESULT 1337 à d .; This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, contral nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABE99989, ABH00010-ABH99989 and ABI00010-ABH82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at the printed specification, but fire wipo.int/pub/published_pct_sequences SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic. Oligonucleotide primer SEQ ID NO 288923 for detecting SNP TSC0013731. Gaps Oligonuclectide primer SEQ ID NO 314630 for detecting SNP TSC0026470 Set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status. ·; Claim 1; SEQ ID NO 288923; 29pp + Sequence Listing; German. 35.5%; Score 7.8; DB 1; Length 12; 81.8%; Pred. No. 6.8e+02; tive 0; Mismatches 2; Indels Sequence 12 BP; 1 A; 0 C; 5 G; 6 T; 0 U; 0 Other; Berlin K; ABH88930 standard; DNA; 12 BP 07-APR-2000; 2000DE-01019173. 06-APR-2001; 2001WO-IB000713. ABI14657 standard; DNA; 12 (first entry) Best Local Similarity 81.8 Matches 9; Conservative 736 AAACAGAACAC 746 Olek A, Piepenbrock C, 11 AACCACACAC 1 (EPIG-) EPIGENOMICS AG 12 AAACACAACCC WPI; 2001-657177/75 WO200177384-A2. Homo sapiens. 22-FEB-2002 22-FEB-2002 18-OCT-2001. ABH88930; ABI14657; Query Match RESULT 1336 ABI14657/c 엄 ö g

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosite methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC9989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but the wipo int/pub/published_pct_sequences
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SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           set of oligonucleotides, useful for diagnosis and cell typing, idesigned to detect single-nucleotide polymorphisms and cytosine methylation status.
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ABI16501 standard; DNA; 12
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Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single-nucleotide polymorphisms and cytosine methylation status.
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABF3073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but the was obtained in electronic formmat from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Oligonuclectide primer SEQ ID NO 347970 for detecting SNP TSC0045385.
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Pred. No. 6.8e+02;
0; Mismatches 2; Indels
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Best Local Similarity 81.8%;
Matches 9; Conservative
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                                                                                                               Berlin K;
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                                                                                                               Piepenbrock C,
                                              (EPIG-) EPIGENOMICS AG.
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acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligomerlocities are used for disponsis and/or prognosis of cancer and a range of disposes including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABE09989, ABF00010-ABE9989, ABH0010-ABE9989 and ABI00010-ABE82073 represent the oligomers described in the invention. NOTE: The sequence was obtained in electronic format from WIPO at the printed specification, but the wipo.int/pub/published_pct_sequences
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Claim 1; SEQ ID NO 347243; 29pp + Sequence Listing; German.

Berlin K;

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99889, ABF00010-ABF99989, ABH00010-ABF99989 and ABI00010-ABF82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic formmat from WIPO at fire printed specification, but fire wipo.int/pub/published_pct_sequences
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                                                                                                                                                                          SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; 88; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                               Oligonucleotide primer SEQ ID NO 372540 for detecting SNP TSC0059450.
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ABI72567 standard; DNA; 12 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                           Length 12;
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Sequence 12 BP; 1 A; 0 C; 2 G; 9 T; 0 U; 0 Other;
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This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, aardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99889, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but the was obtained in electronic formmat from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                Set of oligonucleotides, useful for diagnosis and cell typing, addesigned to detect single-nucleotide polymorphisms and cytosine
                                                                                                                                         Claim 1; SEQ ID NO 268953; 29pp + Sequence Listing; German
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligomucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory,

Olek A, Piepenbrock C, Berlin K;

(EPIG-) EPIGENOMICS AG

06-APR-2001; 2001WO-IB000713 07-APR-2000; 2000DE-01019173

WO200177384-A2 Homo sapiens

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Claim 1; SEQ ID NO 294352; 29pp + Sequence Listing; German.

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central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010 -ABC99989, ABF00010-ABF9989, ABF00010-ABF9989, ABF00010-ABF9989, ABF00010-ABF9989, ABF00010-ABF9989 and ABI00010-ABF82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at this printed specification, but ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SNP; single nuclectide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABE99999, ABF00010-ABE99999, ABF00010-ABE99999, ABF00010-ABE99999 and ABI00010-ABE32073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but twipo.int/pub/published_pot_sequences
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                                                                                                                                                      SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                          Oligonucleotide primer SEQ ID NO 270025 for detecting SNP TSC0001962.
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Pred. No. 6.8e+02;
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Best Local Similarity 81.8%;
Matches 9; Conservative
                              ABH70048 standard; DNA; 12
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Set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status.

Berlin K;

Piepenbrock C,

olek A,

WPI; 2001-657177/75.

(EPIG-) EPIGENOMICS AG

06-APR-2001; 2001WO-IB000713. 07-APR-2000; 2000DE-01019173. German.

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SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
          Oligonucleotide primer SEQ ID NO 295186 for detecting SNP TSC0016477.
                                                                                                                                                                                                                                                    Set of oligonucleotides, useful for diagnosis and cell typing, idesigned to detect single-nucleotide polymorphisms and cytosine methylation status.
                                                                                                                                                                                                                                                                                              Claim 1; SEQ ID NO 295186; 29pp + Sequence Listing; German.
                                                                                                                                           06-APR-2001; 2001WO-IB000713.
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                                                                                                                                                                                                           Piepenbrock C,
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Berlin K;

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC9989, ABR00010-ABE9989 and ABI0010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from NIPO at
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ABH97185 standard; DNA; 12 BP ABH97185 RESULT 1348 ABH97185/ XX ABH9 XX ABH9 XX Z2-F XX C19 XX C19 XX SNP; XW PEPT XW CENT XX CENT XX HOWC XX HOW

(first entry) 22-FEB-2002

SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic. Oligonucleotide primer SEQ ID NO 297178 for detecting SNP TSC0017472

Homo sapiens

WO200177384-A2

18-OCT-2001.

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF99899, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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ftp.wipo.int/pub/published_pct_sequences
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                                                                                   This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABH99989 and ABI00010-ABH82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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                                 Claim 1; SEQ ID NO 297824; 29pp + Sequence Listing; German.
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                                                                                                                                                                                                                                                                                                                                                                                                          SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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designed to detect single-nucleotide polymorphisms and cytosine
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                                                                                                                                                                                                                                                  SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                                                                                                      Oligonucleotide primer SEQ ID NO 298300 for detecting SNP TSC0018015
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                                                               ABH98307 standard; DNA; 12 BP.
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central nervous system; gastrointestinal; respiratory; immune; metabolic
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designed to detect single-nucleotide polymorphisms and cytosine
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Pred. No. 6.8e+02;
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              olek A,
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and cytosine methylation status in chemically pretreated genomic DNA. The oligonuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF99889, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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Sequence 12 BP; 2 A; 4 C; 0 G; 6 T; 0 U; 0 Other;

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, astdowascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABE99999, ABF00010-ABE99999, ABF00010-ABE99999, ABF00010-ABE99999, and ABI00010-ABE82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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                                                                                                                               SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                           Oligonuclectide primer SEQ ID NO 303263 for detecting SNP TSC0020412.
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ABH78687 standard; DNA; 12 BP.
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ABH78687/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                  Gaps
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Score 7.8; DB 1; Length 12;
Pred. No. 6.8e+02;
0; Mismatches 2; Indels
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    35.5%;
81.8%;
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                                                  9; Conservative
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RESULT 1357
ABI 01737/c
ABI 01737/c
AC ABI 01737/c
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XX SNP; Sil
XX SNP; Sil
XX SNP; Sil
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RESULT 1358 ABI03290/c ID ABI03290 XX

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ABH79704 standard; DNA; 12 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            designed to detect methylation status.
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                                                                                                                   This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF9989, ABH00010-ABH99389 and ABI00010-ABI82073 trepresent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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Set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status.
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designed to detect single-nucleotide polymorphisms and cytosine
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                                                                                  + Sequence Listing; German.
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                                                                                    SEQ ID NO 279697; 29pp
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(first entry)

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SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                                                                                                                                            Oligonucleotide primer SEQ ID NO 334498 for detecting SNP TSC0038193.
                                                                                                                                                         ABI34525 standard; DNA; 12 BP.
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                                                                                                         RESULT 1363
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
-ABC39989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data_for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at the printed specification, the ftp.wipo.int/pub/published_pot_sequences
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designed to detect single-nucleotide polymorphisms and cytosine
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                                                                                                                                                                                                                35.5%; Score 7.8; DB 1; Length 12; 81.8%; Pred. No. 6.8e+02; ive 0; Mismatches 2; Indels
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                                                                                                                                                              Sequence 12 BP; 8 A; 3 C; 1 G; 0 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                         Local Similarity 81.8
les 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         designed to detect methylation status.
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Best Local Similarity
Matches 9; Conserv
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                                                                                                                                                                                                                      Query Match
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ABI09227/C
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ABI09227/C
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ABI0922
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ABI0922
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ABI0922
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BDT 22-FEB-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Set of oligonucleotides, useful for diagnosis and cell typing, i
designed to detect single-nucleotide polymorphisms and cytosine
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 12 BP; 10 A; 2 C; 0 G; 0 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  was obtained in electronic format from Wiftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                    Berlin K;
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Best Local Similarity 81.8
Matches 9; Conservative
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                                                        WO200177384-A2.
Homo sapiens.
                                                                                                                 18-OCT-2001.
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ABH87869/c
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABE99989, ABF00010-ABE99989, ABH00010-ABE99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                                                                                                                             Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single-nucleotide polymorphisms and cytosine methylation status.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 35.5%; Score 7.8; DB 1; Length 12; Best Local Similarity 81.8%; Pred. No. 6.8e+02; Matches 9; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                 Claim 1; SEQ ID NO 313091; 29pp + Sequence Listing; German.
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                                                                                                       07-APR-2000; 2000DE-01019173
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) eligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99899, ABF00010-ABF99989, ABF00010-ABF99989 and ABI00010-ABF82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                           SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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Mon Oct 18 14:40:07 2004
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Gaps

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ABI53296 standard; DNA; 12 BP.

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22-FEB-2002 (first entry)

0; Gaps

Similarity 81.8%; Score 7.8; DB 1; Length 12; Similarity 81.8%; Pred. No. 6.8e+02; 9; Conservative 0; Mismatches 2; Indels

737 AACAGAACACC 747

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Best Local Similarity Matches 9; Conserv

Query Match

Sequence 12 BP; 1 A; 0 C; 6 G; 5 T; 0 U; 0 Other;

ABI53296;

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SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                                                                                                                                                                                                                    Oligonucleotide primer SEQ ID NO 353269 for detecting SNP TSC0048413.
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RESULT 1366
ARI53296
XX
AC ABI53296
AC ABI5329
AC ABI53296
AC ABI5329
AC ABI53296
AC ABI53
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SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.

06-APR-2001; 2001WO-IB000713

WO200177384-A2

18-OCT-2001

Homo sapiens.

Oligonucleotide primer SEQ ID NO 313091 for detecting SNP TSC0025474.

(first entry)

22-FEB-2002

ABI13118;

BP.

ABI13118 standard; DNA; 12

RESULT 1365

Claim 1; SEQ ID NO 353269; 29pp + Sequence Listing; German

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Sequence 12 BP; 1 A; 0 C; 4 G; 7 T; 0 U; 0 Other;
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AB115474474
AB115474474
AB115474474
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AB1154744474
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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Pred. No. 6.8e+02;
0; Mismatches 2; Indels
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81.8%;
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Best Local Similarity
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ABI53718/C
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ABI53718/C
DT 22-FEB-;
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SNP; sin
KW POPLide
KW Central
XX
SNP; sin
KW POPLide
KW COOLOT
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KW WOZOOLOT
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CC COLOT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Oligonucleotide primer SEQ ID NO 354717 for detecting SNP TSC0049243.
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Score 7.8; DB 1; Length 12;
Pred. No. 6.8e+02;
0; Mismatches 2; Indels
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   Query Match 35.5%;
Best Local Similarity 81.8%;
Matches 9; Conservative
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Best Local Similarity
Matches 9; Conserv
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RESULT 1369

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABE99989, ABF00010-ABE99989, ABH00010-ABE99989 and ABI00010-ABE82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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Pred. No. 6.8e+02;
0; Mismatches 2; Indels
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Best Local Similarity 81.8%;
Matches 9; Conservative
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Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99999, ABF00010-ABF99999, ABH00010-ABH99999 and ABI00010-ABH82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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                                                                                                                                                                                                 SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                                                         Oligonucleotide primer SEQ ID NO 354911 for detecting SNP TSC0049361.
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                     ABI54938 standard; DNA; 12 BP
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range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH999899 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at fire printed specification, but ftp.wipo.int/pub/published_pct_sequences
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                                                                 Set of oligonucleotides, useful for diagnosis and cell typing, idesigned to detect single-nucleotide polymorphisms and cytosine
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Pred. No. 6.8e+02;
0; Mismatches 2; Indels
                                                                                                                                                          Claim 1; SEQ ID NO 363052; 29pp + Sequence Listing;
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                                                                                                                                                                                                                                                                                                                                                                                                                        was obtained in electronic format from Wiftp.wipo.int/pub/published_pct_sequences
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Matches 9; Conservative
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                       WPI; 2001-657177/75
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, ardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC90989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABF82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 7.8; DB 1; Length 12; Pred. No. 6.8e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Seguence 12 BP; 1 A; 3 C; 0 G; 8 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ftp.wipo.int/pub/published_pct_sequences
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81.8%;
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Best Local Similarity
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a

Claim 1; SEQ ID NO 364613; 29pp + Sequence Listing; German.

Matches

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RESULT 1374

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC9989, ABF00010-ABF9989, ABH00010-ABF9989 and ABT00010-ABI82073 the preparent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                     SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                             Oligonucleotide primer SEQ ID NO 296894 for detecting SNP TSC0017337.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status.
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22-FEB-2002 (first entry)
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Matches 9, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                 SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                                                                                                                                                                        Oligonucleotide primer SEQ ID NO 380436 for detecting SNP TSC0063822.
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                                          733 GAGAAACAGAA 743
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RESULT 1375

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useful for diagnosis and cell typing, is

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligomucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, ardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABH82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                                                                                                                                       Claim 1; SEQ ID NO 297286; 29pp + Sequence Listing; German
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                                                                   This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABE99989, ABF00010-ABE99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC9989, ABF00010-ABF9989, ABH00010-ABF9989 and ABI00010-ABF82071 represent the oligomers described in the invention. NOTE: The sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                   Claim 1; SEQ ID NO 323067; 29pp + Sequence Listing; German.
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Pred. No. 6.8e+02;
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methylation status.
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Score 7.8; DB 1; Length 12; Pred. No. 6.8e+02; 0; Mismatches 2; Indels

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, ardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                                                                                                                                   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                                                         Oligonucleotide primer SEQ ID NO 300551 for detecting SNP TSC0019086.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status.
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                                                                                        ABI00578 standard; DNA; 12
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                                                                                                                                                                                (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Olek A, Piepenbrock C,
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                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
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                                                                                                                                     ABI00578;
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                                               RESULT 1380
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Oligonucleotide primer SEQ ID NO 275389 for detecting SNP TSC0003880.
                                                                                                                                                                                  Gaps
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                                                                                                                                     Length 12;
                                                                                                                                                                                2; Indels
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                                                                                        Sequence 12 BP; 6 A; 6 C; 0 G; 0 T; 0 U; 0 Other;
                                                                                                                                Score 7.8; DB 1;
Pred. No. 6.8e+02;
0; Mismatches 2;
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                                                                                                             Query Match
Best Local Similarity 81.0.
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                                                                                                                                                                                                                                                                      2 AACCACAACAC 12
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Matches 9; Conserv
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SNP; single nucleotide polymorphism; human; diagnosis; FNA; cancer; CNS;
Gaps
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99889, ABF00010-ABF99989, ABH00010-ABF99989 and ABI00010-ABF3073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but the was obtained in electronic format from WFPO at the printed specification, but ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This invention describes novel oligonucleotide primers or peptide nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Oligonucleotide primer SEQ ID NO 330120 for detecting SNP TSC0035350.
                                                                                                  Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single-nucleotide polymorphisms and cytosine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Set of oligonucleotides, useful for diagnosis and cell typing, idesigned to detect single-nucleotide polymorphisms and cytosine methylation status.
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                                                                                                                                                                     Claim 1; SEQ ID NO 326225; 29pp + Sequence Listing; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  35.5%; Score 7.8; DB 1; Length 12; 81.8%; Pred. No. 6.8e+02; Artive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 12 BP; 0 A; 0 C; 5 G; 7 T; 0 U; 0 Other;
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es 9; Conservative
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(EPIG-) EPIGENOMICS AG
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                                 Piepenbrock
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                                                                                                                      designed to detect a methylation status.
                                                                  WPI; 2001-657177/75
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                                                                                                                                                                                                                                                                                                                                                                                                                                 This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABH99989 and ABI00010-ABH82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
peptide nucleic acid, cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Oligonucleotide primer SEQ ID NO 326225 for detecting SNP TSC0032964.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                              ligonucleotides, useful for diagnosis and cell typing, to detect single-nucleotide polymorphisms and cytosine
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                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; SEQ ID NO 275859; 29pp + Sequence Listing; German.
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                                                                                                                                                                                                                                                                                                                                    of oligonucleotides,
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                                                                                                                                                                                                                                                                                                                                                     designed to detect methylation status.
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acid (PNA) oligomers for detecting single nuclectide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory. central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99889, ABF00010-ABF99889, ABH0010-ABH99889 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form art of the printed specification, but tho was obtained in electronic format from WIPO at
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Best Local Similarity 81.0
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ABI30627 standard; DNA; 12 22-FEB-2002 (first entry) ABI30627; RESULT 1384

Oligonucleotide primer SEQ ID NO 330600 for detecting SNP TSC0035613.

SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.

Homo sapiens.

WO200177384-A2

18-0CT-2001

Set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status.

Claim 1; SEQ ID NO 285246; 29pp + Sequence Listing; German.

06-APR-2001; 2001WO-IB000713.

07-APR-2000; 2000DE-01019173.

(EPIG-) EPIGENOMICS AG.

Olek A, Piepenbrock C,

WPI; 2001-657177/75.

Berlin K;

Set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status.

Claim 1; SEQ ID NO 330600; 29pp + Sequence Listing; German.

This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABE99899, ABR00010-ABH99999 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences

Sequence 12 BP; 8 A; 2 C; 0 G; 2 T; 0 U; 0 Other;

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                                                                                                                                                                           SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                          Oligonucleotide primer SEQ ID NO 285246 for detecting SNP TSC0012209.
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Length 12;
Score 7.8; DB 1; Length 12
Pred. No. 6.8e+02;
0; Mismatches 2; Indels
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                                                                                                    ABH85253 standard; DNA; 12 BP.
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35.5%;
81.8%;
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Query Match 35.5
Best Local Similarity 81.8
Matches 9; Conservative
                                    736 AAACAGAACAC 746
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                                                                                                                                                                                                                                                                                                            (EPIG-) EPIGENOMICS AG.
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ö This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at Gaps ·, Query Match 35.5%; Score 7.8; DB 1; Length 12; Best Local Similarity 81.8%; Pred. No. 6.8e+02; Matches 9; Conservative 0; Mismatches 2; Indels Sequence 12 BP; 0 A; 0 C; 3 G; 9 T; 0 U; 0 Other; ftp.wipo.int/pub/published_pct_sequences 734 AGAAACAGAAC 744 AAAAACAAAAC 1 ਨੇ

0974/c ABI10974 standard; DNA; 12 RESULT 1386 ABI10974/ ID ABI1

WO200177384-A2.

18-OCT-2001.

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and oytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                            SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                             Oligonucleotide primer SEQ ID NO 310947 for detecting SNP TSC0024237.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Oligonucleotide primer SEQ ID NO 336609 for detecting SNP TSC0039445.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; SEQ ID NO 310947; 29pp + Sequence Listing; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 7.8; DB 1; Length 12;
Pred. No. 6.8e+02;
0; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                    Berlin K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABI36636 standard; DNA; 12 BP.
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                                               22-FEB-2002 (first entry)
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Best Local Similarity 81.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     methylation status.
                                                                                                                                                                                                                 WO200177384-A2.
                                                                                                                                                                                  Homo sapiens
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cycosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF99899, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from MIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                                                           Berlin K;
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                                                            06-APR-2001; 2001WO-IB000713.
                                                                                           07-APR-2000; 2000DE-01019173.
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Best Local Similarity 81.8
Matches 9; Conservative
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                                                                                                                            (EPIG-) EPIGENOMICS AG
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                                                                                                                                                                                                                                                            methylation status.
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ABH87873/c
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WPI; 2001-657177/75

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretracted genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC9989, ABF00010-ABF9989, ABH00010-ABH99899 and ABI00010-ABH82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form par to f the printed specification, but ftp.wipo.int/pub/published_pct_sequences
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                                Set of oligonucleotides, useful for diagnosis and cell typing, idesigned to detect single-nucleotide polymorphisms and cytosine methylation status.
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                                                                                                                                                                                  Claim 1; SEQ ID NO 287866; 29pp + Sequence Listing; German.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 35.5%; Score 7.8; DB 1; Length 12; Best Local Similarity 81.8%; Pred. No. 6.8e+02; Matches 9; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Seguence 12 BP; 2 A; 1 C; 4 G; 5 T; 0 U; 0 Other;
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AB113569/C
ID AB113565
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oligomers are also used for detecting cell type differentiation. ABC00010
-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at from the printed specification, but ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                                     Sequence 12 BP; 0 A; 2 C; 3 G; 7 T; 0 U; 0 Other;
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Pred. No. 6.8e+02;
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ftp.wipo.int/pub/published_pct_sequences
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12 AAACGAAACAC 2
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                                                                                                                                                                                                                                                                                                            SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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designed to detect single-nucleotide polymorphisms and cytosine
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Best Local Similarity 81.0
  736 AAACAGAACAC 746
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                                        11 AAATATAACAC 1
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                                                                          SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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Oligonucleotide primer SEQ ID NO 352289 for detecting SNP TSC0047796.
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Pred. No. 6.8e+02;
0; Mismatches 2; Indels
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Best Local Similarity
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Claim 1; SEQ ID NO 356575; 29pp + Sequence Listing; German
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                                                                                                                                                                                                                                                                               This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF9989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but the was obtained in electronic format from WIPO at
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                                                                                            Berlin K;
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                  07-APR-2000; 2000DE-01019173.
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                                                                                       Olek A, Piepenbrock C,
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, contral nervous system, ardiovascular and merabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPD at
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF9989, ABH00010-ABH99989 and ABI00010-ABI82073 the represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                                                                                                                                                                                                                SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                                                                                                                      Oligonucleotide primer SEQ ID NO 364768 for detecting SNP TSC0054707.
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RESULT 1397
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AB16,735

AB17, AB17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Oligonucleotide primer SEQ ID NO 360557 for detecting SNP TSC0052132.
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                                                                                                                                 Score 7.8; DB 1; Length 12;
Pred. No. 6.8e+02;
0; Mismatches 2; Indels
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                                                                    Sequence 12 BP; 8 A; 3 C; 0 G; 1 T; 0 U; 0 Other;
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ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                         35.5%;
81.8%;
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                                                                                                       Query Match
Best Local Similarity 81.0
For 20 9; Conservative
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Best Local Similarity
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German.

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                                                                                                                    Gaps
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                                                    35.5%; Score 7.8; DB 1; Length 12; 81.8%; Pred. No. 6.8e+02; ive 0; Mismatches 2; Indels
Sequence 12 BP; 7 A; 3 C; 0 G; 2 T; 0 U; 0 Other;
                                                                                  Pred. No. 6.8e
0; Mismatches
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Gaps

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Matches

736 AAACAGAACAC 746

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AAACACAACTC 12

This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF99899, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic. Oligonucleotide primer SEQ ID NO 318617 for detecting SNP TSC0028770. oligonucleotides, useful for diagnosis and cell typing, is to detect single-nucleotide polymorphisms and cytosine .; 0 Claim 1; SEQ ID NO 318029; 29pp + Sequence Listing; German. Query Match
Best Local Similarity 81.8%; Pred. No. 6.8e+02;
Matches 9; Conservative 0; Mismatches 2; Indels Sequence 12 BP; 8 A; 3 C; 0 G; 1 T; 0 U; 0 Other; BP. 06-APR-2001; 2001WO-IB000713. 06-APR-2001; 2001WO-IB000713. 07-APR-2000; 2000DE-01019173. 07-APR-2000; 2000DE-01019173 ABI18644 standard; DNA; 12 (first entry) 736 AAACAGAACAC 746 Olek A, Piepenbrock C, 2 AAACAATACAC 12 (EPIG-) EPIGENOMICS AG (EPIG-) EPIGENOMICS WPI; 2001-657177/75 Set of oligonucleot: designed to detect amethylation status. WO200177384-A2. WO200177384-A2. Homo sapiens. Homo sapiens. 22-FEB-2002 18-OCT-2001 18-OCT-2001 ABI18644; ABI18644/ ò 셤

ô This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, ardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC09989, ABF00010-ABF99899, ABH0010-ABF99899 and ABI00010-ABF82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic. Gaps Oligonucleotide primer SEQ ID NO 270046 for detecting SNP TSC0001972 Set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status. .. 0 / Match 35.5%; Score 7.8; DB 1; Length 12; Local Similarity 81.8%; Pred. No. 6.8e+02; nes 9; Conservative 0; Mismatches 2; Indels Claim 1; SEQ ID NO 270046; 29pp + Sequence Listing; German Seguence 12 BP; 0 A; 0 C; 6 G; 6 T; 0 U; 0 Other; Berlin K; ABH70069 standard; DNA; 12 BP 06-APR-2001; 2001WO-IB000713. 07-APR-2000; 2000DE-01019173 22-FEB-2002 (first entry) 737 AACAGAACACC 747 Olek A, Piepenbrock C, 11 AACAAAACCCC 1 (EPIG-) EPIGENOMICS AG. WPI; 2001-657177/75 WO200177384-A2 Homo sapiens. 18-OCT-2001. ABH70069; Query Match RESULT 1400 Best Loca Matches ò 셤

100 mm (100 mm) (100

Set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status.

Berlin K;

Piepenbrock C,

olek A,

WPI; 2001-657177/75

Claim 1; SEQ ID NO 318617; 29pp + Sequence Listing; German.

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Gaps

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Indels

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Sequence 12 BP; 1 A; 1 C; 2 G; 8 T; 0 U; 0 Other;
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35.5%; Score 7.8; DB 1; Length 12;

Query Match

ABH75097;

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABE09989, ABF00010-ABE99989, ABF00010-ABE99989 and ABI00010-ABE32073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but the was obtained in electronic format from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                                                                                                                                                                                                                                                               Oligonucleotide primer SEQ ID NO 274205 for detecting SNP TSC0003476.
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Pred. No. 6.8e+02;
0; Mismatches 2;
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     81.8%;
                                                                                                                                                                                                                                                                      ABH74220 standard; DNA; 12
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     Best Local Similarity 81.8
Matches 9; Conservative
                                                                                735 GAAACAGAACA 745
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  oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABF82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at fitp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligoners for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABH82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                                                                                                                                                                                                                     Query Match 35.5%; Score 7.8; DB 1; Length 12; Best Local Similarity 81.8%; Pred. No. 6.8e+02; Matches 9; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                      Sequence 12 BP; 9 A; 2 C; 0 G; 1 T; 0 U; 0 Other;
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ABH98381;

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35.5%; Score 7.8; DB 1; Length 12; 81.8%; Pred. No. 6.8e+02; tive 0; Mismatches 2; Indels
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC091019999, ABF00010-ABF99999, ABH00010-ABH99999 and ABI00010-ABH82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                      SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                     Oligonucleotide primer SEQ ID NO 275084 for detecting SNP TSC0003780.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single-nucleotide polymorphisms and cytosine methylation status.
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                                                                                                                                                                                                                                                                                                                            07-APR-2000; 2000DE-01019173.
                (first entry)
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                                                                                                                                                                      Homo sapiens.
                22-FEB-2002
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Gaps ; 0 Query Match
Best Local Similarity 81.8%; Pred. No. 6.8e+02;
Matches 9; Conservative 0; Mismatches 2; Indels

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ABI26253 standard; DNA; 12 (first entry) 22-FEB-2002 ABI26253; 1404

BP.

Oligonucleotide primer SEQ ID NO 326226 for detecting SNP TSC0032965.

SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.

Homo

WO200177384-A2

06-APR-2001; 2001WO-IB000713. 18-OCT-2001

07-APR-2000; 2000DE-01019173

(EPIG-) EPIGENOMICS

Berlin K; Olek A, Piepenbrock C,

WPI; 2001-657177/75.

Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single-nucleotide polymorphisms and cytosine methylation status.

Claim 1; SEQ ID NO 326226; 29pp + Sequence Listing; German.

This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA)/oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABF99989 and ABI00010-ABF82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic formmat from WIPO at

Sequence 12 BP; 7 A; 4 C; 0 G; 1 T; 0 U; 0 Other;

0; Gaps Query Match 35.5%; Score 7.8; DB 1; Length 12; Best Local Similarity 81.8%; Pred. No. 6.8e+02; Matches 9; Conservative 0; Mismatches 2; Indels

736 AAACAGAACAC 746

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ABI02575 standard; DNA; 12 BP. ABI02575; RESULT 1405

(first entry) 22-FEB-2002

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Oligonucleotide primer SEQ ID NO 302548 for detecting SNP TSC0020056.

SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.

Homo sapiens

WO200177384-A2.

18-OCT-2001.

06-APR-2001; 2001WO-IB000713.

07-APR-2000; 2000DE-01019173.

(EPIG-) EPIGENOMICS

ĸ Berlin Olek A, Piepenbrock C,

WPI; 2001-657177/75

۲. ک Set of oligonuclectides, useful for diagnosis and cell typing,

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically prefracted genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
designed to detect single-nucleotide polymorphisms and cytosine methylation status.
                                    Claim 1; SEQ ID NO 302548; 29pp + Sequence Listing; German.
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Oligonucleotide primer SEQ ID NO 303624 for detecting SNP TSC0020559.
BP.
ABI03651 standard; DNA; 12
                                                                                                            22-FEB-2002 (first entry)
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SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.

06-APR-2001; 2001WO-IB000713

07-APR-2000; 2000DE-01019173

Set of oligonucleotides, useful for diagnosis and cell typing, addesigned to detect single-nucleotide polymorphisms and cytosine Berlin K; WPI; 2001-657177/75.

Claim 1; SEQ ID NO 303624; 29pp + Sequence Listing; German.

This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF99989, ABF00010-ABF99989 and ABI00010-ABI82073

ö SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic. represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at fitted in the fitter. The wise obtained in the population of the printed properties of the wipe. Oligonucleotide primer SEQ ID NO 329107 for detecting SNP TSC0034763. Gaps . 0 Length 12; 2; Indels Seguence 12 BP; 0 A; 1 C; 5 G; 6 T; 0 U; 0 Other Score 7.8; DB 1; Pred. No. 6.8e+02; 0; Mismatches 2; ABI29134 standard; DNA; 12 BP. Query Match
Best Local Similarity 81.8%;
Matches 9; Conservative (first entry) 735 GAAACAGAACA 745 11 GAAACACACCA 1 22-FEB-2002 Homo sapiens. ABI29134; 1407 AB129134/
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Score 7.8; DB 1; Length 12; Pred. No. 6.8e+02; 0; Mismatches 2; Indels

35.5%; 81.8%;

Berlin 06-APR-2001; 2001WO-IB000713. 07-APR-2000; 2000DE-01019173. Piepenbrock C, (EPIG-) EPIGENOMICS AG WPI; 2001-657177/75. WO200177384-A2. 18-OCT-2001. olek A,

Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single-nucleotide polymorphisms and cytosine methylation status.

Claim 1; SEQ ID NO 329107; 29pp + Sequence Listing; German.

This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligonare are also used for detecting cell type differentiation. ABC0010-ABE09989, ABF00010-ABE99989 and ABI00010-ABE32073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but the wipo.int/pub/published_pct_sequences

Seguence 12 BP; 1 A; 1 C; 3 G; 7 T; 0 U; 0 Other;

Gaps .. Score 7.8; DB 1; Length 12; Pred. No. 6.8e+02; 0; Mismatches 2; Indels ; 35.5%; Query Match
Best Local Similarity 81.8
Matches 9; Conservative

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735 GAAACAGAACA 745

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC9989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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ftp.wipo.int/pub/published_pct_sequences
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Mon Oct 18 14:40:07 2004

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Set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status.
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                                  methylation status.
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Claim 1; SEQ ID NO 287131; 29pp + Sequence Listing; German.

Berlin K;

Piepenbrock C,

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99999, ABF00010-ABF99999, ABH00010-ABH99999 and ABI00010-ABI32073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but two, int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                                                                               This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligomucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABH82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                                                                                               Set of oligonucleotides, useful for diagnosis and cell typing, i
designed to detect single-nucleotide polymorphisms and cytosine
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                                                                                                                                                                                                                                                                                                     Claim 1; SEQ ID NO 336561; 29pp + Sequence Listing; German
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                                                                                              Berlin K;
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                                                                                        Piepenbrock C,
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                                            (EPIG-) EPIGENOMICS AG
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schultz1-727.rng

SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.

Oligonucleotide primer SEQ ID NO 316351 for detecting SNP TSC0027404.

(first entry)

22-FEB-2002

ABI16378;

ABI16378 standard; DNA; 12 BP.

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                                                                                                                                                                                                                                                                                                                                     SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                                                                                                                                        Oligonucleotide primer SEQ ID NO 315101 for detecting SNP TSC0026717.
                                                                Gaps
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                                  Length 12;
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                                                              2; Indels
Sequence 12 BP; 8 A; 4 C; 0 G; 0 T; 0 U; 0 Other;
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                            Score 7.8; DB 1;
Pred. No. 6.8e+02;
0; Mismatches 2;
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                                35.5%;
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             Query Match
Best Local Similarity 81.5-
Best Local 9; Conservative
                                                                                             734 AGAAACAGAAC 744
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Set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status.

Berlin K;

Olek A, Piepenbrock C,

(EPIG-) EPIGENOMICS

WPI; 2001-657177/75.

06-APR-2001; 2001WO-IB000713. 07-APR-2000; 2000DE-01019173.

WO200177384-A2.

18-OCT-2001

Homo sapiens.

Claim 1; SEQ ID NO 316351; 29pp + Sequence Listing; German

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, contral nervous system, cardiovascular and metabolic disonders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC9989, ABF00010-ABF9989, aBH00010-ABH99989 and ABI00010-ABI82073 data for this patent did not form part of the printed specification, but the blub published prefrom MIPO at the printed specification, but fitp.wipo.int/pub/published_pref_sequences
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Matches 9; Conservative
                        oligonucleotides,
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WPI; 2001-657177/75
                                              methylation status.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                               Berlin K;
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                                                                                                                               Piepenbrock C,
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tides, useful for diagnosis and cell typing, single-nucleotide polymorphisms and cytosine
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peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic. SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;

06-APR-2001; 2001WO-IB000713. 07-APR-2000; 2000DE-01019173

WO200177384-A2 Homo sapiens.

18-OCT-2001

(EPIG-) EPIGENOMICS AG.

Oligonucleotide primer SEQ ID NO 377792 for detecting SNP TSC0062498

ABI77819 standard; DNA; 12

22-FEB-2002

ABI77819;

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This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, acadiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF9989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic from WIPO at
central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABE9989, ABR00010-ABE9989, ABR00010-ABE9989, ABR00010-ABE9989, ABR00010-ABE9989, and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at fig. wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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Query Match 35.5%; Score 7.8; DB 1; Length 12; Best Local Similarity 81.8%; Pred. No. 6.8e+02; Matches 9; Conservative 0; Mismatches 2; Indels

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99999, ABF00010-ABF99999, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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                                               SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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              Oligonucleotide primer SEQ ID NO 364679 for detecting SNP TSC0054651.
                                                                                                                                                                                                                                                                                                                                                                                          ligonucleotides, useful for diagnosis and cell typing, :
to detect single-nucleotide polymorphisms and cytosine
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This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, ardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC9989, ABF00010-ABF99989, ABH0010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic formmat from WIPO at
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                                                             This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC9989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABH82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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                       Claim 1; SEQ ID NO 380433; 29pp + Sequence Listing; German.
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                                                                                                                                                        Score 7.8; DB 1; Length 12;
Pred. No. 6.8e+02;
0; Mismatches 2; Indels
                                                                                               Sequence 12 BP; 1 A; 3 C; 0 G; 8 T; 0 U; 0 Other;
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was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                            Query Match
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Matches 9; Conservative
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ABH68427/c
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central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                  This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC9989, ABF0010-ABF9989, ABH0010-ABH99989 and ABI0010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                            SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
                                                                                                        Oligonucleotide primer SEQ ID NO 320366 for detecting SNP TSC0029676.
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                                    ABI20393 standard; DNA; 12 BP.
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, contral nervous system, ardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 data for this patent did not form part of the printed specification, but was obtained in electronic format from MIPO at
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   was obtained in electronic format from WI
ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          designed to detect methylation status.
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This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABH99989 and ABI00010-ABH82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but the wipo.int/pub/published_pct_sequences eet or oligonucleotides, useful for diagnosis and cell typing, is designed to detect single-nucleotide polymorphisms and cytosine methylation status. Claim 1; SEQ ID NO 275474; 29pp + Sequence Listing; German. Sequence 12 BP; 9 A; 3 C; 0 G; 0 T; 0 U; 0 Other; Piepenbrock WPI; 2001-657177/75 Á olek

Berlin

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Query Match 35.5%; Score 7.8; DB 1; Length 12; Best Local Similarity 81.8%; Pred. No. 6.8e+02; Matches 9; Conservative 0; Mismatches 2; Indels 734 AGAAACAGAAC 744

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ABI28569 standard; DNA; 12 BP (first entry) 22-FEB-2002 ABI28569; RESULT 1428

SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic. Oligonucleotide primer SEQ ID NO 328542 for detecting SNP TSC0034382.

Homo sapiens.

WO200177384-A2.

18-OCT-2001.

06-APR-2001; 2001WO-IB000713

07-APR-2000; 2000DE-01019173

(EPIG-) EPIGENOMICS AG.

X, Berlin Olek A, Piepenbrock C,

WPI; 2001-657177/75.

typing, i cytosine Set of oligonuclectides, useful for diagnosis and cell designed to detect single-nuclectide polymorphisms and methylation status.

Claim 1; SEQ ID NO 328542; 29pp + Sequence Listing; German.

This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)

and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF9989, ABF00010-ABF9989, ABF00010-ABF9989 and ABI00010-ABF9973 represent the oligomers described in the invention. NOTE: The sequence was obtained in electronic format from WIPO at the printed specification, but the wipo.int/pub/published_pct_sequences 8×333333333333333

Seguence 12 BP; 9 A; 0 C; 2 G; 1 T; 0 U; 0 Other;

Gaps . 0 Length 12; Query Match 35.5%; Score 7.8; DB 1; Length 12
Best Local Similarity 81.8%; Pred. No. 6.8e+02;
Matches 9; Conservative 0; Mismatches 2; Indels

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735 GAAACAGAACA 745 GAAAAAGAAAA 12 N

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ABH79548 standard; DNA; 12 BP.

ABH79548;

22-FEB-2002 (first entry)

Gaps

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Oligonucleotide primer SEQ ID NO 279541 for detecting SNP TSC0007466.

SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.

Homo sapiens

WO200177384-A2.

18-OCT-2001.

36-APR-2001; 2001WO-IB000713.

07-APR-2000; 2000DE-01019173.

(EPIG-) EPIGENOMICS AG.

Berlin K; Olek A, Piepenbrock C,

WPI; 2001-657177/75.

Set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status.

Claim 1; SEQ ID NO 279541; 29pp + Sequence Listing; German.

This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00110-ABC9989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABF82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic formmat from WIPO at ABH779548/A
XX ABH77

12 BP; 0 A; 0 C; 2 G; 10 T; 0 U; 0 Other;

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SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                          Oligonucleotide primer SEQ ID NO 280455 for detecting SNP TSC0008655.
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 ABH80462;
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                                                                                                                                                                                                                                                                                 SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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Score 7.8; DB 1; Length 12;
Pred. No. 6.8e+02;
0; Mismatches 2; Indels
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 35.5%;
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                                                                                                                                                                ABH80335 standard; DNA; 12
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 Query Match
Best Local Similarity 81.6
Matches 9; Conservative
                                                          736 AAACAGAACAC 746
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                                                                                      1-1 AAACAAAAAC 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                designed to detect methylation status.
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Matches 9; Conserv
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                                                                                                                                                                                              ABH80335;
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ABH80335/c
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Berlin K;

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Oligonucleotide primer SEQ ID NO 305623 for detecting SNP TSC0021534.
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ABI05650 standard; DNA; 12
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es 9; Conservative
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WO200177384-A2.

RESULT 1431 ABH80462/c ID ABH80462 standard; DNA; 12 BP. XX

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AACCATAACAC 1

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, contral nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99999, ABF00010-ABF99999, ABH00010-ABF99999 and ABI00010-ABF82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ö SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic. Oligonucleotide primer SEQ ID NO 306155 for detecting SNP TSC0021828. 0; Gaps Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single-nucleotide polymorphisms and cytosine methylation status. Claim 1; SEQ ID NO 305623; 29pp + Sequence Listing; German. Query Match 35.5%; Score 7.8; DB 1; Length 12; Best Local Similarity 81.8%; Pred. No. 6.8e+02; Matches 9; Conservative 0; Mismatches 2; Indels Sequence 12 BP; 1 A; 3 C; 0 G; 8 T; 0 U; 0 Other; ĸ Berlin K; Berlin BP. 06-APR-2001; 2001WO-IB000713. 06-APR-2001; 2001WO-IB000713 07-APR-2000; 2000DE-01019173 07-APR-2000; 2000DE-01019173 182/c ABI06182 standard; DNA; 12 22-FEB-2002 (first entry) 733 GAGAACAGAA 743 Olek A, Piepenbrock C, Olek A, Piepenbrock C, 12 GAGAAATAAAA 2 (EPIG-) EPIGENOMICS AG (EPIG-) EPIGENOMICS WPI; 2001-657177/75. WPI; 2001-657177/75 WO200177384-A2 18-OCT-2001 18-OCT-2001 ABI06182; RESULT 1433 Homo à d

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99999, ABF00010-ABF99999, ABH00010-ABH99999 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from wIPO at
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Set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status.
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                                                                                                                                                   Claim 1; SEQ ID NO 306155; 29pp + Sequence Listing; German.
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ABI32093 standard; DNA; 12 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11 AAACATAATAC 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Oligonucleotide primer SEQ ID NO 284544 for detecting SNP TSC0011875.
                                                                                                                                                                                                     0; Gaps
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                                                                                                                                                           Query Match 35.5%; Score 7.8; DB 1; Length 12; Best Local Similarity 91.8%; Pred. No. 6.8e+02; Matches 9; Conservative 0; Mismatches 2; Indels
                                                                                                                        Sequence 12 BP; 1 A; 6 C; 0 G; 5 T; 0 U; 0 Other;
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                                                                                                                                                                     SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                     Oligonucleotide primer SEQ ID NO 313448 for detecting SNP TSC0025771.
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designed to detect single-nucleotide polymorphisms and cytosine
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                                   ABI13475 standard; DNA; 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  methylation status.
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RESULT 1436
ABI13475
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Matches
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Oligonucleotide primer SEQ ID NO 290443 for detecting SNP TSC0014352.

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Gaps

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35.5%; Score 7.8; DB 1; Length 12; 81.8%; Pred. No. 6.8e+02; trive 0; Mismatches 2; Indels

Local Similarity 81.8

Matches

Query Match

735 GAAACAGAACA 745

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MOII OCC 10 T4:40.07 700M
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, ardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF9989, ABH00010-ABH99989 and ABI00010-ABH82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic. Set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status. Claim 1; SEQ ID NO 290443; 29pp + Sequence Listing; German. Sequence 12 BP; 5 A; 5 C; 0 G; 2 T; 0 U; 0 Other; ftp.wipo.int/pub/published_pct_sequences Berlin K; 06-APR-2001; 2001WO-IB000713. 07-APR-2000; 2000DE-01019173 Olek A, Piepenbrock C, (EPIG-) EPIGENOMICS AG WPI; 2001-657177/75 WO200177384-A2 Homo sapiens

Gaps · 0 35.5%; Score 7.8; DB 1; Length 12; 81.8%; Pred. No. 6.8e+02; ive 0; Mismatches 2; Indels Query Match
Best Local Similarity 81.0-

737 AACAGAACACC 747 2 AACACAACTCC 12 ò g

ABI15662 standard; DNA; 12 ABI15662; RESULT 1438

ВP

(first entry) 22-FEB-2002 Oligonucleotide primer SEQ ID NO 315635 for detecting SNP TSC0027012.

SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.

Homo sapiens

WO200177384-A2

18-OCT-2001.

06-APR-2001; 2001WO-IB000713

07-APR-2000; 2000DE-01019173

scnuttzi-///rrg

AG. (EPIG-) EPIGENOMICS Berlin K; Piepenbrock C, olek A,

WPI; 2001-657177/75

Set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status.

Claim 1; SEQ ID NO 315635; 29pp + Sequence Listing; German.

This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretraeted genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99889, ABF00010-ABF99899, ABH00010-ABH99899 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but the was obtained in electronic format from WIPO at

Sequence 12 BP; 6 A; 3 C; 0 G; 3 T; 0 U; 0 Other;

0; Gaps Length 12; 35.5%; Score 7.8; DB 1; Length 12 81.8%; Pred. No. 6.8e+02; ive 0; Mismatches 2; Indels Query Match Best Local Similarity 81.8 Matches 9; Conservative

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736 AAACAGAACAC 746 AAACTTAACAC 12 ઠે g

RESULT 1439

ABI49818 standard; DNA; 12 BP.

ABI49818;

22-FEB-2002 (first entry)

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Oligonucleotide primer SEQ ID NO 349791 for detecting SNP TSC0046328.

SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.

Homo sapiens

WO200177384-A2.

18-OCT-2001

06-APR-2001; 2001WO-IB000713.

07-APR-2000; 2000DE-01019173.

(EPIG-) EPIGENOMICS AG.

Berlin Olek A, Piepenbrock C,

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WPI; 2001-657177/75.

Set of oligonuclectides, useful for diagnosis and cell typing, is designed to detect single-nuclectide polymorphisms and cytosine methylation status.

Claim 1; SEQ ID NO 349791; 29pp + Sequence Listing; German.

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Gaps

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Score 7.8; DB 1; Length 12; Pred. No. 6.8e+02; 0; Mismatches 2; Indels

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(EPIG-) EPIGENOMICS AG
                                                                                                                                      WPI; 2001-657177/75.
                                        Query Match
Best Local Similarity
                                                                                                                                                 methylation status
                                                                                                        WO200177384-A2
                                                                                                   Homo sapiens
                                                                              22-FEB-2002
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Sequence 12 BP; 1 A; 0 C; 3 G; 8 T; 0 U; 0 Other;
                                              Ouery Match
Best Local Similarity 81.8%;
Matches 9; Conservative (
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                                                                                                                                                                                                                                                              RESULT 1441
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99899, ABF00010-ABF99899, ABH00010-ABH99989 and ABI00010-ABH82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but the was obtained in electronic format from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nuclectide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABC0010-ABE9989, ABM0010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form par of the printed specification, but typ.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Oligonucleotide primer SEQ ID NO 352030 for detecting SNP TSC0047642.
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designed to detect single-nucleotide polymorphisms and cytosine
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Pred. No. 6.8e+02;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                             Sequence 12 BP; 6 A; 0 C; 5 G; 1 T; 0 U; 0 Other;
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81.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                           9; Conservative
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                                                                                                                                                                                                                                                                                                            SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                                                                Oligonucleotide primer SEQ ID NO 352679 for detecting SNP TSC0048031.
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ABI52706 standard; DNA; 12 BP.
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Matches 9; Conserv
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RESULT 1442

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99999, ABF00010-ABH99999 and ABI00010-ABH82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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                                                                                                                                                                                                                                                                                                                              SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                                                                                                                                                           Oligonucleotide primer SEQ ID NO 353148 for detecting SNP TSC0048333.
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                                           ABI53175 standard; DNA; 12 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens.
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                                                                                                                  ABI53175;
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ABI53175/C
XX
AC ABI53175/C
XX
AC ABI5317
XX
COLIGOD
CC COLIGOD
CC
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XX
AC ABI7
XX ABI7
XX ABI7
XX Olig
XX Olig
XX SNP;
XW SNP;
XW SNP;
XW Cent
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The cligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, ardiovascular and metabolic disorders. The coingomers are also used for detecting cell type differentiation. ABC00010-ABC99889, ABF00010-ABF99899, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at fitte wipo.int/pub/published_pct_sequences

Sequence 12 BP; 1 A; 0 C; 3 G; 8 T; 0 U; 0 Other;

Set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status.

Berlin K;

Olek A, Piepenbrock C,

(EPIG-) EPIGENOMICS

WPI; 2001-657177/75.

06-APR-2001; 2001WO-IB000713.

WO200177384-A2

18-OCT-2001

Homo sapiens

07-APR-2000; 2000DE-01019173

Claim 1; SEQ ID NO 376788; 29pp + Sequence Listing; German.

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                                                                                                                                                                                                                           SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                Gaps
                                                                                                                                                                                                        Oligonucleotide primer SEQ ID NO 378343 for detecting SNP TSC0062733.
                                  ..
        35.5%; Score 7.8; DB 1; Length 12; 81.8%; Pred. No. 6.8e+02; rive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                  Berlin K;
                                                                                                                                      ABI78370 standard; DNA; 12 BP.
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                                                                                                                                                                                   22-FEB-2002 (first entry)
Query Match
Best Local Similarity 81.6
                                                      736 AAACAGAACAC 746
                                                                                                                                                                                                                                                                                                                                                                                                                 Olek A, Piepenbrock C,
                                                                                                                                                                                                                                                                                                                                                                                            (EPIG-) EPIGENOMICS AG.
                                                                          11 AAACAAAATAC
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WPI; 2001-657177/75

range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF99989, ABF00010-ABF99989, ABF00010-ABF99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic forms from WIPO at

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Gaps

; 0

2; Indels

35.5%; Score 7.8; DB 1; Length 12; 81.8%; Pred. No. 6.8e+02;

0; Mismatches

9; Conservative 736 AAACAGAACAC 746

Matches

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Local Similarity

Query Match

Sequence 12 BP; 0 A; 1 C; 6 G; 5 T; 0 U; 0 Other;

ftp.wipo.int/pub/published_pct_sequences

8888888888888

German.

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABH82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Oligonucleotide primer SEQ ID NO 378374 for detecting SNP TSC0007374.
                                                Set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status.
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                                                                                                                                                                                                                                                                                                                                                                                                          35.5%; Score 7.8; DB 1; Length 12; 81.8%; Pred. No. 6.8e+02; Live 0; Mismatches 2; Indels
                                                                                                                     Claim 1; SEQ ID NO 378343; 29pp + Sequence Listing;
                                                                                                                                                                                                                                                                                                                                                                            Sequence 12 BP; 1 A; 0 C; 4 G; 7 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                              9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligomucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic discorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABE99989, ABF00010-ABE99989, ABH00010-ABE99989 and ABI00010-ABI32073 represent the oligomers described in the invention. NOTE: The sequence was obtained in electronic formm part of the printed specification, but the wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Oligonucleotide primer SEQ ID NO 366118 for detecting SNP TSC0055549
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Query Match 35.5%; Score 7.8; DB 1; Length 12; Best Local Similarity 81 8%; Pred No. 6.8e+02; Sequence 12 BP; 1 A; 0 C; 6 G; 5 T; 0 U; 0 Other;

This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, ardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABF82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                      SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                           Oligonucleotide primer SEQ ID NO 317667 for detecting SNP TSC0028158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Set of oligonucleotides, useful for diagnosis and cell typing, idesigned to detect single-nucleotide polymorphisms and cytosine methylation status.
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                                                                                                                                                                                                                                                                                                                                                                                                  SNP, single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                                                                                                                                                                                          Oligonucleotide primer SEQ ID NO 382008 for detecting SNP TSC0009339.
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RESULT 1448

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Indels

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Mismatches

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Matches

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Gaps

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                                                                                                                                                                                  This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99999, ABF00010-ABF99999, ABH00010-ABH99999 and ABI00010-ABH82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                                                                Claim 1; SEQ ID NO 292984; 29pp + Sequence Listing; German.
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Pred. No. 6.8e+02;
0; Mismatches 2; Indels
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81.8%;
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This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nuclectide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but the was obtained in electronic format from WIPO at
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Claim 1; SEQ ID NO 294498; 29pp + Sequence Listing; German.
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Pred. No. 6.8e+02;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 12 BP; 1 A; 0 C; 4 G; 7 T; 0 U; 0 Other;
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81.8%;
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RESULT 1453
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                                                                                                                                                                                                                                                                                                                                SNP, single nucleotide polymorphism, human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pot_sequences
                                                                                                                                                                                                                                                                                                      Oligonuclectide primer SEQ ID NO 271728 for detecting SNP TSC0002600.
                                                                                                         0; Gaps
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                                                                             Query Match 35.5%; Score 7.8; DB 1; Length 12; Best Local Similarity 81.8%; Pred. No. 6.8e+02; Matches 9; Conservative 0; Mismatches 2; Indels
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                                                    Sequence 12 BP; 1 A; 6 C; 0 G; 5 T; 0 U; 0 Other;
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Best Local Similarity 81.8
Matches 9; Conservative
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Set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status.

Berlin K;

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(EPIG-) EPIGENOMICS

Olek A, Piepenbrock C,

WPI; 2001-657177/75.

06-APR-2001; 2001WO-IB000713. 07-APR-2000; 2000DE-01019173.

WO200177384-A2. Homo sapiens.

18-OCT-2001.

Claim 1; SEQ ID NO 272307; 29pp + Sequence Listing; German.

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                                                       Gaps
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                        35.5%; Score 7.8; DB 1; Length 12; 81.8%; Pred. No. 6.8e+02; ive 0; Mismatches 2; Indels
Sequence 12 BP; 8 A; 3 C; 0 G; 1 T; 0 U; 0 Other;
                                                                                                                                                                              ВР.
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                       Query Match
Best Local Similarity 81.8
Matches 9; Conservative
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736 AAACAGAACAC 746

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2 AAACAAATCAC 12

This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically prereated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC9989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but the was obtained in electronic format from WIPO at the printed specification, but the wipo int/pub/published_pot_sequences

SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.

Oligonucleotide primer SEQ ID NO 272307 for detecting SNP TSC0002774.

(first entry)

22-FEB-2002

ABH72328;

BP.

ABH72328 standard; DNA; 12

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, contral nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF9989, ABH0010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from MIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This invention describes novel oligonuclectide primers or peptide nucleic
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                                                                                                     Set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status.
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                                                                                                                                                                                                                                                                                                                                                                                                                                      was obtained in electronic format from WI
ftp.wipo.int/pub/published_pct_sequences
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                                     Piepenbrock C,
(EPIG-) EPIGENOMICS AG
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Best Local Similarity
Matches 9; Conserv
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                                     olek A,
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ABH76081/c
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  peptide nucleic acid, cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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Pred. No. 6.8e+02;
0; Mismatches 2; Indels
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81.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                     designed to detect methylation status.
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acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory. Central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99889, ABC0010-ABE9989, ABR0010-ABE9989, ABR0010-ABE9989 and ABI0010-ABI82073 tepresent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Oligonucleotide primer SEQ ID NO 326688 for detecting SNP TSC0033234.
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Best Local Similarity 81.0
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                                                                                                                                                                                                                                                                                                                              SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                                                                                                                                  Oligonucleotide primer SEQ ID NO 302632 for detecting SNP TSC0020091.
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 Length 12;
Score 7.8; DB 1; Length 12
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0; Mismatches 2; Indels
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81.8%;
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ID ABI03308 standard, DNA, 12
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 Query Match
Best Local Similarity 81.8
Matches 9; Conservative
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, aradiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC9989, ABF00010-ABF9989, ABH00010-ABH99989 and ABI00010-ABI82073 tepresent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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                                                                                                                            SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                            Oligonucleotide primer SEQ ID NO 303281 for detecting SNP TSC0020420.
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ABI28965 standard; DNA; 12
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Berlin K;

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(first entry)

Homo sapiens

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC9989, ABR0010-ABH89989 and ABI0010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from MIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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Matches 9; Conservative
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                                                                                                                              This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC9989, ABF00010-ABF9989, ABF00010-ABF9989, and ABI0010-ABF8273 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from NIPO at
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                                                                                               Claim 1; SEQ ID NO 279799; 29pp + Sequence Listing; German.
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oligomers are also used for detecting cell type differentiation. ABC00010-ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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designed to detect single-nucleotide polymorphisms and cytosine
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81.8%; Pred. No. 6.8e+02;
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC9989, ABF00010-ABE9989, ABH00010-ABE9989 and ABI00010-ABI82073 tapeseen the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from NIPO at
                                                                                                                                                                                                                                                 SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                                                     Oligonucleotide primer SEQ ID NO 306225 for detecting SNP TSC0021880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Set of oligonucleotides, useful for diagnosis and cell typing, idesigned to detect single-nucleotide polymorphisms and cytosine methylation status.
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                                                                                                                  ABI06252 standard; DNA; 12 BP
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736 AAACAGAACAC 746
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                                AAACTAAACAC 11
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, azdiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99999, ABF00010-ABF99999, ABH00010-ABH99999 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but they wipo int/pub/published_pct_sequences
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                                SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
Oligonucleotide primer SEQ ID NO 309521 for detecting SNP TSC0023558.
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Claim 1; SEQ ID NO 288670; 29pp + Sequence Listing; German.
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                                                                                                                                                                 This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC9989, ABF00010-ABF9989, ABH00010-ABH99989 and ABI00010-ABH82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SNP, single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                       set or oligonucleotides, useful for diagnosis and cell typing, is designed to detect single-nucleotide polymorphisms and cytosine methylation status.
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This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genemic DNA. The cligonuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, contral nervous system, cardiovascular and metabolic disorders. The coingomers are also used for detecting cell type differentiation. ABC00010-ABE99989, ABF00010-ABE99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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Matches 9; Conservative
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                                                                                                                                                                                                                                                                                     SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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designed to detect single-nucleotide polymorphisms and cytosine
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                                               Score 7.8; DB 1; Length 12;
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35.5%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 6.8e+02;
Matches 9; Conservative 0; Mismatches 2; Indels
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                         Sequence 12 BP; 8 A; 4 C; 0 G; 0 T; 0 U; 0 Other;
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methylation status.
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, contral nervous system, cardiovascular and metabolic disorders. The ABC99989, ABF0010-ABF9989, ABH0010-ABH99999 and ABI0010-ABF3973 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from MIPO at
                                                                                                                                                                                                                     SNP, single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                                                                          Oligonucleotide primer SEQ ID NO 346435 for detecting SNP TSC0044583.
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81.8%; Pred. No. 6.8e+02;
ative 0; Mismatches 2;
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ABI46462 standard; DNA; 12 BP.
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Olek A, Piepenbrock C,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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Set of oligonucleotides, useful for diagnosis and cell typing, idesigned to detect single-nucleotide polymorphisms and cytosine methylation status.
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Best Local Similarity 81.8%; Pred. No. 6.8e+02;
Matches 9; Conservative 0; Mismatches 2; Indels
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35.5%; Score 7.8; DB 1; Length 12;
Query Match
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Sequence 12 BP; 1 A; 2 C; 0 G; 9 T; 0 U; 0 Other;

AAF92714;

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range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers ealso used for detecting cell type differentiation. ABC00010-ABC99889, ABC00100-ABF99889 and ABI00010-ABF82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form par of the printed specification, but was obtained in electronic format from WIPO at fire wipo.int/pub/published_pct_sequences
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       oligonucleotides are used for diagnosis and/or prognosis of cancer and a
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ABI68631/C
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073 targement the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from MIPO at
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                                                                       ABI57978 standard; DNA; 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (EPIG-) EPIGENOMICS AG
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Best Local Similarity
Matches 9; Conserv
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                                                                                                                                              ABI57978;
RESULT 1475
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The invention relates to a method for the expression of tumour associated antigens (TAA) or virus-associated antigens (VAA) by dendritic cells comprising; preparing a recombinant influenza virus containing a nucleotide sequence comparing a recombinant influenza virus containing a nucleotide sequence conding for the TAA or VAA; and infecting dendritic cells with the recombinant virus. The method is used for expressing TAA or VAA in dendritic cells. The cells are used for preparing a medicament for treating tumours or viral infections. A vaccine can be created by using dendritic cells presenting tumour antigens to induce an immune response. This polymucleotide sequence represents a 3' conserved RNA region of the wild-type influenza C virus of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to a method for the expression of tumour associated antigens (TAA) or virus-associated antigens (VAA) by dendritic cells comprising: preparing a recombinant influenza virus containing a nucleotide sequence coding for the TAA or VAA; and infecting dendritic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cytostatic, antiviral; tumour associated antigen; TAA; dendritic cell; virus-associated antigen; VAA; recombinant influenza virus; vaccine; viral infection; immune; Influenza A virus; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                            Expressing tumor or viral associated antigens by dendritic cells, use for treating tumors or viral infections, comprises using recombinant influenza virus containing nucleic acid encoding the antigens.
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                   Grassmann
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                 Strobel I,
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                   Steinkasserer A,
                                                                                                                                                                                 Disclosure; Page 5; 33pp; English
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ses 9; Conservative
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                   Hopom G,
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                   Schuler G,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention relates to human leukocyte antigen (HLA) typing. The method involves detecting polymorphic residues by sequence specific oligonucleotide probe hybridization (SSOPH) with labeled oligonucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cytostatic; antiviral; tumour associated antigen; TAA; dendritic cell; virus-associated antigen; VAA; recombinant influenza virus; vaccine; viral infection; immune; wild-type; influenza C virus; ss.
                                                                                                 Human; leukocyte antigen; HLA; typing; sequence specific probe; SSOPH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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Pred. No. 6.8e+02;
0; Mismatches 2; Indels
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                                                          Mutilple allele detection probe #4.
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Best Local Similarity 81.8%;
Matches 9; Conservative
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AAL37779 standard; RNA; 12
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                   (first entry)
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CTGGAGAGACA 11
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                                                                                                                                                               Homo sapiens
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                   16-MAY-2001
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Three classes of cell-based luminescent reporter molecules such as detectors, classifiers and identifiers are described and serve as reporters of toxic threat agents. The first two levels of characterisation ensure a rapid readout of toxin class without sacrificing the ability to detect many new mutant toxins or dissect several complex mixtures of known toxins. This sequence encodes a protease bissensor recognition site used in the cell-based screening

system

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cells with the recombinant virus. The method is used for expressing TAA or VAA in dendritic cells. The cells are used for preparing a medicament for treating tumours or viral infections. A vaccine can be created by using dendritic cells presenting tumour antigens to induce an immune response. This polymuchotide sequence represents a modified 3' RNA region of the Influenza A virus of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Detection; classification; identification; toxin detection; protease; ADP-ribosylating toxin; cytotoxic phospholipase; exfoliative toxin;
                                                                                                                                                                                                                                                                                                                                    Gaps
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99US-0122152P.
99US-0123399P.
99US-00352171.
99US-0151797P.
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P-PSDB; ABG94454.
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The invention describes methods of automated detection, classification and identification comprising treating cells containing luminescent reporter molecules (I) in array of locations with a test substance, where (I) are detectors, classifiers or identifiers, imaging cells in each location to obtain luminescent signals and converting optical information into digital data to interpret presence of toxins in the test substance. The method are useful for detection of toxins chosen from proteases, ADP-ribosylating toxins, cytotoxic phospholipases, and exfoliative toxins.

Example 10; Fig 29B; 214pp; English.

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The present invention describes a human influenza virus (I) comprising an RA-sequence encoding a modified RNA-polymerase that differs from the wild-type RNA-polymerase of the human influenza virus in that at least 1 of the amino acid residues distinguishing the wild-type RNA-polymerase of the human influenza virus from FPV Bratislava RNA-polymerase of corresponding amino acid residue(8) as present in FPV Bratislava RNA-polymerase of Bratislava RNA-polymerase of C Bratislava RNA-polymerase. (I) has virucide, cytostatic, anti-H1V hepatotropic, anti-H1V hamacory and immunomodulator activities and can be used in gene therapy and vaccines. The influenza virus is useful for preparing agents for: (a) gene transfer into cells, preferably into mammalian cells, particularly into human cells, by viral infection; (b) gene transfer into antigen-presenting cells, and the use of the obtained concluding therapeutic and prophylactic vaccination; in vivo vaccination, including therapeutic and prophylactic vaccination; (c) eliciting an immune response, including the induction of a T-cell
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New human influenza virus comprising an RNA-sequence encoding a modified RNA-polymerase, useful for preparing agents for therapeutic and prophylactic vaccination, or treating a growing tumor or a chronic infectious disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Influenza virus; transcription; replication; RNA polymerase; vaccine; gene therapy; cytostatic; anti-HIV; hepatotropic; antiinflammatory; immunomodulator; virucide; infectious disease; ss.
                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Modified influenza virus A 3' conserved region SEQ ID NO:4.
                                                                                                                                                                                                                  Score 7.8; DB 1; Length 12;
Pred. No. 6.8e+02;
                                                                                                                                                                                                                                                    2; Indels
                                                                                                                                                                                Sequence 12 BP; 6 A; 1 C; 3 G; 2 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                      0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                   ABQ75462 standard; RNA; 12 BP.
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81.8%;
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                                                                                                                                                                                                                     Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Influenza virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200264757-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       07-NOV-2002
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                                                                                                                                                                                                                                                        Matches
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schultz1-727.rng

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response; (d) treating a growing tumour or a chronic infectious disease; (e) immunotherapy, preferably for autologous immunotherapy; (f) transfer and expression of foreign genes into cells infected by such viruses; or viruses; preferably the RNA molecules into cells infected by such viruses; or double-strand sequences relative to the target cellular mRNA molecules, and/or the agent is suitable for sequence-specific gene silencing, preferably by antisense RNA or RNA interference mechanisms such as ribozyme cleavages of target RNAs. The recombinant viruses can be made for use in vaccines against HIV, hepatitis B or C virus, herpes viruses or papilloma viruses. The present sequence represents a modified a conserved region of an influenza virus, given in the exemplification
                                                                                                                                                                                                                                                                                                                                                         the present invention
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Sequence 12 BP; 1 A; 3 C; 1 G; 0 T; 7 U; 0 Other;

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  Length 12;
                        2; Indels
Score 7.8; DB 1;
Pred. No. 6.8e+02;
0; Mismatches 2
 Query Match
Best Local Similarity 81.8%;
Matches 9; Conservative
                                                731 AGGAGAAACAG 741
                                                                      N
                                                                      12 AGTAAAAACAG
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461/c ABQ75461 standard; RNA; 12 BP. (first entry) 07-NOV-2002 ABQ75461; RESULT 1481 ABQ75461

Influenza virus C 3' conserved region SEQ ID NO:3. gene therapy;

Influenza virus, transcription, replication, RNA polymerase, vaccine, gene therapy, cytostatic, anti-HIV, hepatotropic, antiinflammatory, immunomodulator; virucide; infectious disease; ss.

Influenza virus.

WO200264757-A2.

22-AUG-2002.

07-FEB-2002; 2002WO-EP001257

09-FEB-2001; 2001EP-00103060.

(ARTE-) ARTEMIS PHARM GMBH.

Menke A; Hobom G,

WPI; 2002-657594/70.

New human influenza virus comprising an RNA-sequence encoding a modified RNA-polymerase, useful for preparing agents for therapeutic and prophylactic vaccination, or treating a growing tumor or a chronic infectious disease.

Disclosure; Page 15; 172pp; English.

The present invention describes a human influenza virus (I) comprising an RNA-sequence encoding a modified RNA-polymerase that differs from the wild-type RNA-polymerase of the human influenza virus in that at least 1 of the amino acid readduse distinguishing the wild-type RNA-polymerase the human influenza virus from FPV Bratislava RNA-polymerase of the human influenza virus from FPV Bratislava RNA-polymerase of Bratislava RNA-polymerase of beatslalava RNA-polymerase. (I) has virucide, cytostatic, anti-HIV, hepatotropic, antiinflammatory and immunomodulator activities and can be used in gene therapy and vaccines. The influenza virus is useful for preparing agents for: (a) gene transfer into cells, preferably into mammalian cells, particularly into human cells, by viral infection; (b)

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gene transfer into antigen-presenting cells, and the use of the obtained propaduct for ex vivo immunotherapy; in vivo somatic gene therapy; in vivo vaccination, including therapeutic and prophylactic vaccination; (c) eliciting an immune response, including the induction of a T-cell response; (d) treating a growing tumour or a chronic infectious disease; (e) immunotherapy; preferably to autologous immunotherapy; (f) transfer and expression of RNA molecules into cells infected by such viruses; or (g) transfer and expression of RNA molecules into cells infected by such viruses, preferably the RNA molecules to be expressed are antisense squences or double-strand sequences relative to the target cellular mRNA molecules; and/or the agent is suitable for sequence specific gene silencing, preferably by antisense RNA or RNA interference mechanisms such as ribozyme cleavages of target RNAs. The recombinant viruses can be made for use in vaccines against HIV, hepatitis B or C virus, herpes viruses or papilloma viruses. The present sequence represents a 3' conserved region of a wild type influenza virus, given in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              exemplification of the present invention
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Sequence 12 BP; 0 A; 5 C; 2 G; 0 T; 5 U; 0 Other;

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Gaps

Gaps 0 Query Match 35.5%; Score 7.8; DB 1; Length 12; Best Local Similarity 81.8%; Pred. No. 6.8e+02; Matches 9; Conservative 0; Mismatches 2; Indels

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731 AGGAGAAACAG 741 AGCAGAAGCAG 12

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ABK99290 standard; RNA; 12 BP. 21-OCT-2002 ABK99290; ABK99290

ID ABK9

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Hepatitis C virus (HCV) NS5B replicase RNA synthesis template #20.

Hepatitis C virus; HCV; NS5B replicase; ss; RNA polymerase

Synthetic.

US2002064771-A1.

30-MAY-2002

06-APR-2001; 2001US-00828034.

07-APR-2000; 2000US-0195852P.

(HONG/) HONG Z. (FERR/) FERRARI E. ZHONG W. (ZHON/)

Ferrari E; Zhong W, Hong Z,

WPI; 2002-582330/62.

Novel replicase complex comprising hepatitis C virus NS5B replicase, a 3 nucleotide-long template to which a 2 nucleotide-long primer is annealed, and template and primer which do not form a stable duplex in the absence HCV NS5B

Example; Page 6; 17pp; English.

The invention relates to a replicase complex comprising a hepatitis C virus (HCV) NSBs replicase protein, a linear nucleic acid template and a complementary nucleic acid primer which is annealed to the 3' terminus of the template, where the template is at least three nucleotides and the primer is two or three nucleotides, and the template and primer do not form a stable duplex in solution in the absence of the HCV NSSB protein. The complex is useful for detecting HCV replicase activity and permits

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                      and evaluate antiviral inhibitors and to improve the specificity and efficacy of the inhibitors. The complex is also useful in the development of a reliable system for determining kinetic and thermodynamic constants of HCV NSSB-catalysed nucleotide incorporation and investigation of mechanistic inhibitors for mis-incorporation or chain termination. Specifically, the short RNA template and primer pairs are useful in screening assays which are used for determining kinetic, thermodynamic and mechanistic properties of NSSB replication and ultimately in the development of inhibitors of NSSB. Newly identified inhibitors of replicase activity may be used for development and ultimately in the replicase activity may be used for development and inhibitors of sevelopment of inhibitors of NSSB. Newly identified inhibitors of seveloping anti-HCV pharmaceuticals. Sequences ABK99271-ABK99296 represent HCV NSSB replicase RNA synthesis
sensitive RNA-dependent RNA polymerase assays to screen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Recombinant influenza virus for transfer and expression of foreign genes and RNA molecules into cells and for preventing, treating influenza, has biscistronic viral RNAs coding for two genes in tandem arrangement.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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Pred. No. 6.8e+02;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 12 BP; 8 A; 2 C; 1 G; 0 T; 1 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Page 6; 39pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    35.5%;
81.8%;
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Best Local Similarity
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antisense or double-stranded sequences relative to the target cell cellular mRNA molecules, and/or the agent is suitable for sequence-specific gene silencing, preferably by antisense RNA or RNA interference mechanisms. (I) gives high-yield expression for foreign genes. This sequence represents the 3' conserved region of influenza C virus, described in the method of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New recombinant vector containing sequence for small nuclear RNA, useful e.g. for identifying variant snRNA that suppresses expression of transcription products.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to a recombinant vector which comprises DNA, consisting of an insertion cassette contained between at least two insertion sites, that encodes a small nuclear (sn) RNA. The invention is used to identify snRNA modifications that inhibit expression of transcription products (and the identified snRNA are used to suppress expression) for delivering antisense sequences to the nucleus and to create transgenic animals. The present sequence is Luc (luciferase) 1547/10+2 construct DNA. (Updated on 07-AUG-2003 to correct OS field.)
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                                                                                                                                              35.5%; Score 7.8; DB 1; Length 12; 81.8%; Pred. No. 6.8e+02; Arive 0; Mismatches 2; Indels
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Pred. No. 6.8e+02;
0; Mismatches 2; Indels
                                                                                                                  Sequence 12 BP; 0 A; 5 C; 2 G; 0 T; 5 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                   AAD39657 standard; DNA; 12 BP.
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81.8%;
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(first entry)
                                                                                                                                    Query Match
Best Local Similarity 81.0.
Best Local 9, Conservative
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                                                                                                                                                                                                                                                 12 AGCAGAAGCAG 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  transgenic animal;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unidentified.
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22-OCT-2002
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The invention describes a recombinant influenza virus (I), stable in the absence of any helper virus, that has a viral RNA segment being a biscistronic RNA molecule coding for two genes in tandem arrangement (tandem RNA segment, TRS). (I) is useful for expression of incorporated foreign gene(s) and RNA molecules in cells. (I), preferably a recombinant influenza A virus is useful for: preventing and/or treating influenza, and for preparing a medicament for vaccination purposes; somatic gene therapy, and as immunoden for inducing antibodies; as an expression vector for producing proteins or glycoproteins; preparing agents for somatic gene therapy; immunotherapy, preferably autologous immunotherapy; transfer and expression of foreign genes and RNA molecules into cells infected by such viruses, where the RNA molecules to be expressed include

08-MAY-2003 (first entry)

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Expression which comprises binding complexes, formed between a single-
expression which comprises binding complexes, formed between a single-
extranded gene product and an individual primer, or many different
primers, to a surface in a random arrangement. Cyclic extension of the
complementary strand of the gene product is then performed using one or
more polymerases by treating the bound complexes with a solution
containing a polymerase and 1-4 modified on that if one NTx; labeled with
fluorescent dyes. NTx are base-modified so that if one NTx; is
containing a polymerase then a second can not be incorporated into the
same strand. The method is used for quantitative analysis of the
expression of many genes, e.g. for identifying genes involved in
tumorigenesis. The gene products can be bound to any position on the
cumorigenesis. The gene products can be bound to any position on the
cumplementary positions. Analysis is performed on a standardised surface,
expression of unknown genes can be determined, since many molecules are
expression weakly expressed genes can be detected, only small amounts
of starring material are required (MRNA from a single cell) and all steps
are suitable for automation. Only short sequences (10-50 nucleotides)
created to the determined for identification of genes, if their sequences are
available in databases. This sequence represents an oligonic location.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          available in databases. This sequence represents an oligonucleotide used to illustrate the method of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Parallel analysis; gene expression; tumorigenesis; detection; ss
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                                                                                                                                                                                                                                                                                                                                                                                                              Sequencing oligonucleotide #1
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                                                                                                       ABQ77279 standard; DNA; 12
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RESULT 1485
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Query Match 35.5%; Score 7.8; DB 1; Length 12; Best Local Similarity 81.8%; Pred. No. 6.8e+02; Matches 9; Conservative 0; Mismatches 2; Indels
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BP. ABQ77340 standard; DNA; 12 ABQ77340; RESULT 1486

This invention describes a novel method for parallel sequencing of nucleic acid fragments which comprises: (i) binding fragments of about 50 nucleic acid fragments which comprises: (i) binding fragments of about 50 complex with an individual primer, or many different primers, to a complex with an individual primer, or many different primers, to a complex with an individual primer, or many different primers, to a complementary strand of the nucleic acid fragment is then performed using containing polymerases and 1-4 modified nucleotides rate used, then fluorescent signals from each can be measured separately, (ii) then modified nucleotides are used, then fluorescent signals from each can be neasured separately, (iii) then modified nucleotides is a clavable sterically bulky lignad, (iv) the surface the same strand, fluorescent dye and complementary strand is extended by one unclectide, then washed to remove unincorporated modification in the nuclectide, then washed to remove unincorporated modification in the nuclectide, then washed to remove unincorporated modification in the nuclectide, then washed to remove unincorporated modification in the nuclectide, then washed to sequence of from a fluorescent dye and the bulky ligand are removed from complementary strand; (iv) the surface using the cycle respected, (vi) The relative positions, on the surface washed to envelope the surface used to sequence of the nucleic acid fragments in them are determined by correlation of the signals detected in many cycles at a cell single-nucleotide polymorphisms in a sequence, also more ach position. The method provides a cheaper, quicker and more efficient analysis of sequences, many sequences can be determined in corporated, there is little risk of errors as a result of easymentomis site is progressing or not. The molecules as a result of fixed to the carrier in a defined pattern, since the signal determined is recorded from individual molecules rather than from a polyanchiour mis sequence. Parallel sequencing of nucleic acid fragments, useful e.g. for analysis of single-nucleotide polymorphisms, by cyclical extension of primers with Parallel sequencing associated oligonucleotide SEQ ID Parallel sequencing; cyclical extension; ds. Example 4; Page 59; 121pp; German. 26-APR-2002; 2002WO-EP004659 27-APR-2001; 2001DE-01020797 population. This sequence illustrate the method of t (GENO-) GENOVOXX GMBH of single-nucleotide | modified nucleotides. WPI; 2003-183839/18. WO200288382-A2. Icherkassov 07-NOV-2002 Synthetic.

Sequence 12 BP; 6 A; 6 C; 0 G; 0 T; 0 U; 0 Other;

Gaps ö 35.5%; Score 7.8; DB 1; Length 12; llarity 81.8%; Pred. No. 6.8e+02; Conservative 0; Mismatches 2; Indels Local Similarity nes 9; Conserv Query Match Best Loca Matches

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737 AACAGAACACC 747

EST; expressed sequence tag; ss; polymorphic repeat; tandem repeat; polymorphic marker prediction of ubiquitous simple sequences; POWPOUS; Rep.-K; human; genetic disease; drug-treatment; Machado-Joseph; Haw River syndrome; Huntington's disease; fragile-X syndrome; Fredreich's ataxis; myotonic dystrophy; hyperandrogenemia; spinal atrophy; bulbar atrophy; spinocerebellar ataxia.

EST polymorphic DNA repeat polynucleotide #59.

(first entry)

17-APR-2003

ABX79734 standard; cDNA; 12 BP.

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The invention discloses a method for identifying a candidate polymorphic repeat within a coding sequence (expressed sequence tag, EST), which comprises detecting tandem repeats in a target coding sequence, scoring the repeats for polymorphic probability and generating a dataset correlating the repeats with polymorphic probability to identify a candidate polymorphic repeat. The computational methods (polymorphic repeats) which can be useful for identifying and detecting candidate polymorphic repeats in human genes, which can be used to understand, treat or eliminate genetic diseases, predispositions or adverse drug-treatment reactions. Examples of diseases linked to nucleotide repeats are Machado-Joseph, Haw River syndrome, Huntington's disease, fragile-X syndrome, Predicich's ataxis, myotonic dystrophy, hyperandrogenaemia, spinal and bulbar atrophy and spinocereballar ataxia. The sequences presented in ABX79676-ABX80022 are the polymorphic repeats identified for a search of human ESTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Identifying a candidate polymorphic repeat within a coding sequence, understanding or treating genetic disease, comprises detecting tandem repeats in a target coding sequence and scoring the repeats for
                                                                                                                                                                                                                                                  polymorphic marker prediction of ubiquitous simple sequences; POMPO Rep-X; human; genetic disease; drug-treatment; Machado-Joseph; Haw River syndrome; Huntington's disease; fragile-X syndrome; Fredreich's ataxis; myotonic dvstronhy.
                                                                                                                                                                                                                                                                                                                                             Fredreich's ataxis; myotonic dystrophy; hyperandrogenaemia; spinal atrophy; bulbar atrophy; spinocerebellar ataxia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         35.5%; Score 7.8; DB 1; Length 12; 81.8%; Pred. No. 6.8e+02; tive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 12 BP; 0 A; 7 C; 0 G; 5 T; 0 U; 0 Other;
                                                                                                                                                                                                                              EST polymorphic DNA repeat polynucleotide #329.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fondon JW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example; Col 1163; 588pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Minna JD,
                                                                                                                     ABX80004 standard; cDNA; 12 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99US-00475947
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                                                                                                                                                                                            17-APR-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (TEXA ) UNIV TEXAS SYSTEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            polymorphic probability.
Wren JD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2003-208818/20
                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  31-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        31-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                        US6472154-B1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29-OCT-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Garner HR,
                                                                                                                                                        ABX80004,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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Identifying a candidate polymorphic repeat within a coding sequence, funderstanding or treating genetic disease, comprises detecting tandem repeats in a target coding sequence and scoring the repeats for

Example; Col 267; 588pp; English.

for tandem

polymorphic probability.

Fondon JW;

Minna JD,

Wren JD,

Garner HR,

WPI; 2003-208818/20

(TEXA) UNIV TEXAS SYSTEM

99US-00475947 99US-00475947

31-DEC-1999; 31-DEC-1999;

Homo sapiens.

US6472154-B1

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The invention discloses a method for identifying a candidate polymorphic repeat within a coding sequence (expressed sequence tag, EST), which comprises detecting trandem repeats in a target coding sequence, scoring the repeats for polymorphic probability and generating a dataset correlating the repeat. The computational methods (polymorphic repeat.) are useful for identifying and detecting candidate polymorphic repeats in human genes, which can be used to understand, treat or eliminate genetic diseases, predispositions or adverse durg-treatment reactions. Examples of diseases linked to nucleotide repeats are Machado-Joseph, Haw River syndrome, Huntington's disease, fragile-X syndrome, Fredreich's ataxis, myotonic dystrophy, hyperandrogensemia, spinal and bulbar atrophy and spinocereballar ataxia. The sequences presented in ABX79676-ABX80022 are the polymorphic repeats identified for a search of human ESTs
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Pred. No. 6.8e+02;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 12 BP; 6 A; 4 C; 2 G; 0 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              35.5%;
81.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity 81.8
es 9; Conservative
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20-NOV-2003 (first entry)

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Gaps

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Conservative GGAGAAACAGA 742

Local Similarity les 9; Conser

Best Loc Matches

N

12 GGAGAGAGAGA

RESULT 1488

ABX79734

732

à g

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recombinant fusion protein; fusion protein; binding; detection; localisation domain; binding domain; subcellular compartment localisation; gene; ds.

Protein binding domain nucleotide sequence SEQ ID NO:359.

entry)

(first

18-DEC-2003

ADC22510;

ADC22510 standard; DNA; 12 BP.

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This invention described a novel method for parallel sequencing analysis of nucleic acids in which single-stranded fragments, of 50-1000 bases, are generated, representing overlapping fragments of a complete sequence. The fragments are then attached, as a complex with one or primers, in random fashion to a reaction surface. The complementary strand of the single stranded fragment is constructed using one or more DNA polymerases on a cycle involving incubating the bound complex with a least one of in a cycle involving incubating the bound complex with a fluorescenc different for each modified nucleotides on be detected from the conflormation in its parallel with a fluorescence of individual incorporated modified nucleotides can be detected from the contracteristic fluorescence, with simultaneous detection of the relative positions of the complex on the surface and optionally repeating the entire cycle. Detection in is by broad-field epifluorescence, laser-contracted in successive cycles. Bach fragment includes a primer binding stee (BBS), one in each strand for double-stranded sequences, and this site is the same for all fragments. The method is used (i) to identify mitteriors, particularly all single-nucleotide polymorphisms in a gene and (ii) for analysis of gene expression. Compared with known methods, this process is less expensive, quicker and more efficient, especially it allows many fragments to short fragments for mutational analysis, in the same process single nucleic acid molecules can be detected, the risk of errors through failure of synchronization in a population is avoided, molecules do not have to be fixed at specific positions, and multiple conjust sequenced and pRN). Even weakly expressed, or unknown, genes can be sequenced and only a tring sequence and fearting method only a ting sequence and errors through failure of synchronization in a population, and multiple conjust a process of the nucleic acid to not need to be made (eliminating and pRN) is ensured. The method is used only a ting sequen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Parallel sequencing of nucleic acid fragments, useful e.g. for detecting mutations, comprises sequential single-base extension of immobilized fragment-primer complex.
                                           parallel sequencing; fluorescence; detection; mutational analysis; NSKF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sequence to illustrate the method of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 12 BP; 6 A; 6 C; 0 G; 0 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 2; Page 56; 114pp; German.
                                                                                                                                                                                                                                                              28-AUG-2002; 2002WO-EP009614.
                                                                                                                                                                                                                                                                                                              29-AUG-2001; 2001DE-01042256.
NSKF target DNA sequence
                                                                                                                                                                                                                                                                                                                                                            (GENO-) GENOVOXX GMBH
                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2003-290205/28.
                                                                                                                                                             WO2003020968-A2.
                                                                                                                                                                                                                                                                                                                                                                                                         Tcherkassov D;
                                                                                                                  Unidentified.
                                                                                                                                                                                                                13-MAR-2003
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New recombinant fusion protein comprising detection and first localization domains and a binding domain for the molecule of interest, useful for detecting binding of a molecule of interest.

Chen Y;

Bright G, Premkumar DR,

WPI; 2003-248174/24.

P-PSDB; ADC22511

(CELL-) CELLOMICS INC.

01-AUG-2002; 2002WO-US024572 01-AUG-2001; 2001US-0309395P. 13-DEC-2001; 2001US-0341589P.

WO2003012068-A2.

13-FEB-2003

Homo sapiens.

Disclosure; SEQ ID NO 359; 101pp; English.

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The present invention describes a recombinant fusion protein (1) for detecting binding of a molecule of interest. (1) comprises: (a) a detecting binding of a molecule of interest. (1) comprises: (a) a detection domain, the first localisation domain, the first localisation domain and the binding domain for the molecule of interest. The detection domain, the first constituting the recombinant this on protein for detecting binding of a molecule of interest are operably linked. The binding domain for the molecule of interest is separated from the first localisation domain by 0 comming acid residues. The first localisation domain by 0 comming for the molecule of interest both do not occur in a single non-recombinant protein with the same spacing as in the recombinant fusion protein for detecting binding of a molecule of interest. Also described:

(1) a recombinant endoleic acid enocding the recombinant fusion protein;
(2) a recombinant expression vector comprising the nucleic acid control sequences operably linked to the recombinant mucleic acid molecule;
(3) a genetically engineered host cell transfected with the recombinant compression vector; (4) a kit for detecting binding of the molecule of interest; and (5) a method for identifying compounds that alter the binding of the molecule of interest. The recombinant tusion protein is useful for detecting binding of a molecule of interest. The recombinant protein eliminates the monitoring of biochemical events in live, intact the binding of the molecule of interest. The recombinant protein because the need to construct two or more chimering the binding of the molecule of succession weak and enables the monitoring of biochemical events in live, intact the binding of the molecule of succession were chimering of the molecule of succession were succession of the molecule of succession were succession were chimering the binding of succession were succession were chimering the binding of succession were construct two or more chimering the binding of the molecule of successio
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Best Local Similarity 81.5-
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Score 7.8; DB 1; Length 12; Pred. No. 6.8e+02; 0; Mismatches 2; Indels

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35.5%;

Query Match
Best Local Similarity 81.8
Matches 9; Conservative

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RESULT 1490 ADC22510/c

ADC18377

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97US-00810983.
98US-0031271.
99US-0123399P.
99US-0133399P.
99US-00338965.
99US-0051797P.
99US-00480656.
                                                    19-MAR-2002; 2002US-00100957.
                                                                                           (CELL-) CELLOMICS INC.
                                         US2003096322-A1.
                                   Unidentified.
                                                                                     25-FEB-2000;
                                                          27-FEB-1997;
                                              22-MAY-2003
                                                                         31-AUG-1999
17-SEP-1999
                                                                 26-FEB-1999
                                                                   08-MAR-1999
     ADC18377;
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ds; cell based toxin; luminescent reporter molecule; biosensor; microchip; drug discovery; MAP4; epitope; affinity tag; protease recognition site; caspase; target domain.
                                                                                                                                                                                                                                                    Protease recognition site for caspase-6 DNA #1.
ADC18377 standard; DNA; 12 BP.
                                                                                                                                                                       18-DEC-2003 (first entry)
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Giuliano K, Kapur R; WPI; 2003-786988/74. P-PSDB; ADC18378

Cell based toxin characterization method for e.g. in drug discovery paradigm, involves treating cells possessing luminescent reporter molecules with fluorescence based molecules reagents to detect presence of toxins.

The invention relates to characterising cell based toxins, where the cell possessing luminescent reporter molecules (biosensors) are provided on a microchip, and are treated with fluorescence based molecular reagents.

The cells are photographed with fluorescence optics, and the optical information is converted into digital data. The presence of the toxin in a reagant, is detected using the digital data. The presence of the toxin in closalisation, distribution structure of identifier, detector and closalisation, distribution structure of identifier, detector and closalisation storing a cell based toxin characterisation program, and a kit for cell based toxin detection. The method is used for characterising or detecting a biological cell based toxin that affect particular biological functions and for preparing molecular biochemical arrays for new drug discovery paradigm. It is also used in automated DNA sequencing, PCR application, positional cloning, hybridisation arrays and bioinformatics using cell based quantity and soreaming system. The method improves the target validation and candidate optimisation by combining many cell crased quantity and speed of data collection, shortened cycle times and faster evaluation of promising drug candidates. The method also provides increased throughput while decreasing the volumes of centering it to microtubules) or detectable signal (epitope or affinity temply, a protease recognition site (e.g. for a caspase protein) and a comparise a signal component (fluorescence parages protein) and a caspase protein) and comparison of comparison and candidate optimisation a particular cellular component for a historian a daspase protein) and a historian of the biosensor or a particular cellular. Example 10; SEQ ID NO 65; 98pp; English. or a biosensor of the invention

Gaps ; 0 Score 7.8; DB 1; Length 12; Pred. No. 6.8e+02; 0; Mismatches 2; Indels Sequence 12 BP; 6 A; 1 C; 3 G; 2 T; 0 U; 0 Other; .; 0 35.5%; 81.8%; Query Match
Best Local Similarity 81.8
Matches 9; Conservative 732 GGAGAAACAGA 742 1 GTAGAAATAGA 11 엄

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Search completed: October 18, 2004, 14:07:21 Job time : 8 secs

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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwD42 (gilfy132114[gb]AR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coll X110-Gold (Stratagene) cells and selected for ampicillin resistance."
             AZ386064 linear GSS 02-OCT-2000 linear GSS 02-OCT-2000 linear GSS 02-OCT-2000 lineary Mus musculus genomic close UUGCIM0145C04 F, genomic survey sequence.
                                                                                                                   Mus musculus (house mouse)

Mus musculus

Mus musculus

Bukaryota, Metazoa, Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

(bases 1 to 19)

Unni, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,

Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,

Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von

Miderhausern, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb
                                                                                                                                                                                                                                                                                                                                 Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /lab host="B. Coli strain XLIO-Gold, Tl-resistant, F-" /clone lib="Mouse 10kb plasmid UUGCIM library" /note="Vector: PWD42nry, Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
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Fax: 801 585 7177
Insert Length: 10000 Std Error: 0.00
Plate: 0145 row: C column: 04
Seg primer: CGTTGTAAACGACGCCAGT
Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Mus musculus"
/mol type="genomic DNA"
/strain="C57BL/6J"
/db xref="taxon:1009"
/clone="UUGCIM0145C04"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   High quality sequence stop: 19.
Location/Qualifiers
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DEFINITION
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ACCESSION: CF30888
ACCESSION: CF543159
ACCESSION: B07112
ACCESSION: CF277997
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ACCESSION: CF318771
ACCESSION: CF33649
ACCESSION: CF313731
ACCESSION: CF313731
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ACCESSION: B07312
ACCESSION: BQ587766
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ACCESSION: CA794225
ACCESSION: CA851674
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ACCESSION: BQ585171
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ACCESSION: CF302851
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                                                                                                                           October 18, 2004, 14:39:47 ; Search time 0.001 Seconds (without alignments) 38.836 Million cell updates/sec
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                 GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 27 summaries
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Match Length DB
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73
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1 (bases 1 to 13)
Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
and Radelof,U.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                B07312 G360T3 MVAT4 sheared genomic library Trypanosoma brucei rhodesiense genomic clone G360, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="Vector: pCMVSPORT6; Site_1: Sall; Site_2: NotI; ontData library from sugar beet, lTbrary provided by KWS Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact: b.schulz@kws.de; cloning sites Sall-NotI, primer sites and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Trypanosoma.
I (bases 1 to 12)
El-Sayed, N.M.A. and Donelson, J.E.
A survey of the Trypanosoma brucei rhodesiense genome using shotgun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       orientation:
SP6-SalI-CCACGCTCCG-Sprime-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-Beet
project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database: http://gabi.rzpd.de"
                                                                                                                                                                 Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes Plant J. 32 (5), 845-857 (2002)
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/culTivar="KWS2320 (double haploid, monogerm breeding
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Eukaryota, Euglenozoa, Kinetoplastida, Trypanosomatidae,
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Pred. No. 3.4;
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                                                                                                                                                                                                                                                                                                                            Contact: Weisshaar B
ADIS DNA core facility at MPIZ
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weisshaa@mpiz-koeln.mpg.de
Insert Length: 13
Std Brror: 0.00
Plate: 1 row: J column: 02
Seq primer: SP6; CATACGATTAGGTGACACTATAG.
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97237559
       Caryophyllales; Amaranthaceae; Beta.
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/organism="Beta vulgaris"
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Contact: E1-Sayed NMA
John Donelson's Laboratory
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ilarity 83.3%;
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BQ589768 13 bp mRNA linear EST 06-DEC-2002 E012680-024-020-D03-SP6 MPIZ-ADIS-024-storage root Beta vulgaris cDNA clone 024-020-D03 5-PRIME, mRNA sequence.
                                                                                                                                                                                                                                       Enterprise 1 Tracheophyta; Embryophyta; Tracheophyta; Enkaryota; Viridiplantae; Streptophyta; Endicotyledons; core eudicots; Caryophylales; Amaranthaceae; Beta.

1 (bases 1 to 13)
Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M., and Radelof,U.
Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes Plant J. 32 (5), 845-857 (2002)
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/note="vector: pcMvSPORT6; Site_2: NotI; Site_3: NotI;
/note="vector: pcMvSPORT6; Site_3: NotI; Sit
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Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
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E012207-024-001-J02-SP6 MPIZ-ADIS-024-inflorescence Beta vulgaris cDNA clone 024-001-J02 5-PRIME, mRNA sequence.
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/mol type="mRNA"
/cultivar="KW82320 (double haploid, monogerm breeding
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ADIS DNA core facility at WPIZ
ADIS DNA core facility at WPIZ
MAX-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 0049221506281,
Email: weisshaa@mpiz-koeln.mpg.de
Insert Length: 13 Std Error: 0.00
Plate: 20 row: D column: 03
Seq primer: SP6; CATACGATTAGGTGACACTATAG.
Location/Qualifiers
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Pred. No. 2;
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Best Local Similarity 84.6
Matches 11; Conservative
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CDNA_library from sugar beet, library provided by KWS
Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites Sall-NotI, primer sites and
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                                                                                                                                                                                                                                                              orientation:
SP6-SalI-CCACGCGTCCG-Sprime-cDNA-polyA-CC-NotI-T7; Note:
SP6-SalI-CCACGCGTCCG-Sprime-cDNA-polyA-CC-NotI-T7;
Sequence of the GABI-Beet
project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database:http://gabi.rzpd.de"
         cultivar="KWS2320 (double haploid, monogerm breeding
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/clone lib="tmf"
/note="Vector: PCR 4Blunt-TOP; 0.8-1.2 kb methylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Trachec
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
Pooideae, Triticae, Aegilops.
1 (bases 1 to 12)
Li,W., Zhang,P., Fellers,J., Friebe,B. and Gill,B.S.
Sequence composition, organization and evolution of a basic
Triticaea genome of the grass family
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Li, W
Dr. Bikram S. Gill's Lab
Wheat Genetics Resource Center, Kansas State University
4024 Throckmorton, Manhattan, KS 66506-5502, USA
Tel: 785-532-1108
Fax: 785-532-5692
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Pred. No. 4.6;
0; Mismatches 2; Indels
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/mol_type="genomic DNA"
/strain="AL 8/18"
/db xref="taxon:37682"
/clone="tmf17C15"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 filtered genomic DNA library"
                                                                     /db_xref="taxon:161934"
/clone="024-010-M01"
/tissue_type="leaf"
                                                 /db xref="GABI:185095"
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Location/Qualifiers
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ilarity 81.8%;
Conservative
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Seq primer: T7
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CG677120
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CG677120
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Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Garyophylales, Amaranthaceae, Beta.
1 (bases 1 to 12)
1 (bases 1 to 12)
1 (bases)
1 to 12)
1 bringowski,M., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
Drungowski,M., Schil,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
and Radelof,U.
Construction of a 'unigne' cDNA clone set by oligonucleotide
fingerprinting allows access to 25 000 potential sugar beet genes
Plant J. 32 (5), 845-857 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BQ587766 12 bp mRNA linear BST 06-DEC-2002 E012340-024-010-M01-SP6 MPIZ-ADIS-024-leaf Beta vulgaris cDNA clone 024-010-M01 5-PRIME, mRNA sequence.
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                             IA
Howard Hughes Medical Institute
300 EMRB, Dept. of Biochemistry, University of Iowa, Iowa City,
52.24.
721: 319 335 6918
Fax: 319 335 6764
Email: nelsaye@waxa.weeg.uiowa.edu
Insert Length: 700 Std Brror: 200.00
Seg primer: 13 primer
Class: shotgun.
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o
                                                                                                                                                                                                                                   /organism="Trypanosoma brucei rhodesiense"
/mol_type="genomic DNA"
/sub_species="rhodesiense"
/db_xref="taxon:31286"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 8.4; DB 1; Length 12; Pred. No. 3.4;
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ADIS DNA core facility at MPIZ
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weisshaa@mpiz-koeln.mpg.de
Insert Length: 12 Std Error: 0.00
Plate: 10 row: M column: 01
Seg primer: SP6; CATACGATTTAGGTGACACTATAG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches

    .12
    /organism="Beta vulgaris",
/mol_type="mRNA"

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BQ587766.1 GI:26117348
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Best Local Similarity 90.0
Matches 9; Conservative
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This GSS is part of a random genomic sequencing program of thirteen yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces servazzii, Zygoasccharomyces rouxii, Saccharomyces kluyveri, Kluyveromyces thermotolerans, Kluyveromyces lactis var. lactis, Kluyveromyces marxianus var. marxianus, Pichia angusta, Debaryomyces hansenii, var. hansenii, Pichia sorbitophila, Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to 5 kb were prepared and both extremities were sequenced. See keywords for description of this sequence and for the sequence of the other extremity of this insert.
                                                                                                                                                                                                                                                                                                           SM Zygosaccharomyces rouxii

Butaryota; Rungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Zygosaccharomyces.

E. 1 (bases 1 to 9)
S Souciet,J.L., Aigle,M., Artiguenave,F., Blandin,G.,
Bolotin-Fukuhara,M., Bon,E., Brottier,P., Casaregola,S.,
de-Montigny,J., Dujon,B., Durrens,P., Lepingle,A., Llorente,B.,
Malpertuy,A., Neuveglise,C., Ozier-Kalogeropoulos,O., Potier,S.,
Saurin,W., Tekaia,F., Toffano-Nioche,C., Wesolowski-Louvel,M.,
Wincker,P. and Weissenbach,J.
Genomic exploration of the hemiascomycetous yeasts: 1. A set of
yeast species for molecular evolution studies

E. 20584711

E. 20584711
                                                                                                                                                    CNSO6E5N 1 inear GSS 17-JUN-2001
T3 end of clone AROAA018H04 of library AROAA from strain CBS 732 of
Zygosaccharomyces rouxii, genomic survey sequence.
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Minoker, P., Straub, M., Potier, S., Tekaia, F., Dujon, B., Winoker, P., Ariguenave, F. and Souciet, J.

Genomic exploration of the hemiascomycetous yeasts: 8.
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FEBS Lett. 487 (1), 52-55 (2000)
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Enrhartoideae; Oryzeae; Oryza.

Enrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 10)

S Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

Lupublished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University

YongIn, KyeongGi, Korea

Tel: 82 31 321 6355

Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Oryza sativa"
/organism="Oryza sativa"
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CF311011
ABF--06-B02.b1 ABF3-overexpressing transgenic rice plasmid cDNA
Library (ABF) Oryza sativa cDNA clone ABF--06-B02, mRNA sequence.
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Micotiana benthamiana
Nicotiana benthamiana
Nicotiana benthamiana
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; Iamiids; Solanales; Solanaceae; Nicotiana.
1 (bases 1 to 10)
Buell,C.R.; Hart,A., Zismann,V., Karamycheva,S.A., Day,B.,
Staskavicz,B., Jin,H. and Baker,B.
Graskavicz,B., Jin,H. and Baker,B.
Unpublished (2003)
Chher_Estr servick1693
Contact: Robin Buell
The Institute for Genomic Research
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                                                                                                                                               CF311011.1 GI:33682772
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Best Local Similarity 88.9
Matches 8; Conservative
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// Reinmanzlebener Saatsucht AG Einbeck, Germany, contact:
// Boschulz@kws.de; cloning sites Sal1-Not1, primer sites and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CF299850
7LEAF--04-A13.g1 Rice leaf plasmid cDNA library II (7LEAF) Oryza sativa cDNA clone 7LEAF--04-A13, mRNA sequence.
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Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzae, Oryza,
1 (bases 1 to 11)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
                                                                                                                                                                                                                                                                      orientation:
SP6-SalI-CCACGCGCCCG-Sprime-cDNA-polyA-CC-NotI-T7; Note:
SP6-SalI-CCACGCGCCCG-Sprime-cDNA-polyA-CC-NotI-T7;
Sequencing granted in the context of the GABI-Beet
project, local Pi: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database: http://gabi.rzpd.de"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Nature 1.2. (Contact: Nature 1.2.)
Contact: Nature 1.2. (Contact: Nature 1.2.)
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yorgin, KyeongGi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6155
Fax: 82 31 321 6255
Email: bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
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Pred. No. 4.6;
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/organism="Oryza sativa"
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88.9%;
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                                                                                                                                                                                                                                 /done="MBMDJ48"
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callus tissue and root tissue"
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/lab host="DH10B-TonA"
/lab host="DH10B-TonA"
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supplier: RNA was isolated from Nicotiana benthamiana
tissues that include callus, roots from liquid culture
grown plants, heat-estessed leaves (38 C, 3 hr and 6 hr),
cold-stressed leaves (5 C 3 hr, and pathogen
challenged leaves (Pseudomonas syringae pv tomato 12 hr;
Xanthomonas campestris pv campeetris 12 hr, 18hr;
Pseudomonas syringae pv phaseolicola 18hr, and Xanthomonas
campestris pv vesicatoria 18hr). RNA was isolated from
these tissues and pooled in approximately equal molar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BQS85171 11 bp mRNA linear EST 06-DEC-2002 S014222-024-001-J02-SP6 MPIZ-ADIS-024-inflorescence Beta vulgaris CDNA clone 024-001-J02 5-PRIME, mRNA sequence.
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Beta vulgaris
Beta vulgaris
Beta vulgaris
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Caryophyllales; Amaranthaceae; Beta.
1 (Bases I to 11)
1 (Bases I to 11)
1 (Bases I to 11)
2 Ebases I to 11)
Prungowski,M., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H. and Radelof,U.
Construction of a 'unigene' cDNA clone set by oligonucleotide
fingerprinting allows access to 25 000 potential sugar beet genes
Plant J. 32 (5), 845-857 (2002)
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                            Email: potato-array@tigr.org
Clones can be requested from TIGR via potato@tigr.org
Seg primer: GTA ATA CGA CTC ACT ATA GGG C.
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Pred. No. 3.6;
0; Mismatches 1; Indels
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ADIS DNA core facility at MPIZ
ADIS DNA core facility at MPIZ
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weisshaa@mpiz-koeln.mpg.de
Insert Length: 11 Std Error: 0.00
Plate: 1 row: J column: 02
Seq primer: SP6; CATACGATTAGGTGACACTATAG.
9712 Medical Center Dr, Rockville, MD 20850, USA
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                                                                                                           Location/Qualifiers
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ACCESSION VERSION KEYWORDS

RESULT 12 CF304450/c LOCUS DEFINITION

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CFE43159 11 bp mRNA linear EST 22-SEP-2003 S014678-024-030-006-SP6 MPIZ-ADIS-024-leaf Beta vulgaris cDNA clone 024-030-006 5-PRIME, mRNA sequence.
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1 Chasea 1 to 11)

1 Chasea 1 to 11)

1 Weisshaar, B., Hennig, S., Steinfath, M., Drungowsti, M., Stahl, D., Wruck, W., Menze, A., O'Brien, J., Lehrach, H. and Radelof, U.
                       Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, KyeongGi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="Wector: pCR4-TOPO, Site 1: EcoRI; Leaf was dried for 2hrs. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was prepared from ABA-responsive element binding transcription factor 3 overexpression line."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Construction of a 'unigene' cDNA clone set by oligonucleotide
fingerprinting allows access to 25 000 potential sugar beet genes
Plant J. 32 (5), 845-857 (2002)
                                                                                                                                                                                                                                                                                                                                                          db_xref="taxon:4530"

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cDNA library (ABF)"
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/culTivar="KWS2320 (double haploid, monogerm breeding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10.1%; Score 7.4; DB 1; Length 11; 88.9%; Pred. No. 4.6; tive 0; Mismatches 1; Indels
                                                                                                                                                                                          Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
    Location/Qualifiers
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ADIS DNA core facility at MPIZ
MAx-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 0042215062851
Email: weisshaa@mpiz-koeln.mpg.de
Insert Length: 11 Etd Error: 0.00
Plate: 30 row: O column: 06
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                                                                                                                                                                                                                                                                                                        /mol_type="mRNA"
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Unpublished (2003)
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/mol type="mRNA"
/cultivar="NackGong"
/db xref="taxon:4530"
/clone="ABF1--05-A03"
/tissue_Type="deaf"
/dav_stage="14 days after germination"
/dav_stage="14 days after germination"
/dav_stage="18.coli SOLM"
/dav_stage="Scoversypeessing transgenic rice lambda phage cDNA library (ABF1)"
/clone lib="ABF2-overexypeessing transgenic rice lambda phage cDNA library (ABF1)"
/nofe="vertor: pBluescript SK(+); Site_1: EcoRI; Site_2: XhoI; Leaf was dried for Zhrs. cDNA was inserted into lamda Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhoI site. mRNA was prepared from ABA-responsive element binding transcription factor 3 overexpression line."
                                                                                                          CF304450
ABF1--05-A03.gl ABF3-overexpressing transgenic rice lambda phage cDNA library (ABF1) Oryza sativa cDNA clone ABF1--05-A03, mRNA
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ABF--04-E09.g1 ABF3-overexpressing transgenic rice plasmid cDNA
library (ABF) Oryza sativa cDNA clone ABF--04-E09, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Enhartoidaes; Oryzae; Oryzae.

1 (bases 1 to 11)

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Sang, S.I., Kim, J.K., and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTs
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1 (bases 1 to 11)

(bases 1 to 11)

(kin,J.S., Vun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs
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Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
YongJin, KyeongJi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
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REFERENCE AUTHORS

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CF277997 Bbp mRNA linear EST 14-AUG-2003
J4ETL--03-L19.g1 Rice etiolated leaf plasmid cDNA library (14ETL)
Oryza sativa cDNA clone 14ETL--03-L19, mRNA sequence.
CF277997
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1 (bases 1 to 8)

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)
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Oryza sativa
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yorgin, KyeongJi, Korea
Tel: 82 31 330 6193
Fax: 82 31 31 21 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
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fragments were cloned into the pCR-Script vector (Stratagene)."
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/cultivar="Nackdong"
/db xref="taxon:4530"
/clone="14FTL-03-L19"
/tissue_type="1eaf"
/dev_stage="14 days after germination"
/lab_host="E_coli DH108"
                                                                         Score 7.4; DB Pred. No. 5.6;
                                                                                                                       0; Mismatches
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87.5%; Pred. No. 39;
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ilarity 88.9%;
Conservative
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CF301888/c
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CF277997
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                                                /tissue_type="leaf"
/tab.host="EmbH10B"
/clone_lih="MPDH10B"
/clone_lih="WPDH2AD15-024-leaf"
/note="Vector: pCMVSPORT6; Site_1: Sall; Site_2: Not1;
/note="Vector: pCMVSPORT6; Site_1: Sall; Site_2: Not1;
/note="Vector: pCMVSPORT6; Site_1: Sall; Site_2: Not1;
/contain_the supers Saatzeucht Ad Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites Sall-Not1, primer sites and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Trypanosoma.
1 (bases 1 to 12)
El-Sayed,N.M.A. and Donelson,J.E.
A survey of the Trypanosoma brucei rhodesiense genome using shotgun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12 bp DNA linear GSS 26-MAR-1997 G360T3 WVAT4 sheared genomic library Trypanosoma brucei rhodesiense genomic clone G360, genomic survey sequence.
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                                                                                                                                                                                                                                  SP6-Sall-CCACGCGTCCG-Sprime-cDNA-polyA-CC-Not1-T7; Note: Sequencing granted in the context of the GAB1-Beet project, local Pir. Dr. Katharina Schneider, coordinator: Prof. Christian Unig; Sequence submission managed by RZPD/GAB1-Primary database:http://gabi.rzpd.de"
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Howard Hughes Medical Institute
300 EMRB, Dept. of Biochemistry, University of Iowa, Iowa City, IA
                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
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Mol. Bichem. Parasitol. 84 (2), 167-178 (1997)
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Fax: 319 335 6764
Fax: 319 335 6764
Insert Length: 700 Std Error: 200.00
Seg primer: T3 primer
Class: shotgun.
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Contact: E1-Sayed NMA
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Best Local Similarity 87.5
Matches 7; Conservative
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7LEAF--08-MO7.g1 Rice leaf plasmid cDNA library II (7LEAF) Oryza sativa cDNA clone 7LEAF--08-MO7, mRNA sequence.
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                                                                                                                                                                        Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University YongJi, KveongJi, Korea Tel: 82 31 330 6193
Pax: 82 31 321 6355
                                                                                                                                                                                                                                                                                                                                                                        /mol_type="mrNa"
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/note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for
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Genomics and Generics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Yongin, Kyeonggi, Korea
Fax: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.

1. (bases 1 to 8)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C. Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
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Location/Qualifiers
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/mol_type="mRNA"
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CF302851.1 GI:33674612
                                                                                                                                                               Contact: Nahm B.H.
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Surviva sativa Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Enrhartophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Enrhartoldeae; Oryzae; Oryza.

Enrhartoldeae; Orozae; Oryza.

Enryophyta; Tracheophyta; Enrhartor Enry Sonles; Poaceae;

Enryophyta; Enry Sonles; Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bloscience and Bloinformatics, MyongJi University Yongin, Kyeongqi, Korea

Tel: 82 31 330 6193

Fax: 82 31 31 6355
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Cac_BL_1208 Cac_BL (Bean and Leaf from Amelonardo type Cacao)
Theobroma cacao cDNA clone Cac_BL_1208 5', mRNA sequence.
CA794225.
CA794225.1 GI:26051301
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ABF--08-L15.g1 ABF3-overexpressing transgenic rice plasmid CDNA library (ABF) Oryza sativa CDNA clone ABF--08-L15, mRNA sequence.
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/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)" /note="Vector: pCR4-TOPO; Site_l: BcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."
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Best Local Similarity 87.5%; Pred. No. 39;
Matches 7; Conservative 0; Mismatches
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/cultivar="NacKdong"

/db xref="taxon:4530"

/clone="ABF--08-L15"
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Gaps

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CF312817

9 bp mRNA linear BST 15-AUG-2003
ABF--08-L15.b1 ABF3-overexpressing transgenic rice plasmid cDNA
Library (ABF) Oryza sativa cDNA clone ABF--08-L15, mRNA sequence.
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Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehrhartoideae; Oryzaee; Oryzae.

1 (bases 1 to 9)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs
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/note="Vector: pBluescript SK-; cDNA clones from mRNA
extracted from Peking roots 2 and 4 days past invasion."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
Genomics and Bioinformatics, MyongJi University
YongJi, KyeongJi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Exax: 82 31 321 6355
Email: bhnahm@pio.myongji.ac.kr.
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/ dev_stage="ladf"
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/ clone lib="ABF3-overexpressing transgenic rice plasmid
cona lib=ary (ABF)"
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                                                organism="Glycine max"
    Location/Qualifiers
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CF312817.1 GI:33684578
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Best Local Similarity 87.5%;
Matches 7; Conservative
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Analysis of expressed sequence tags from roots of resistant soybean infected by the soybean cyst nematode
Unpublished (2002)
Contact: Alkharouf, N.W.
Soybean Genomics and Improvement Laboratory (SGIL)
US Department of Agriculture (USDA), ARS, PSI
Bldg.006, Rm 118, 10300 Baltimore Ave., Beltsville, MD 20705-2350,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CA851674 1 10 mRNA linear EST 01-AUG-2003 D16C10 F22 05.abl cDNA Peking library 2, 4 day SCN3 Glycine max cDNA cIone D16C10 5', mRNA sequence. CA851674.1 GI:33388467
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/lab_host="XL-1 Blue MRF"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bikarycca; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
                                                                         Tracheophyta;
                                              Eukaryotta, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta Spermatophyta, Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Malvales; Malvaceae; Byttnerioideae; Theobroma.

1 (bases 1 to 9)
Jones, P.G., Allaway, D., Gilmour, D.M., Harris, C., Rankin, D., Gene discover, and Jones, C.A.

Gene discovery and microarray analysis of cacao (Theobroma cacao D.)
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3d Dundee Road, Slough, Berkshire, UK, SL1
Tel: +44 1664 416644
Email: Paul.Jones@eu.effem.com
Seg primer: T3
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Best Local Similarity 87.5%; Pred. No. 35;
Matches 7; Conservative 0; Mismatches 1;
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Fax: 301 504 5728
Email: alkharon@ba.ars.usda.gov.
                                                                                                                                                                                                                                                                               Planta 216 (2), 255-264 (2002)
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                          cacao (cacao)
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                          Theobroma cacao
Theobroma cacao
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CA794554/c
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                                                         9 Dp mRNA linear EST 15-AUG-2003 HD--09-A13.g1 OsHDAC1-overexpressing transgenic rice plasmid cDNA library (HD) Oryza sativa cDNA clone HD--09-A13, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /tissue_type="callus"
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                                                                                                                                                                                                                                                                                                             Eukaryotativa
Eukaryotativa
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Shrhartoideee; Oryzeae; Oryza.
1 (bases 1 to 9)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,Y.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTS
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, MyongJi University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrartoideae; Oryzae; Liliopsida; Poales; Poaceae; Dryzae; Li (bases 1 to 9) (bases 1 to 9) (bases 1 to 9) (bases 2 to 9) (bases 2 to 9) (bases 3 to 9) (bases 3 to 9) (bases 3 to 9) (bases 3 to 8) (bases 3 to 9) (bases 3 to 8) (bases 3 to 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cDNA lTbrary (HD)"

/note="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was treated with ABA(20um) for 1hr. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was derived from rice Histone Deacetylase overexpression line."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
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/mol_type="mRNA"
/cultivar="Nackdong"
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                                                                                                                                                                                             CF318771.1 GI:33690532
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Best Local Similarity 87.5
Matches 7; Conservative
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RESULT 23
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/organism="ncryza sativa"
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/mol type="mRNA"
/mol type="mRNA"
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/db xref="taxon:4530"
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/lab host="E.coli DH10B"
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Gac_BL_1496 Cac_BL (Bean and Leaf from Amelonardo type Cacao)
Theobroma cacao cDNA clone Cac_BL_1496 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Theobroma cacao
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 (bases 1 to 8)
Jones, P.G., Allaway, D., Gilmour, D.M., Harris, C., Rankin, D.,
Retzel, B.R. and Jones, C.A.
Gene discovery and microarray analysis of cacao (Theobroma cacao
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /mol_type="miNA"
/mol_type="miNA"
/malonado type"
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/clone="Cac_BL|1496"
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/closue type="Mhole organ"
/dev_scage="maturity"
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/clone="Cac_BL (Bean and Leaf from Amelonardo type
cacao)"
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of Bioscience and Bioinformatics, MyongJi University Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
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3d Dundee Road, Slough, Berkshire, UK, SL1 4LG
Tel: +44 1664 416644
Seq primer: T3.
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/organism="Theobroma cacao"
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Planta 216 (2), 255-264 (2002)
2337596
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resistant soybean
                                  1. (James 1 to 8)
Alkharouf, N.W., Khan, R. and Matthews, B.F.
Analysis of expressed sequence tags from roots of resistant soybean infected by the soybean cyst nematode
Unpublished (2002)
Contact: Alkharouf, N.W.
Soybean Genomics and Improvement Laboratory (SGIL)
US Department of Agriculture (USDA), ARS, PSI
BldG.006, Rm 118, 10300 Baltimore Ave., Beltsville, MD 20705-2350,
                                                                                                                                                                                                                                                                                                                                                                        / organism="Glycine max"
/ organism="Glycine max"
/ mol type="mRNA"
/ clulivar="Peking"
/ db xref="taxon:3847"
/ clone="D12G08"
/ tissue type="Roots"
/ dev stage="Seedlings"
/ clone lib="con8 Peking library 2, 4 day SCN3"
/ note="Wector: pBluescript SK-; cDNA clones from mRNA
/ mote="Wector: pBluescript SK-; cDNA clones from mRNA
extracted from Peking roots 2 and 4 days past invasion."
  rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
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                                                                                                                                                                                                                                                   USA
Tel: 301 504 5750
Fax: 301 504 5758
Email: alkharom@ba.ars.usda.gov.
Location/Qualifiers
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SM Oryza sativa

Sukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, Liliopsida; Poales, Poaceae; Ehrhartoideae, Oryzeae, Oryza.

El (bases I to 8)

S Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

Lungulished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bloscience and Bioinformatics, MyongJi University

YongIn, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Fax: 82 31 321 6355
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/dev stage="proliferated callus on 2N6 media for 2 weeks"
/lab_nost="E.coll DH10B"
/clone lib="OsHDAC1-overexpressing transgenic rice plasmid
cDNA library (HD)"
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HD--01-P12.g1 OSHDAC1-overexpressing transgenic rice plasmid cDNA
library (HD) Oryza sativa cDNA clone HD--01-P12, mRNA sequence.
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Glycine max
Glycine max
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots;
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Location/Qualifiers
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                                                 0; Indels
8.2%; Score 6; DB 1; Length 8; 100.0%; Pred. No. 39; Azive 0; Mismatches 0; Indel.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Oryza sativa"
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CF313731.1 GI:33685492
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                   Best Local Similarity 100.
Matches 6; Conservative
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Matches 6; Conserv
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RESULT 1 US-09-106-038A-54/C i Sequence 54, Application US/09106038A i Patent No. 6007995 i GENERAL INFORMATION: APPLICANT: Brenda F. Baker and Lex M. Cowsert ITILE OF INVENTION: ANTISENSE MODULATION OF TIREL ITILE OF INVENTION: EXPRESSION NUMBER OF SEQUENCES: ADDRESSEE: 1518 Pharmaceuticals, Inc. STREET: 2592 Faraday Avenue	STATE: CALIEDAGE STATE: CALLEDAGE COUNTRY: U.S.A. ZIP: 92008 COMPUTER: BADABLE FORM: MEDIUM TYPE: 3.5 inch disk, 1.44 Mb COMPUTER: IBM PC compatible OPERATING SYSTEM: Mindows NT SOFTWARE: Microsoft Word 97 CURRENT APPLICATION NDATA: APPLICATION NUMBER: US/09/106,038A FILING DATE: June 26, 1998 CLASSIPICATION: NUMBER: US/09/106,038A FILING DATE: June 26, 1998 CLASSIPICATION: THORMATION: NAME: Laurel Spear Bernstein REGISTRATION NUMBER: 37, 280 REFERENCE/DOCKET NUMBER: RTS-0004 TELECOMMUNICATION INFORMATION: TELECOMMUNICATI	Query Match Best Local Similarity 100.0%; Pred. No. 5.9; Matches 18; Conservative 0; Mismatches 0; In Matches 18; Conservative 0; Mismatches 0; In Qy 906 CATTTCTTTGGTCTTTG 923
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Best Local Similarity 100.0%; Pred. No. 5.9;
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Sequence 58, Application US/09106038A

Patent No. 600799

GENERAL INFORMATION:
APPLICANT: Brenda F. Baker and Lex M. Cowsert
TITLE OF INVENTION: EXPRESSION
TITLE OF INVENTION: EXPRESSION
NUMBER OF SEQUENCES: 91

CORRESPONDENCE ADDRESS:
ADDRESSEE: Isis Pharmaceuticals, Inc.
STREET: 2292 Faraday Avenue
CITY: Carlsbad
                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT:
APPLICANT:
Brenda F. Baker and Lex M. Cowsert
TITLE OF INVENTION: ANTISENSE MODULATION OF THERI
TITLE OF INVENTION: EXPRESSION
NUMBER OF SEQUENCES: 91
CORRESPONDENCE ADDRESS:
ADDRESSE: Isis Pharmaceuticals, Inc.
STREET: 2292 Faraday Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: U.S.A.
ZIP: 92008
COMPUTER READABLE FORM:
MEDLUM TYPE: 3.5 inch disk, 1.44 Mb
COMPUTER: 1BW PC compatible
COMPUTER: 1BW PC compatible
OPERATING SYSTEM: Windows NT
SOFTWARE: MICTOSOFE WORD 97
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/106,038A
FILING DATE: JUNE 26, 1998
CLASSIFICATION: 514
ATTONNEY, AGGNT INFORMATION:
NAME: LAUREL SPEAT BETIEFEIN
REGISTRATION NUMBER: 237,280
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MEDIUM TYPE: 3.5 inch disk, 1.44 Mb
COMPUTER: IBM PC compatible
                                                                                                                                        US-09-106-038A-57/c
; Sequence 57, Application US/09106038A
; Patent No. 6007995
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REFREENCE/DOCKET NUMBER: RTS-(
TELECOMMUNICATION INFORMATION:
TELEPHONE: (760) 931-9200
INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
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US-09-106-038A-57
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 3
US-09-106-038A-56/C

1 Sequence 56, Application US/09106038A
1 Patent No. 6007995
1 Patent No. 6007995
1 TILE OF INVENTION: BARET and Lex M. Cowsert
1 TILE OF INVENTION: EXPRESSION
1 TILE OF INVENTION: EXPRESSION
1 NUMBER OF SEQUENCES: 91
1 CORRESPONDENCE ADDRESS:
1 ADDRESSE: Isis Pharmaceuticals, Inc.
2222 Faraday Avenue
1 CITY: Carlsbad
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READBLE FORM:
MEDIUM TYPE: 3.5 inch disk, 1.44 Mb
COMPUTER: IBM PC comparable
OPERATING SYSTEM: Windows NT
SOFTWARE: Microsoft Word 97
CURRENY APPLICATION DATA:
APPLICATION NUMBER: US/09/106,038A
FILING DATE: June 26, 1998
CLASSIFICATION: 514
ATTORNEY AGENT INFORMATION:
NAME: LAURE! Spear Bernstein
RESTERRITON NUMBER: 37,280
RESTERRICON NUMBER: ATS-0004
TELECOMMUNICATION INPORMATION:
TELECOMMUNICATION INPORMATION:
TELECOMMUNICATION INPORMATION:
TELECOMMUNICATION INPORMATION:
                                                                                    TILING DALE:

CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Laurel Spear Bernetein
REGISTRATION NUMBER: 37,280
REFERENCE/DOCKET NUMBER: RTS-0004
TELECHONE: (760) 931-9200
TELEFAX: (760) 603-3820
INFORMATION FOR SEQ ID NO: 55:
SEQUENCE CHARACTERISTICS:
SOFTWARE: Microsoft Word 97
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/106,038A
FILLING DATE: June 26, 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  911 TCTTTGGTCTTTGCCTTT 928
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 100.(
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                single
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STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                TYPE: nucleic acid
STRANDEDNESS: singl
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                    ;
US-09-106-038A-55
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                                                                                                                                                                                                                                                                                                                                                   GENERAL INCENTATION:
APPLICANT: Pavco, Pamela
APPLICANT: Pavco, Pamela
APPLICANT: Stinchcomb, James
APPLICANT: Stinchcomb, James
APPLICANT: Stinchcomb, Jame
TITLE OF INVENTION: METHOD AND REAGENT FOR THE
TITLE OF INVENTION: CONDITIONS RELATED TO LEVELS
TITLE OF INVENTION: OF VASCULAR ENDOTHELIAL
TITLE OF INVENTION: GROWTH PACTOR
NUMBER OF SEQUENCES: 8502
CORRESPONDENCE ADDRESS:
ADDRESSE: Lyon & Lyon
STREET: SQUENCE ADDRESS:
ATREET: SQUENCE ADDRESS:
ADDRESSE: Lyon & Lyon
STREET: SQUENCE ADDRESS:
ATREET: SQUENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: SQUENCE ADDRESS:
ATREET: SQUENCE ADDRESSEE
ATREET: SQUENCE ADDRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: LOS ANGELS
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: 8torage
COMPUTER: IBM COMPALIALE
COMPUTER: IBM P.C. DOS 5.0
SOFTWARE: World Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/0854,040
FILING DATE: January 11, 1996
CLASSIFTCATION: 5.4
PRIOR APPLICATION NUMBER: 60/005,974
FILING DATE: COCLOBE: 26, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
RECESTRATION NUMBER: 26, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
RECOMMUNICATION INFORMATION:
TELEFAX: (213) 955-040
TELEFAX: (213) 955-040
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
   APPLICANT: Ribozyme Pharmaceuticals, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 8
US-09-371-772B-3066/c
'S Sequence 3066, Application US/09371772B
; Patent No. 6566127
                                                                                                                                                                                                                                                      US-08-584-040-7257/c
; Sequence 7257, Application US/08584040
; Patent No. 6346398
                                                   952 ATGIATCGCTACCAACGG 969
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
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US-08-584-040-7257
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24.7%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 5.9;
Matches 18; Conservative 0; Mismatches 0; Indels
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US-09-106-038A-59/C

Sequence 59, Application US/09106038A

Patent No. 6007995

GENERAL INFORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSE: 18is Pharmaceuticals, Inc.
STREET: 2222 Faraday Avenue
CITY: Carlsbad
STREET: CA
COUNTRY: U.S.A.
ZIP: 92008
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch disk, 1.44 Mb
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: Microsoft Word 97
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/106,038A
FILING DATE: June 26, 1998
CLASSIFICATION NUMBER: 37.280
FILING PRANTION POR SEQ ID NO: 59:
SEQUENCE CHARACTERISTICS:
LENGTH: 18
OPERATING SYSTEM: Windows NT
SOSTWARE: Microsoft Word 97
CURRENT APPLICATION DATE:
APPLICATION DATE: US, 1998
FILING DATE: Unne 26, 1998
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: LAUREI Spear Bernstein
REGISTRATTON NUMBER: ATS-0004
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (760) 931-9200
TELEPHONE: (760) 603-3820
INFORMATION FOR SEQ ID NO: 58:
SEQUENCE CHARACTERISTICS:
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Matches 18; Conservative
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linear
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STRANDEDNESS: singl
TOPOLOGY: linear
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STRANDEDNESS: sing:
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TOPOLOGY:
US-09-106-038A-59
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Patent No. 5994069
GENERAL INFORMATION:
APPLICANT: Hall, Jeff G.
APPLICANT: Brow, March al.
TITLE OF INVENTION: Detection Of Nucleic Acids By Multiple
TITLE OF INVENTION: Sequential Invasive Cleavages
NUMBER OF SEQUENCES: 163
CORRESPONDENCE ADDRESS:
ADDRESSEE: Medlen & Carroll, LLP
STREET: 220 Montgomery Street, Suite 2200
CITY: San Francisco
STREET: California
COUNTRY: United States Of America
ZIP: 94104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
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                                                                                                                                                              STATE: Callicania
STATE: Callicania
ZIP: 94104
ZIP: 1BM PC Compatible
COMPUTER: IBM PC Compatible
SOFTWARE: Patentin Release #1.0, Version #1.30
SOFTWARE: Patentin Release #1.0, Version #1.30
ZURENT APPLICATION DATA:
APPLICATION NUMBER: US/08/757,653
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Ingolia, Diane E.
REGISTRATION NUMBER: FORS-02565
TELEPHONE: (415) 397-9338
INFORMATION FOR SEQ ID NO: 180:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 base pairs
TYPE: MICHOLIC acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER FRADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: END FO COMPATIBLE
COMPUTER: END FO COMPATIBLE
COPERATION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTION NUMBER: US/08/823,516
FILING DATE: 24-MAR-1997
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: PCT/US97/01072
              NUMBER OF SEQUENCES: 190
CORRESPONDENCE ADDRESS:
ADDRESSEE: Medlen & Carroll, LLP
STREET: 220 Montgomery Street, Suite 2200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
20.0%; Score 14.6; D
Best Local Similarity 81.0%; Pred. No. 31;
Matches 17; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLGGY: linear MOLECULE TYPE: other nucleic acid DESCRIPTION: /desc = "DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           917 GICTITGCCTTTTATCCCTCC 937
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                                                                                                                         CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-757-653-180
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APPLICANT: McSwiggen, Jim
APPLICANT: Escobed, Jaim
APPLICANT: Escobed, Jaim
APPLICANT: Escobed, Jaime
APPLICANT: Escobed, Jaime
TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
CURRENT FILING DATE: 1999-08-10
PRIOR APPLICATION NUMBER: US 60/005,974
PRIOR APPLICATION NUMBER: US 60/005,974
PRIOR APPLICATION NUMBER: US 68/584,040
PRIOR APPLICATION NUMBER: US 08/584,040
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US-09-068-319-5
i Sequence 5, Application US/09068319A
i Patent NO. 6277560
j GENERAL INFORMATION:
APPLICANT: Jean Marie Andrieu
j APPLICANT: Wei Lu
i TITLE OF INVENTION: METHOD AND KIT
ITLE OF INVENTION: METHOD AND KIT
FILE REFERENCE: 31736 PCT USA 072995
CURRENT APPLICATION NUMBER: US/09/068,319A
CURRENT FILING DATE: 1998-05-04
j EARLIER APPLICATION NUMBER: PCT/FR96/01736
j EARLIER FILING DATE: 1996-11-05
j EARLIER FILING DATE: 1996-11-05
j NUMBER OF SEQ ID NOS: 6
j NUMBER OF SEQ ID NOS: 6
j SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 20.5%; Score 15; DB 1; Length 23; Best Local Similarity 78.3%; Pred. No. 29; Matches 18; Conservative 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Indels
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US-08-757-653-180
US-08-757-653-180
Squence 180. Application US/08757653
GENERAL INFORMATION:
APPLICANT: Kaiser, Michael W.
APPLICANT: Lyamichev, Victor I.
APPLICANT: Lyamichev, Natasha
TITLE OF INVENTION: Cleavage Of Nucleic Acid Using
TITLE OF INVENTION: Thermostable FEN-1 Endonucleases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
21.1%; Score 15.4; Di
Best Local Similarity 94.1%; Pred. No. 17;
Matches 16; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA ORGANISM: Human Immunodeficiency Virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 910 ITCTITGGICTITGCCTITIAIC 932
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      921 TEGCCTTTTATCCCTCC 937
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TYPE: RNA
; ORGANISM: Mus sp.
US-09-371-772B-3066
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ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: APERICATION DATA:
APPLICATION NUMBER: US/08/758,314
FILING DATE: 02-DEC-1996
FLING APPLICATION DATA:
APPLICATION NUMBER: US 08/
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/
FILING DATE: 22-NOV-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/682,853
FILING DATE: 12-UL-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/599,491
FILING DATE: 24-UAN-1996
ATTONINY/AGRATI INFORMATION:
ANAME: TRONINY/AGRATION:
ANAME: TRONINY/AGRATION:
ANAME: TRONINY/AGRATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Generoce 119, Application US/08758314

Factor No. 6090606

GENERAL INFORMATION:

APPLICANT: Kaiser, Michael W.

APPLICANT: Lyamichev, Victor I.

APPLICANT: Lyamichev, Natasha

TITLE OF INVENTON: Improved Cleavage Agents

NUMBER OF SEQUENCES: 134

CORRESPONDENCE ADDRESS:

ADDRESSEE: Addlen & Carroll, LLP

STREET: 220 Montgomery Street, Suite 2200

CITY: San Francisco

STATE: California

CONNTR: United States Of America
                  APPLICATION NUMBER: US 08/682,853
FILING DATE: 12-UUL-1996
PRIOR APPLICATION DATA: 12-UUL-1996
APPLICATION NUMBER: US 08/59,491
FILING DATE: 24-JAN-1996
ATTORNEY,AGENT INFORMATION:
NAME: Ingolia, Diane E.
REGISTRATION NUMBER: 40,027
REFERENCE/DOCKET NUMBER: FORS-02574
TELEPHONE: (415) 705-8410
TELEPHONE: (415) 397-8338
INFORMATION FOR SEQ ID NO: 119:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 base pairs
TYPE: nucleic acid
STRANDENBESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Ingolia, Diane E.
REGISTRATION NUMBER: 40,027
REFERENCE/DOCKET NUMBER: FORS-02575
TELECOMMUNICATION INPORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     917 GICITIGCCITITATCCCTCC 937
PRIOR APPLICATION DATA:
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CITY: San Francisco
CONTRY: United States Of America
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 12
US-08-759-038-119
is genence 119, Application US/08759038
genence 119, Application US/08759038
genence 119, Application US/08759038
genence No. 6090543
GENERAL INFORMATION:
APPLICANT: Hall, Jeff G.
APPLICANT: Hall, Jeff G.
APPLICANT: Brow, Mary Ann D.
APPLICANT: Brow, Mary Ann D.
TILLE OF INVENTION: Cleavage Of Nucleic Acids
NUMBER OF SEQUENCES: 134
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/759,038
FILING DATE: 02-DEC-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/758,314
FILING DATE: 02-DEC-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/756,386
FILING DATE: 29-NOV-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/682,853
FILING DATE: 12-JUL-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: other nucleic acid DESCRIPTION: /desc = "DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              917 GICITIGCCTTTTAICCCTCC 937
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CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION UMMER: US 01
FILING DATE: 29-NOV-1996
21-JAN-1997
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Gaps
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                                                                                                                                                                                 ö
                                                                                                                                  Length 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 21;
                                                                                                                                                                                 4; Indels
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                                                                                                                                    DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Kaiser, Michael W.
APPLICANT: Lyamichev, Victor I.
APPLICANT: Lyamichev, Natasha
TITLE OF INVENTION: Lyamichev, Natasha
TITLE OF INVENTION: Lyamichev, Natasha
FILE REFERENCE: FORS-03755
CURRENT FAPLICATION NUMBER: US/09/308,825A
CURRENT FILING DATE: 1999-10-08
PRIOR PILING DATE: 1996-110-08
PRIOR APPLICATION NUMBER: 08/757,653
PRIOR PELING DATE: 1996-112-0
PRIOR PELING DATE: 1996-112-0
PRIOR PELING DATE: 1996-112-0
PRIOR FILING DATE: 1997-11-29
NUMBER OF SEQ ID NOS: 188
                                                                                                                                                                                                                                                                                                                                                                       Sequence 119, Application US/09684938
Sequence 119, Application US/09684938
Patent No. 655357
GENERAL INFORMATION:
APPLICANT: Edser, Michael W.
APPLICANT: Lyamichev, Victor I.
APPLICANT: Lyamichev, Natshar
TITLE OF INVENTION: Improved Cleavage Agents
TITLE OF INVENTION: Improved Cleavage Agents
FILE REFERENCE: FORS 03755
CURRENT FILING DATE: 2000-10-06
FRIOR APPLICATION NUMBER: 08/757
FRIOR FILING DATE: 1999-05-25
FRIOR PILING DATE: 1999-05-25
FRIOR PELICATION NUMBER: 08/757, 653
FRIOR PILING DATE: 1999-05-25
FRIOR APPLICATION NUMBER: 08/758, 314
FRIOR PILING DATE: 1996-11-29
FRIOR APPLICATION NUMBER: DE/US97/21783
FRIOR FILING DATE: 1996-11-29
NUMBER OF SEQ ID NOS: 188
SOFTWARE PATENTIN VET: 2.0
                                                                                                                                    Score 14.6; D
Pred. No. 31;
0; Mismatches
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. Sequence 119. Application US/09308825A
. Patent No. 6562611
. GENERAL INFORMATION:
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                                                                                                                                    Query Match
Best Local Similarity 81.0%;
Matches 17; Conservative
                       ENGTH: 21
TYPE: DNA
CRGANISM: Hepatitis B virus
US-09-306-420C-16
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Matches 17; Conserv
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US-09-684-938-119
SEQ ID NO 16
LENGTH: 21
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APPLICANT: LOCAZNINI, STEPHEN A
APPLICANT: BARTHOLOWEUSZ, ANGELINE I
APPLICANT: BARTHOLOWEUSZ, ANGELINE I
APPLICANT: AYE, THEIN T
APPLICANT: DEMAN, OLDERT A
TITLE OF INVENTION: UIRAL VARIANTS AND METHODS FOR DETECTING SAME
FILE REFERENCE: 2551-28
CURRENT APPLICATION NUMBER: US/09/306,420C
CURRENT FILING DATE: 1999-05-06
PRIOR PELICATION NUMBER: PCT/AU97/00520
PRIOR APPLICATION NUMBER: PO3519
PRIOR FILING DATE: 1996-11-08
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                                                                                                                                                                                                                                                  Cuery Match 20.0%; Score 14.6; DB 1; Best Local Similarity 81.0%; Pred. No. 31; Matches 17; Conservative 0; Mismatches 4;
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20.0%; Score 14.6;
Best Local Similarity 81.0%; Pred. No. 31
Matches 17; Conservative 0; Mismatche
TELEFAX: (415) 397-8338
; INFORMATION FOR SEQ ID NO: 119:
SEQUEBNCE CHARACTERISTICS:
LENGTH: 21 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "DNA"
US-08-758-314-119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Sequence 12, Application US/09306420C; Patent No. 6555311; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 15
NS-09-304-20C-16/c
Sequence 16, Application US/09306420C
Patent No. 6555311
                                                                                                                                                                                                                                                                                                                                        917 GICITIGCCTTITAICCCICC 937
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA ORGANISM: Hepatitis B virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS:
SOFTWARE: Patentin Ve
SEQ ID NO 12
LENGTH: 21
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APPLICANT: LOCARNIJ
APPLICANT: BARTHOL(
                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 14
US-09-306-420C-12
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; TYPE: DNA
; ORGANISM: Human
US-09-249-730-134
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US-09-249-247-134
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                                                                                                                                                                                                                 OTHER INFORMATION: Description of Artificial Sequence: Synthetic
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APPLICANT: Wright, Jim A.
APPLICANT: Wright, Jim A.
APPLICANT: Young, Aiping H.
TITLE OF INVENTION: ANTITUMOR ANTISENSE SEQUENCES DIRECTED
TITLE OF INVENTION: AGAINST RIBONUCLEOTIDE REDUCTASE
NUMBER OF SEQUENCES: 163
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                          Query Match
20.0%; Score 14.6; DB 1; Length 21;
Best Local Similarity 81.0%; Pred. No. 31;
Matches 17; Conservative 0; Mismatches 4: Tndele
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Farminton Hills
COUNTRY: Wichigan
STATE: Michigan
COUNTRY: US
COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM CCOMpatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/904,901
FILING DATE:
CLASSIFICATION: 514
ATTORNEY APAGENT INFORMATION:
NAME: Kohn, Kenneth I.
REGISTRATION NUMBER: 0227.0004
TELEPHONE: (248) 539-5050
TELEPHONE: (248) 539-5055
INFORMATION FOR SEQ ID NO: 134:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: MUCHAIC ACID STORES TO THE TYPE: 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
ANTI-SENSE: YES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 19
US-09-249-730-134/c
; Sequence 134, Application US/09249730
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US-08-904-901-134/c
; Sequence 134, Application US/08904901
; Patent No. 5998383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 GCCTATGCCCTTTATTCCTCC 21
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                                                                                                                                           ORGANISM: Artificial Sequence FEATURE:
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 119
LENGTH: 21
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Best Local Similarity
Matches 15; Conserv
                                                                                                                                                                                                                                                    US-09-308-825A-119
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                                                                                                                DNA
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NESULT 20

US-09-149-247-134/C

Sequence 134, Application US/09249247

Sequence 134, Application US/09249247

Sequence 134, Application US/09249247

Sequence 134, Application US/09249247

GENERAL INFORMATION:

APPLICANT: WIGHT, UM A.

TITLE OF INVENTION: Antitumor Antisense Sequences Directed Against R1 and TITLE OF INVENTION: Accomponents of Ribonucleotide Reductase

TITLE OF INVENTION: August H.

TITLE OF INVENTION: BAPLICATION NUMBER: US/09/249,247

CURRENT APPLICATION NUMBER: US 60/023,040

EARLIER FILING DATE: 1996-08-02

EARLIER FILING DATE: 1997-08-01

EARLIER FILING DATE: 1997-08-01

MUMBER OF SEQ ID NOS: 220

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 134

TENTION OF 134
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GENERAL INFORMATION:
APPLICANT: WRIGHT, Jim A.
APPLICANT: WRIGHT, Jim A.
APPLICANT: VOUG, Alping H.
TITLE OF INVENTION: Altitumor Antisense Sequences Directed Against R1 and
TITLE OF INVENTION: R2 Components of Ribonucleotide Reductase
FILE REFERENCE: 032396-040
CURRENT APPLICATION NUMBER: US/09/249,730
CURRENT FILING DATE: 1999-02-11
NUMBER OF SEQ ID NOS: 220
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 134
LENGTH: 20
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Patent No. 6258790
GENERAL INFORMATION:
APPLICANT: Bennett, C. Frank
APPLICANT: Cowsert, Lex M.
TITLE OF INVENTION: ANTISENSE MODULATION OF INTEGRIN 4 EXPRESSION
FILE REFERENCE: ISPH-0390
CURRENT APPLICATION UMBER: US/09/377,309B
CURRENT FILING DATE: 1999-08-19
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19.7%; Score 14.4; I
Best Local Similarity 93.8%; Pred. No. 32;
Matches 15; Conservative 0; Mismatches
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Best Local Similarity 93.8
Matches 15, Conservative
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TYPE: DNA
ORGANISM: Chlamydia pneumoniae
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Best Local Similarity 80.0%;
Matches 16; Conservative
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ORGANISM: Artificial Sequence
FEATURE:
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US-09-198-452A-4603
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US-09-792-251-23/c
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                                                                                                                                                                                    TYPE: DNA
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18.6%; Score 13.6; DB 1; Length 20;
Best Local Similarity 80.0%; Pred. No. 46;
Matches 16; Conservative 0; Mismatches 4; Indels
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APPLICANT: MCHIBDA, EISUKE
APPLICANT: MCHIBDA, EISUKE
APPLICANT: MATGUCHI, Tetsuo
APPLICANT: MATGUCHI, Tetsuo
TITLE OF INVENTION: No. 6465618e1 MAPK Kinase
FILE REFERENCE: 98-1027US
CURRENT APPLICATION NUMBER: US/09/446,754
CURRENT FILING DATE: 1999-12-27
PRIOR APPLICATION NUMBER: UP 9-193207
PRIOR FILING DATE: 1997-07-03
PRIOR PILING DATE: 1997-07-03
PRIOR APPLICATION NUMBER: PCT/UP98/03016
PRIOR PILING DATE: 1998-07-03
NUMBER: PRIOR FILING DATE: 1998-07-03
NUMBER: PRIOR FILING DATE: 1998-07-03
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Patent No. 6465618
GENERAL INFORMATION
GENERAL INFORMATION
GENERAL INFORMATION
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GENERAL INFORMATION
GENERAL MARSUZAKI, Osamu
TILLE OF INVENTION: No. 6465618e1 MAPK Kinase
FILE REFERENCE: 98-10270S
GURRENT APPLICATION NUMBER: US/09/446,754
GURRENT APPLICATION NUMBER: JP 9-367640
FRIOR FILING DATE: 1997-12-26
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80.0%; Pred. No. 46;
tive 0; Mismatches
                                                                                                                                                                                    CTHER INFORMATION: antisense sequence US-09-377-309-87
  09/166,203
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EARLIER APPLICATION NUMBER: 09/:
EARLIER FILING DATE: 1998-10-05
NUMBER OF SEQ ID NOS: 99
                                                                                                                  TYPE: DNA
ORGANISM: Artificial Sequence
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Best Local Similarity 80.0
Matches 16; Conservative
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US-09-446-754-11
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US-09-446-754-17
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LENGTH: 20
                                                                    SEQ ID NO 87
LENGTH: 20
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Sequence 4603, Application US/09198452A

Sequence 4603, Application US/09198452A

Sequence 4603, Application US/09198452A

Sequence 100, 6559294

GENERAL INFORMATION:

APPLICANT: Griffals, R.

APPLICANT: Griffals, R.

TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prever TITLE OF INVENTION: and treatment of infection

FILE REFERENCE: 9710-003-999

CURRENT APPLICATION NUMBER: US/09/198,452A

CURRENT APPLICATION NUMBER: 1998-11-24

NUMBER OF SEQ ID NOS: 6849

LENGTH: 20
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Patent No. 6664074

GENERAL INFORMATION:
APPLICAMT: Youngman, Philip
APPLICAMT: Youngman, Duz-Maria
TITLE OF INVENTION: USE OF YACM AND YOEJ, ESSENTIAL BACTERIAL GENES AND POLYPEPTIDES:
TITLE OF INVENTION: USE OF YACM AND YOEJ, ESSENTIAL BACTERIAL GENES AND POLYPEPTIDES:
FILLE OF INVENTION: USE OF YACM AND YOEJ, ESSENTIAL BACTERIAL GENES AND POLYPEPTIDES:
FILLE OF INVENTION: USE OF YACM AND YOEJ, ESSENTIAL BACTERIAL GENES AND POLYPEPTIDES:
FILLE OF INVENTION: USE OF YACM AND YOEJ, ESSENTIAL BACTERIAL GENES AND POLYPEPTIDES:
FILLE OF INVENTION: USE OF YACM AND YOEJ, ESSENTIAL BACTERIAL GENES AND POLYPEPTIDES
FILLE OF INVENTION: USE OF YACM AND YOEJ, ESSENTIAL BACTERIAL GENES AND POLYPEPTIDES
FILLE PREFERENCE: DOLDER AND YOEJ, ESSENTIAL BACTERIAL GENES AND POLYPEPTIDES
FILLE OF INVENTION: USE OF YACM AND YOEJ, ESSENTIAL BACTERIAL GENES AND POLYPEPTIDES
FILLE OF INVENTION: USE OF YACM AND YOEJ, ESSENTIAL BACTERIAL GENES AND POLYPEPTIDES
FILLE PREFERENCE: DOLDER AND YOEJ, ESSENTIAL BACTERIAL GENES AND POLYPEPTIDES
FILLE OF INVENTION: USE OF YACM AND YOEJ, ESSENTIAL BACTERIAL GENES AND POLYPEPTIDES
FILLE OF INVENTION: USE OF YACM AND YOEJ, ESSENTIAL BACTERIAL GENES AND POLYPEPTIDES
FILLE OF INVENTION: USE OF YACM AND YOEJ, ESSENTIAL BACTERIAL GENES AND POLYPEPTIDES
FILLE OF INVENTION: USE OF YACM AND YOEJ, ESSENTIAL BACTERIAL GENES AND POLYPEPTIDES
FILLE OF INVENTION: USE OF YACM AND YOEJ, ESSENTIAL BACTERIAL GENES AND POLYPEPTIDES
FILLE OF INVENTION: USE OF YACM AND YOEJ, ESSENTIAL BACTERIAL GENES AND POLYPEPTIDES
FILLE OF INVENTION: USE OF YACM AND YOUNGER AND YOUN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: Description of Artificial Sequence: 3' end primer used in OTHER INFORMATION: Example 2 for amplifying the sequence inbetween the 5' and OTHER INFORMATION: 3' sequences of human MKK7
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Best Local Similarity 80.0%; Pred. No. 46;
Matches 16; Conservative 0; Mismatches 4;
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Pred. No. 46;
0; Mismatches
PRIOR APPLICATION NUMBER: JP 9-193207
PRIOR FILING DATE: 1997-07-03
PRIOR PAPLICATION NUMBER: PCT/JP98/03016
PRIOR FILING DATE: 1998-07-03
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patentin Ver: 2.1
SEQ ID NO 17
LENGTH: 20
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US-09-531-000-29
                                                                                                                                                                                                                                                                                                                                                                   GENERAL INCORNATION:
APPLICANT: C. Frank Bennett
APPLICANT: C. Frank Bennett
APPLICANT: David Spector
APPLICANT: Jacqueline Wyatt
TITLE OF INVENTION: ANTISENSE MODULATION OF SR-CYP EXPRESSION
FILE REPERENCE: RTS-0145
CURRENT APPLICATION NUMBER: US/09/706,197
CURRENT FILING DATE: 2000-11-03
SEQ ID NO 37
LENGTH: 20
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18.4%; Score 13.4; DB 1; Length 20;
Best Local Similarity 93.3%; Pred. No. 50;
Matches 14; Conservative 0; Mismatches 1; Indels
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                                                                         Length 20;
                                                                                                                   Indels
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| Patent No. 6461810
| GENERAL INPORMATION:
| APPLICANT: FRESCO, Jacques R.
| TITLE OF INVENTION: FRIPLEX IN-SITU HYBRIDIZATION
| FILE REPERENCE: 2448-103
| CURRENT APPLICATION NUMBER: US/09/531,000
| PRIOR PILICA DATE: 1998-11-10
| PRIOR APPLICATION NUMBER: PCT/US98/23765
| PRIOR APPLICATION NUMBER: 80/64,997
| PRIOR FILING DATE: 1998-11-10
| PRIOR FILING DATE: 1998-11-10
| SEQ ID NOS: 77
| PRIOR FILING DATE: 1997-11-10
| SEQ ID NOS: 77
| SEQ ID NOS: 77
| SEQ ID NOS: 77
                                                                  Query Match
18.6%; Score 13.6; DB 1;
Best Local Similarity 80.0%; Pred. No. 46;
Matches 16; Conservative 0; Mismatches 4;
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COTHER INFORMATION: Antisense Oligonucleotide
US-09-706-197-77
                                                                                                                                                                905 TCATTTTCTTTGGTCTTTGC 924
                                                                                                                                                                                                                                                                                                     US-09-706-197-77; Sequence 77, Application US/09706197; Patent No. 6475797
; OTHER INFORMATION: primer for PCR
US-09-792-251-23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA ORGANISM: Artificial Sequence
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US-09-531-000-29
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US-09-198-452A-2716/c

Sequence 2716, Application US/09198452A

Sequence 2716, Application US/09198452A

Sequence 2716, Application US/09198452A

Sequence 2716, Application US/09198452A

GENERAL INFORMATION:

APPLICANT: Griffais, R.

TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments

TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prever

TITLE OF INVENTION: and treatment of infection

FILE REFERENCE: 9710-003-999

CURRENT APPLICATION NUMBER: US/09/198,452A

CURRENT FILING DATE: 1998-11-24

NUMBER OF SEQ ID NOS: 6849
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (BPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/607,384A
FILING DATE: 77-FEB-1996
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Staphylococcus epidermidis
STRAIN: ATCC 12228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY AGENT INFORMATION:
NAME: BYRNE, THOMAS E
REGISTRATION NUMBER: 32,205
REFERENCE/DOCKET NUMBER: 227-75
TELECOMMUNICATION INFORMATION:
TELEFAX: (703) 816-4000
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 base pairs
TYPE: mucleic acid
STRANEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           929 TATCCCTCCTCTTCATTG 946
1 TTCTCCTTTCTCTTCAT 18
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MOLECULE TYPE: DNA (genomic)
HYPOTHATICAL: NO
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19 rarccrcarcrrcarag
                                                                                                                                                                                                                                                                                                                                                              STREET: 1100 NORTH GLE
CITY: ARLINGTON
STATE: VIGGINA
COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy di
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927 TITAICCICCICTICAL 944

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APPLICANT: Cohen, Daniel
APPLICANT: Blumenfeld, Marta
APPLICANT: Chumakov, Ilya
TITLE OP INVENTION: Biallelic markers for use in constructing a high density...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 1; Length 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2; Indels
                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: Antisense Oligonucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17.5%; Score 12.8; E
87.5%; Pred. No. 58;
iive 0; Mismatches
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US-09-422-978-10295/c
US-09-422-978-10295, Application US/09422978
; Patent No. 6537751
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 8, Application US/09267423
Patent No. 6395878
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                927 TITAICCTICTIC 942
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                                                                                                                                                                                                                                                                                                     ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17 chiggarchiráccar
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Best Local Similarity 87.5
Matches 14; Conservative
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; ORGANISM: Homo sapiens
US-09-267-423-8
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               RESULT 31
US-09-205-144-36
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                                                                                                    Score 13.2; DB 1; Length 20;
Pred. No. 54;
0; Mismatches 3; Indels
                                                                                                                                                                                                                                                               RESULT 30

US-08-239-431A-8/c
Sequence B, Application US/08239431A
Patent No. 5716835
GENERAL INFORMATION:
APPLICANT: Regan, John W.
APPLICANT: Woodward, David F.
TITLE OF INVENTION: NOVEL HUMAN EP PROSTAGLANDIN RECEPTOR
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 1; Length 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Knobbe, Martens, Olson and Bear
STREET: 620 Newport Center Drive 16th Floor
CITY: Newport Beach
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ouery Match 17.5%; Score 12.8; Dest Local Similarity 87.5%; Pred. No. 58; Best Local Similarity 0; Mismatches 14; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER REDABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/239,431A
FILING DATE: 05-MAY-1994
CLASSIFICATION 0435
PRIOR APPLICATION UMBER:
                                                                                                                                                                              917 GTCTTTGCCTTTTATCCC 934
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29,622
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-235-8550
TELEFAX: 619-235-0176
                                                                                                                                                                                                                  18 GICTTIGCICCTIATCCC 1
                                   TYPE: DNA
ORGANISM: Chlamydia pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          912 CTTTGGTCTTTGCCTT 927
                                                                                                        Query Match
Best Local Similarity 83.3%;
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: ISTABLISH: Ned A
REGISTRATION NUMBER: 29,6
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17 crieccicririccar 2
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SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
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MOLECULE TYPE: CI
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; ORIGINAL SOURCE:
US-08-239-431A-8
                                                                      US-09-198-452A-2716
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           92660
SEQ ID NO 2716
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GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: C. Frank Bennett
APPLICANT: Lex M. Cowsert
APPLICANT: Lex M. Cowsert
TITLE OF INVENTION: ANTISENSE MODULATION OF CELLULAR INHIBITOR OF APOPTOSIS-2 EXPRESS)
TITLE REFERENCE: RTS-0021
FILE REFERENCE: RTS-0021
CURRENT APPLICATION NUMBER: US/09/205,144
NUMBER OF SEQ ID NOS: 47
LENGTH: 18
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APPLICANT: Cunningham, Bruce A.
TITLE OF INVENTION: CONTAINING FIBRONECTIN TYPE III REPEATS AND METHODS OF USE
NUMBER OF SEQUENCES: 77
CORRESPONDENCE ADDRESS:
ADDRESSEE: The Scripps Research Institute
STREET: 10550 No. 6313265th Torrey Pines Road, TPC-8
CITY: La Johla
STATE: California
COUNTRY: U.S.
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              Gaps
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PCT-US95-07744A-32/C
Sequence 32, Application PC/TUS9507744A
Sequence 32, Application PC/TUS9507744A
GENERAL INFORMATION:
TITLE OF INVENTION: Plant Genes for Sensitivity to Ethylene
TITLE OF INVENTION: and Pathogens
NUMBER OF SEQUENCES: 82
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz & Norris
STREET: One Liberty Place, 46th floor
CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17.0%; Score 12.4; DB 1; Length 18; 92.9%; Pred. No. 68; ive 0; Mismatches 1; Indels
                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:

WEDIUM TYPE: Floppy disk

WEDIUM TYPE: Floppy disk

COMPUTER: IBM PC Compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/506,296B

FILING DATE: 24-JUL.1995

ATTORNEY/AGENT INPORMATION:

NAME: Fitting, Thomas

REGISTRATION NUMBER: 34.163

REGISTRATION NUMBER: 15RI 488.0

TELEPHONE: (619) 554-2937

TELEPHONE: (619) 554-2937

INFORMATION FOR SEQ ID NO: 12:

SEQUENCE CHARACTERISTICS:

**TOMATH: 18 base pairs
              Mismatches
                                                                                                                                                                                                                                                 Sequence 12, Application US/08506296B; Patent No. 6313265; GENERAL INFORMATION:
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                                                                 933 CCTCCTCTTCATTG 946
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Best Local Similarity 92.99
Matches 13; Conservative
              Matches 13; Conservative
                                                                                                                 17 ccrccrcrrgarid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
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NAME/KEY: primer_bind

CONSTIDENT:

CONSTANDED 1..19

CONSTANDED 1..19

CONSTANDED 10.0966 for SEQ 2430, in complem US-09-422-978-10295
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Sequence 32, Application US/08261822A
Fatent No. 5865053
Fatent No. 5865053
FATENT NORMATION:
APPLICANT: Ecker, Joseph R. et al.
TITLE OF INVENTION: Plant Genes for Sensitivity to Ethylene
TITLE OF INVENTION: and Pathogens
NUMBER OF SEQUENCES: 82
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz & No. 5650553ris
STREET: One Liberty Place, 46th floor
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103
COMPUTER FRADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: DATASET PLOSS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ouery Match
17.5%; Score 12.8; DB 1; Length 19;
Best Local Similarity 87.5%; Pred. No. 61;
Matches 14; Conservative 0; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRALING STRIEM: TC-LOOF MAS-LOOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/261,822A
FILING DATE: 17-JUN-1994
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Beardell, Loos
TELEPHONE: (215) 568-34.93
ITELEPHONE: (215) 568-34.99
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: lines aingle
FILE REFERENCE: GENSET.020CP1
CURRENT APPLICATION NUMBER: US/09/422,978
CURRENT FILING DATE: 1999-10-20
EARLIER APPLICATION NUMBER: US 09/298,850
EARLIER FILING DATE: 1999-04-21
EARLIER FILING DATE: 1999-04-21
EARLIER PILING DATE: 1998-11-23
EARLIER FILING DATE: 1998-11-23
EARLIER FILING DATE: 1998-04-21
EARLIER FILING DATE: 1998-04-21
NUMBER OF SEQ ID NOS: 11796
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                                                                                                                                                                                                                                                                                                                              TYPE: DNA
ORGANISM: Homo Sapiens
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Best Local Similarity
                                                                                                                                                                                                                                                                        SEQ ID NO 10295
LENGTH: 19
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US-08-261-822A-32
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DB 1; Length 17;
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                                                                                                                                         Sequence 65, Application US/08373124A

Patent No. 5646042

GREEAL INFORMATION:
APPLICANT: Stinchcomb, Dan T.
APPLICANT: Braper, Kenneth
APPLICANT: McSwiggen, James
APPLICANT: McSwiggen, James
APPLICANT: McSwiggen, James
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
TITLE OF INVENTION: TREATMENT OF RESTENOSIS AND
TITLE OF INVENTION: CANCER USING RIBOZYMES
NUMBER OF SEQUENCES: 2627
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 41.2%; Pred. No. 70;
Matches 7; Conservative 7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Los Angeles
COUNTY: Los Angeles
COUNTY: U.S.A.
ZIF: 90071
COMPUTER: READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: STORME
COMPUTER: IBM Compatible
OPERATION SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: WORD Perfect 5.1
CURRENT APPLICATION DATA:
PRING DATE: January 13, 1995
FILING DATE: MAY 18, 1994
APPLICATION NUMBER: 08/192, 943
FILING DATE: MAY 18, 1994
APPLICATION NUMBER: 07/991,132
FILING DATE: PEDRUARY 7, 1994
APPLICATION NUMBER: 07/997,132
FILING DATE: ANGUST 10,992
ATTORNEY AGENT INFORMATION:
NAME: WASDLICKET NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 209/035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 39
US-08-435-628-65
; Sequence 65, Application US/08435628
                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 65:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              910 TTCTTTGGTCTTTGCCT 926
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917 GICTITGCCTTTTA 930
                                            19 Grerrigecerria 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TOPOLOGY: linear
US-08-373-124A-65
                                                                                                                                    US-08-373-124A-65
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US-09-422-978-7250/c
; Sequence 7250, Application US/09422978
; Patent No. 6537751
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Chen, Daniel
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallellc markers for use in constructing a high density...
; TILE OF INVENTION: Biallellc markers for use in constructing a high density...
; TILE OF INVENTION: Biallellc markers for use in constructing a high density...
; FILE REFERENCE: GENSET.020CP1
; CURRENT APPLICATION NUMBER: US/09/422, 978
; CURRENT FILING DATE: 1999-04-21
; EARLIER PILING DATE: 1999-04-21
; EARLIER PILING DATE: 1998-04-21
; RARLIER PILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 7250
LENGTH: 19
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1 LOCATION: 1..19

2 OTHER INFORMATION: upstream amplification primer 99-3217 for SEQ 3316,

US-09-422-978-7250
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17.0%; Score 12.4; DB 1; Length 19;
Best Local Similarity 92.9%; Pred. No. 72;
Matches 13; Conservative 0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Indels
              COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 12.4; DB
Pred. No. 68;
0; Mismatches
                                                                                                                                                             опывк: PCT/US95/07744A
15-JUNE-1995
1;
                                                                                                                                                                                   APPLICATION COLLABORATION PRING DATE: 15-JUNE-1995
CLASSIFICATION: 15-JUNE-1995
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 08/261,822
FILING DATE: June 17, 1994
ATTORNEY/AGENT INFORMATION:
NAME: Beardell, Lori Y.
REGISTRATION NUMBER: 34,293
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEFRAX: (215) 568-3499
INFORMATION FOR SEQ ID NO: 32: 25QUENCE CHARACTERISTICS: LENGTH: 18 base pairs
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17.0%;
92.9%;
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Best Local Similarity 92.9°
Matches 13; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PCT-US95-07744A-32
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       COUNTRY:
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TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions ReTILE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor FILE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor CURRENT APPLICATION NUMBER: US/09/31,772B

CURRENT FILING DATE: 1999-08-10

PRIOR PILING DATE: 1999-08-10

PRIOR PILING DATE: 1995-10-26

PRIOR FILING DATE: 1996-01-08

NUMBER OF SEQ ID NOS: 14225

SEQ ID NO 5632

LENGTH: 17
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; Sequence 2, Application US/08384324
; Patent No. 5844110
; GENERAL INFORMATION:
; APPLICANT: Gold, Barry I.
; TITLE OF INVENTION: Synthetic Triple Helix-Forming Compounds
; TOMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dann, Dorfman, Herrell and Skillman
; STREET: 1601 Market Street, Suite 720
; CITY: PALladelphia
; STATE: PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
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ZIF: 19103
COMPUTER PLABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/384,324
FILING DATE: 31-JAN-1995
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: REGG, Janet E.
REGISTRATION NUMBER: 36,252
REGISTRATION NUMBER: 36,252
REGISTRATION NUMBER: 36,252
REGISTRATION NUMBER: 36,262
TELEPAX: (215) 563-4100
TELEPAX: (215) 563-4104
TELEPAX: (215) 563-404
INFORMATION FOR SED ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TYPE: Nucleic acid
TYPE: Nucleic acid
STRANDEDNESS: Single
TYPE: Nucleic acid
TYPE: Nucleic acid
TYPE: Nucleic acid
STRANDEDNESS: Single
TYPE: Nucleic acid
TYPE
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Best Local Similarity 29.4'
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: RNA
CONGANISM: Homo sapiens
US-09-371-772B-5632
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Query Match 16.7%; Score 12.2; D
Best Local Similarity 41.2%; Pred. No. 70;
Matches 7; Conservative 7; Mismatches
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US-09-371-772B-5632
Sequence 5632, Application US/09371772B
Patent No. 6566127
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.; APPLICANT: Pavco, pam
APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: Stinchcomb, Dan
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REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 209/035
TELEPHONE: (213) 489-1600
TELEFA: (213) 955-0440
TELEEX: (7-3510
TELEX: 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             910 TICTTIGGICTTIGCCT 926
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US-08-435-628-65
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APPLICANT: Cohen, Daniel
APPLICANT: Cohen, Daniel
APPLICANT: Cohen, Daniel
APPLICANT: Chumarfeld, Marta
APPLICANT: Chumarkov, Ilya
TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
FILE REFERENCE: GENSET.020CP1
CURRENT PRILING DATE: 1999-10-20
BARLIER APPLICATION NUMBER: US 09/298,850
BARLIER PILING DATE: 1999-04-21
EARLIER FILING DATE: 1999-04-21
EARLIER FILING DATE: 1998-11-23
EARLIER FILING DATE: 1998-11-23
EARLIER FILING DATE: 1998-04-21
NUMBER OF SEQ ID NOS: 11796
SEQ ID NOS: 11796
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; LOCATION: 1..18 —
; OTHER INFORMATION: upstream amplification primer 99-2636 for SEQ 3242,
US-09-422-978-7176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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Sequence 2, Application PC/TUS9601473
GENERAL INFORMATION:
APPLICANT: University of Nebraska, Board of Regents
APPLICANT: Gold, Barry I.
TILLE OF INVENTION: Synthetic Triple Helix-Forming Compounds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
16.7%; Score 12.2; D
Best Local Similarity 82.4%; Pred. No. 74;
Matches 14; Conservative 0; Mismatches
CURRENT APPLICATION NUMBER: US/09/422,978
CURRENT FILING DATE: 1999-10-20
EARLIER APPLICATION NUMBER: US 09/298,850
EARLIER FILING DATE: 1999-04-21
EARLIER FILING DATE: 1998-111-23
EARLIER FILING DATE: 1998-04-21
EARLIER FILING DATE: 1998-04-21
NUMBER OF SEQ ID NOS: 11796
EARLIER FILING DATE: 1998-04-21
NUMBER OF SEQ ID NOS: 11796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 7176, Application US/09422978 Patent No. 6537751 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     929 TATCCTCCTCTTCATT 945
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Best Local Similarity 82.4%;
Matches 14; Conservative
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                                                                                                                                                                                                                                                                  TYPE: DNA
ORGANISM: Homo Sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
ORGANISM: Homo Sapiens
                                                                                                                                                                                                                                                                                                                                    NAME/KEY: primer_bind
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US-09-422-978-7176/c
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                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: VAN DOORN, Leen-Jan et al.
APPLICANT: VAN DOORN, Leen-Jan et al.
TITLE OF INVENTION: Detection and identification.
TITLE OF INVENTION: Specific reverse hybridization.
FILE REFERENCE: 3501-0101P
CURRENT APPLICATION NUMBER: US/09/527,030G
CURRENT APPLICATION NUMBER: US/09/527,030G
SUPPLIES OF SEQ ID NOS: 497
SOFTWARE: Patentin version 3.0
SEQ ID NO 108
LENGTH: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; OTHER INFORMATION: Type specific probe derived from the Human Papillomavirus (HPV) US-09-527-030G-108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 44
US-054-422-978-5922/c
105-054-22-978-5922/c
5 Sequence 5922, Application US/09422978
5 Sequence 5922, Application US/09422978
5 Patent No. 6537751
5 Patent No. 6537751
5 APPLICANT: Choren, Daniel
5 APPLICANT: Blumenfeld, Marta
7 APPLICANT: Chumakov, Ilya
7 TTLE OF INVENTION: Biallelic markers for use in constructing a high density...
5 FILE REFERENCE: GENSET.020CP1
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Patent No. 649213
GRNERAL INFORMATION:
APPLICANT: Lex M. Cowsert
TITLE OF INVENTION: ANTISENSE MODULATION OF CYCLIN D2 EXPRESSION FILE REFERENCE: RTS-0275
CURRENT APPLICATION NUMBER: US/09/920,760
CURRENT FILING DATE: 2001-08-01
NUMBER OF SEQ ID NOS: 89
SEQ ID NO 89
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 1; Length 18;
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.. OTHER INFORMATION: Antisense Oligonuclectide
US-09-920-760-89
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Pred. No. 74;
                                                                                                                                                                       Sequence 108, Application US/09527030G Patent No. 6482588
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82.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14; Conservative
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Best Local Similarity
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Best Local Similarity
Matches 14; Conserv
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US-09-920-760-89/c
                                                                                                                                                        US-09-527-030G-108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PALLICANT: WANG, ALICE M.; DOYLE, MICHAEL V.; MARK, DAVID F.
TITLE OF INVENTION: QUANTITION OF NUCLEIC ACIDS USING THE
POLYMERASE CHAIN REACTION
NUMBER OF SEQUENCES: 64
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/413,623
FILING DATE: 28-SEP-1989
PRIOR PAPLICATION DATA:
PILING DATE: 21-AUG-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16.7%; Score 12.2; DB 1; Length 18; 82.4%; Pred. No. 74; tive 0; Mismatches 3; Indels
                              ONDERSPONDENCE ADDRESS:
ADDRESSEE: Dann, Dorfman, Herrell and Skillman STREET: 1601 Market Street Suite 720
CITY: Philadelphia STREET 1601 Market Street Suite 720
STREET: 1601 Market Street Suite 720
STATE: PA
ZIP: 19103-2307
ZIP: 19103-2307
ZIP: 19103-2307
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: PA EACHLIN Release #1.0, Version #1.30
CURPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: BC-JAN-1996
CLASSIPICATION NUMBER: US 08/384,324
FILING DATE: 01-FEB-1995
ATTORNEY/AGENT INFORMATION:
NAME: Reed, Janet E.
REGISTRATION NUMBER: 36,522
TELEPHONE: (215) 563-4004
INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: mucleic acid
STRANDEDNESS: single
TYPE: uncleic acid
HYPOTHETICAL: YES
WANTER TYPE: CHEER THES
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Matches 14; Conservative
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 14; Conserva
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PCT-US96-01473-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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5219727-64
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RESULT 49
US-09-371-772B-4106

Sequence 4106, Application US/09371772B

Sequence 4106, Application US/09371772B

Sequence 4106, Application US/09371772B

Sequence 4106, Application US/09371772B

Setent No. 6566127

GENERAL INFORMATION:

APPLICANT: Revoco, Pam

APPLICANT: Stinchcomb, Dan

APPLICANT: Stinchcomb, Dan

APPLICANT: Stinchcomb, Dan

TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re

TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor

FILE REFERENCE: MBHB00, 876-J (237/198)
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Sequence 8450, Application US/08584040

Patent No. 6346398

GENERAL INFORMATION:
APPLICANT: Pavco, Pamela
APPLICANT: Bacobach, James
APPLICANT: Bachedon, Dann T.
APPLICANT: Stinchcomb, Dann T.
APPLICANT: Stinchcomb, Dann T.
APPLICANT: Stinchcomb, Dann T.
APPLICANT: Bacobacho, James
ITILE OF INVENTION: METHOD AND REAGENT FOR THE
ITILE OF INVENTION: TREATMENT OF DISEASES OR
ITILE OF INVENTION: CONDITIONS RELATED TO LEVELS
ITILE OF INVENTION: GROWTH FACTOR
NUMBER OF SEQUENCES: 8502
CORRESPONDENCE ADDRESS:
ADDRESSE: LYON & LYON
STREET: SUITE 4700

STREET: Sulle # , vo CITY: Los Angeles STATE: California ZID: 90071-2066 ZID: 90071-2066 COMPUTER READABLE FORM: MEDIUM TYPE: 3.5" Diskette, 1.44 Mb MEDIUM TYPE: 8.5 DISKETTE, 1.44 Mb MEDIUM TYPE: 8.5 DISKETTE, 1.44 Mb MEDIUM TYPE: 1.5 DISKETTE, 1.44 Mb MEDIUM TYPE: 1.5 DISKETTE, 1.44 Mb MEDIUM TYPE: 1.5 DISKETTE, 1.49 PC. DOS 5.0 SOFTWARE: Word Perfect 5.1 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/584,040 FILING DATE: January 11, 1996 CLASSIFICATION: 514 PRIOR APPLICATION: 514 PRIOR APPLICATION NUMBER: 20, 1995 ATTORNEY/AGENT INFORMATION: TELEFAM: (213) 489-160 TELEFAM: (213) 489-160 TELEFAM: (213) 489-160 TELERY: 67-3510 TELERY: 67-3510 TELERY: 67-3510 TELERY: 67-3510 SEQUENCE CHARACTERISTICS: LENGTH: 15 base pairs

TYPE: nucleic acid STRANDEDNESS: single TOPOLOGY: linear

; TOPOLOGY:] US-08-584-040-8450

16.4%; Score 12; DB 1; Length 15; 50.0%; Pred. No. 66; 0; Indels tive 6; Mismatches 0; Indels Best Local Similarity 50.0 Matches 6; Conservative Query Match

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Gaps

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915 TGGTCTTTGCCT 926

RESULT 48

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Pred. No. 76;
6; Mismatches 0; Indels
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APPLICANT: Pavco, Pamela
APPLICANT: Reavingen, James
APPLICANT: Stinchcomb, Dan T.
APPLICANT: Stinchcomb, Dan T.
APPLICANT: Stinchcomb, Dan T.
APPLICANT: Stochedo, Jaime
TITLE OF INVENTION: METHOD MINE PRAGENT FOR THE
TITLE OF INVENTION: TREATMENT OF DISEASES OR
TITLE OF INVENTION: CONDITIONS RELATED TO LEVELS
TITLE OF INVENTION: GROWTH FACTOR
NUMBER OF SEQUENCES: 8502
CORRESPONDENCE ADDRESS:
           CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-206
COMPUTEN READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
                                                                                                                                                                                                                                                  COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/584,040
FILING DATE: January 11, 1996
CLASSIPICATION 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/005,974
FILING DATE: OCCODER 26, 1995
ATTORNEY/AGENT INCORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,32,32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1500, Application US/08584040 Patent No. 6346398
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633 West Fifth Street
Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 1499:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 21.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16.4%;
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Best Local Similarity 50.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                s ugencumaceu 16
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Los Angeles
STATE: California
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US-08-584-040-1500
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STREET:
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Sequence 550, Application US/09371772B

Sequence 550, Application US/09371772B

Settent No. 6566127

GENERAL INFORMATION:

APPLICANT: Ribozyme Pharmaceuticals, Inc.

APPLICANT: Ribozyme Pharmaceuticals, Inc.

APPLICANT: Stinchcomb, Dann

APPLICANT: Stinchcomb, Dann

APPLICANT: Stinchcomb, Dann

APPLICANT: Escobedo, Jaime

TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor

TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor

TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor

CURRENT APPLICATION NUMBER: US/09/371,72B

CURRENT APPLICATION NUMBER: US 60/005,974

PRIOR FILING DATE: 1995-10-26

PRIOR FILING DATE: 1995-00-108

NUMBER OF SEQ ID NOS: 14225

SOFTWARE: Patentin Version 3.0

LENGTH: 16
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Pred. No. 71;
6; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                   Score 12; DB 1; Length 15;
Pred. No. 66;
6; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1496, Application US/08584040

Patent No. 6446398
GENERAL INFORMATION:
APPLICANT: Pavco. Pamela
APPLICANT: Pavco. Pamela
APPLICANT: Stinchcomb. Dan T.
APPLICANT: Stinchcomb. Dan T.
TITLE OF INVENTION: METHOD AND REAGENT FOR THE
TITLE OF INVENTION: TREATMENT OF DISEASES OR
TITLE OF INVENTION: CONDITIONS RELATED TO LEVELS
TITLE OF INVENTION: GROWTH FACTOR
TITLE OF INVENTION: GROWTH FACTOR
  CURRENT APPLICATION NUMBER: US/09/371,772B
                  CURRENT FILING DATE: 1999-08-10
PRIOR APPLICATION NUMBER: US 60/005,974
PRIOR FILING DATE: 1995-10-26
PRIOR FILING DATE: 1996-01-08
NUMBER OF SEQ ID NOS: 14225
SOPTWARE: Patentin version 3.0
LENGTH: 15
                                                                                                                                                                                                                                                                                                       16.4%;
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50.0%;
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Best Local Similarity 50.v.
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Best Local Similarity 50.0
Matches 6; Conservative
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                                                                                                                                                                                                                    TYPE: RNA
CORGANISM: Homo sapiens
US-09-371-772B-4106
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US-08-584-040-1499
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Query Match
16.4%; Score 12; DB 1;
Best Local Similarity 50.0%; Pred. No. 76;
Matches 6; Conservative 6; Mismatches
    REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 218/064
TELEPHONE: (213) 489-1600
FELEFAX: (213) 955-0440
FELEFAX: (213) 955-0440
FELEFX: (213) 955-0440
FELEFX: (213) 955-0440
FELEFX: (7-3510
FELEFX: (
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US-09-371-772B-44
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Sequence 1501, Application US/08584040

Sequence 1501, Application US/08584040

APPLICANT: Pavco, Pamela
APPLICANT: Stinchcomb, Dan T.
APPLICANT: Becobedo, Jaime
TITLE OF INVENTION: CONDITIONS RELATED TO LEVELS
TITLE OF INVENTION: GROWTH FACTOR
TITLE OF INVENTION: LAYON
STREET: 613 West Fifth Street
STREET: 613 West Fifth Street
STREET: Galifornia
COUNTRY: U.S.A.
ZIP: 30071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: STORAGE
COMPUTER: DAN COMPATION:
MEDIUM TYPE: STORAGE
COMPUTER: DAN COMPATION
SOFTWARE: WORD PATE:
CLASSIFICATION NUMBER: US/08/584,040
FILING DATE: October 26, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
NAME: Warburg, Richard J.
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/584,040
FILING DATE: January 11, 1996
CLASSIFICATION DATA:
APPLICATION NUMBER: 06/005,974
FILING APPLICATION DATA:
APPLICATION NUMBER: 21, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 32,027
REJESPHONE: (213) 489-1600
TELLEFAX: (213) 955-0440
INFORMATION FOR SEQ ID NO: 1500:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        915 TGGTCTTTGCCT 926
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US-08-584-040-1500
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US-09-37/-/Ze-44 Application US/09371772B

Sequence 44, Application US/09371772B

Patent No. 6566127

SEGNERAL INFORMATION:
MCGWIGGE, USERBATH TON:
MAPPLICANT: Pavco, Pam
MCGWIGGE, Use Applicant: Pavco, Pam
MCGWIGGE, Use Applicant: Becobedo, Jaime
MAPPLICANT: MAPPLICANT: NUMBER: US 60/005, 974
MAPPLICANT: MAPPLICANT: NUMBER: US 60/005, 974
MAPPLICANT: MAPPLICA
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Pred. No. 76;
6; Mismatches 0; Indels
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50.0%;
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Best Local Similarity 50.0.
Thea 6; Conservative
915 TGGTCTTTGCCT 926
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                                             : | | : | : : : | | | : 2 udgucuuudccu 13
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5 UGGUCUUUGCCU 16
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CRGANISM: Homo sapiens
US-09-371-772B-44
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Length 17;

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APPLICANT: Condon, Tom P.
APPLICANT: Condon, Tom P.
TITLE OF INVENTION: ANTHIESENSE MODULATION OF INTEGRIN 4 EXPRESSION
FILE REFERENCE: ISPH-0323
CURRENT APPLICATION NUMBER: US/09/166,203A
CURRENT FILING DATE: 1998-10-05
NUMBER OF SEQ ID NOS: 60
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81;
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Pred. No. 76;
6; Mismatches 0; Indels
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PRIOR APPLICATION NUMBER: US 60/005,974
PRIOR FILING DATE: 1995-10-26
PRIOR PILING DATE: 1995-01-08
PRIOR FILING DATE: 1996-01-08
NUMBER OF SEQ ID NOS: 14225
SEQ ID NO 4244
LENGTH: 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; FEATURE:
; OTHER INFORMATION: antisense sequence
US-09-166-203-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; OTHER INFORMATION: antisense sequence US-09-377-309-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 21, Application US/09166203A; Patent No. 5968826; GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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Best Local Similarity 50.0
Matches 6; Conservative
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                                                                                                                                                                                                                                                               TYPE: RNA
CORGANISM: Homo sapiens
US-09-371-7728-4244
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US-09-377-309-21/c
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LENGTH: 18
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APPLICANT: Stinchcomb, Dan
APPLICANT: Scobedo, Jaime
TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
CURRENT APPLICATION NUMBER: US/09/371,72B
CURRENT FILING DATE: 1999-08-10
PRIOR FILING DATE: 1995-10-26
PRIOR APPLICATION NUMBER: US 08/584,040
PRIOR FILING DATE: 1996-01-08
NUMBER OF SEQ ID NOS: 14225
SOFTWARE: PATENT VERSION 3.0
SEQ ID NO 46
LENGTH: 17
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APPLICANT: Stinchcomb, Dan
APPLICANT: Stinchcomb, Dan
APPLICANT: Stinchcomb, Jan
APPLICANT: Stoobed, Jaime
TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
PILE REFERENCE MHH800, 876-J (237/198)
CURRENT PELLOGIONE MH800, 876-J (237/198)
CURRENT FILING DATE: 1999-08-10
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Pred. No. 76;
6; Mismatches 0; Indels
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Pred. No. 76;
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      CURRENT FILING DATE: 1999-08-10
PRIOR APPLICATION NUMBER: US 60/005,974
PRIOR FILING DATE: 1995-10-26
PRIOR FILING DATE: 1996-10-8
PRIOR FILING DATE: 1996-11-08
PRIOR FILING DATE: 1996-11-08
NUMBER OF SEQ ID NOS: 14225
SOFTWARE: Patentin version 3.0
SEQ ID NO 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 46, Application US/09371772B Patent No. 6566127 GENERAL INFORMATION: APPLICANT: Ribozyme Pharmaceuticals, Inc. APPLICANT: Pavco, Pam
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Ribbazyme Pharmaceuticals, Inc. APPLICANT: Pavco, Pam
APPLICANT: McGwiggen, Jim
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Best Local Similarity 50.0%;
Matches 6; Conservative
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Best Local Similarity 50.0
The conservative for Conservative
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uccucuucccu 13
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; ORGANISM: Homo sapiens
US-09-371-772B-45
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US-09-371-772B-46
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US-09-371-772B-4244
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US-09-371-772B-46
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APPLICANT: Sanders, Jan W.
APPLICANT: Sanders, Adrianus M.
APPLICANT: Ledeboer, Adrianus M.
APPLICANT: Ledeboer, Adrianus M.
APPLICANT: Ledeboer, Adrianus M.
APPLICANT: Venema, Gerard
APPLICANT: Venema, Gerard
APPLICANT: Kok, Jan
TITLE OF INVENTION: Batterium, and Its Use in a Lacctic Acid Bacterium for TITLE OF INVENTION: Bacterium, and Its Use in a Lacctic Acid Bacterium for TITLE OF INVENTION: Production of Desired Protein
TITLE OF INVENTION NUMBER: US/09/068,195B
CURRENT FILING DATE: 1997-029
EARLIER APPLICATION NUMBER: EP 97200744/7
EARLIER FILING DATE: 1997-03-13
EARLIER FILING DATE: 1997-03-13
EARLIER FILING DATE: 1997-03-05
NUMBER OF SEQ ID NOS: 25
SEQ ID NO 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PEATURE:
NAME/KEY: modified_base
COCATION: 16
COTHER INFORMATION: /mod_base= OTHER
OTHER INFORMATION: /mod_base= OTHER
OTHER INFORMATION: /mod_base= OTHER
OTHER INFORMATION: /mode="T-T, linking group o-xyloso (nucleotides other information: that have xylose sugar linked via the o-xylene PCT-US91-03680-98
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ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: primer NS3-10
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16.2%; Score 11.8; DB 1; Length 16;
Best Local Similarity 66.7%; Pred. No. 78;
Matches 10; Conservative 4; Mismatches 1; Indels
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LOCATION: 3
OCHER INPORMATION: /mod_base= OTHER
OTHER INPORMATION:
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LOCATION: 14
OCHER INFORMATION: /mod_base= OTHER
OTHER INFORMATION:
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Patent No. 6140078; GENERAL INFORMATION:
TELEFAX: 415-377-250
TELEFAX: 415-377-250
TELEFX: 706141
INFORMATION FOR SEQ ID NO: 98: SEQUENCE CHRACTERISTICS: LENGTH: 16 base pairs TYPE: NUCLEIC ACID STRANDEDNESS: single TOPOLOGY: linear
RELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          918 TCTTTGCCTTTTATC 932
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APPLICANT: Krawczyk, Steven
TITLE OF INVENTION: SEQUENCE-SPECIFIC NONPHOTOACTIVATED
TITLE OF INVENTION: SEQUENCE-SPECIFIC NONPHOTOACTIVATED
TITLE OF INVENTION: DUPLEX DNA
NUMBER OF SEQUENCES: 158
CORRESCONDENCE ADDRESS:
ADDRESSEE: Mortison & Foerster
STREET: 545 Middlefield Road, Suite 200
CITY: Menlo Park
STATE: California
COUNTRY: USA
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Fatent No. 6656731
Generce 303, Application US/09479005A
Fatent No. 6656731
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
TITLE OF INVENTION: Nucleic Acid Catalysts with Endonuclease Activity
FILE REPERENCE: MBHB00-884-C
CURRENT APPLICATION NUMBER: US/09/479,005A
CURRENT FILING DATE: 2000-01-07
PRIOR FILING DATE: 1999-11-19
PRIOR FILING DATE: 1999-11-19
PRIOR FILING DATE: 1999-11-19
PRIOR PILING DATE: 1999-09-22
PRIOR FILING DATE: 1997-09-22
NUMBER OF SEQ ID NOS: 1208
SOFTWARE: Patentin version 3.0
SEQ ID NOS: 1208
LENGTH: 16
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                 Query Match 16.4%; Score 12; DB 1; Length 18; Best Local Similarity 100.0%; Pred. No. 81; Matches 12; Conservative 0; Mismatches 0; Indels
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
CORPOTAR: PatentIn Release #1.0, Version #1.25
SOUTHWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US91/03680
FILING DATE: 19910524
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Mureabige, Kate H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 4610-0011.40
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40.0%; Pred. No. 78;
tive 7; Mismatches
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                                                                                                                            901 CTGGTCATTTTC 912
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Best Local Similarity 40.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: RNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                           US-09-479-005A-303
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; Sequence 419, Application US/09371772B
; Patent No. 6566127
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Matches 13; Conservative
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; ORGANISM: Homo sapiens
US-09-371-772B-419
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US-09-529-812A-4/c
                                         US-09-371-772B-419
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Patent No. 6346398

GENERAL INFORMATION:
APPLICANT: Pavco, Pamela
APPLICANT: Pavco, Pamela
APPLICANT: Binchcomb, Dan T.
APPLICANT: Escobedo, Jaime
TITLE OF INVENTION: METHOD AND REAGENT FOR THE
TITLE OF INVENTION: TREATMENT OF DISEASES OR
TITLE OF INVENTION: CONDITIONS RELATED TO LEVELS
TITLE OF INVENTION: GROWTH FACTOR
TITLE OF INVENTION: GROWTH FACTOR
TITLE OF INVENTION: GROWTH FACTOR
                                                                                  16.2%; Score 11.8; D
86.7%; Pred. No. 83;
tive 0; Mismatches
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16.2%; Score 11.8; D
Best Local Similarity 53.3%; Pred. No. 83;
Matches 8; Conservative 5; Mismatches
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ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COMPUTER: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/584,040
FILING DATE: January 11, 1996
CLASSIFTCATION BATA:
APPLICATION STATE
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 60/005,974
FILING DATE: October 26, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 218/064
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 955-0440
TELEFAX: (213) 955-0440
TELEFAX: 67-3510
INFORMATION FOR SEG ID NO: 1874:
SEQUENCE CHARACTERISTICS:
LENGTH: ACCURATERISTICS:
LENGTH: ACCURATERISTICS:
LENGTH: ACCURATERISTICS:
LENGTH: ACCURATERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
                                                                                                                                                                            936 CCTCTTCATTGGTTT 950
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                                                                                     Query Match
Best Local Similarity 86.73
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
; NAME/KEY: primer bind; LOCATION: (1)..(17)
US-09-068-195-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
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US-08-584-040-1874
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APPLICANT: MCSWiggen, Jim
APPLICANT: Stinchcomb, Dan
APPLICANT: Secobed, Jaime
TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Rel
TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
CURRENT APPLICATION NUMBER: US 60/005,974
PRIOR FILING DATE: 1995-10-26
PRIOR PLILNG DATE: 1995-10-26
PRIOR FILING DATE: 1995-01-08
NUMBER OF SEQ ID NOS: 14225
SOFTWARE: Patentin version 3.0
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ORGANISM: Artificial Sequence
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Triplex
OTHER INFORMATION: forming oligonuclectide
OTHER INFORMATION: This oligo may or may not be 3'-monophosphorylated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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Best Local Similarity 53.3%; Pred. No. 83;
Matches 8; Conservative 5; Mismatches 2; Indels
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GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Pavco, Pam
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US-09-422-978-6620

Sequence 6620, Application US/09422978

Patent No. 6537751

GENERAL INFORMATION:
APPLICANT: Blumenfeld, Marta
APPLICANT: Blumenfeld, Marta
APPLICANT: Chen, Daniel
APPLICANT: Blumenfeld, Marta

APPLICANT: Blumenfeld, Marta

APPLICANT: Blumenfeld, Marta

CURRENT APPLICATION NUMBER: US/09/422, 978

CURRENT FILING DATE: 1999-04-21

EARLIER FILING DATE: 1999-04-21

EARLIER FILING DATE: 1998-11-23

EARLIER FILING DATE: 1998-04-21

NUMBER OF SEQ ID NOS: 11796

SEQ ID NO 6620

LEMOTH: 18
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| LOCATION: 1..18
| OTHER INFORMATION: upstream amplification primer 99-14093 for SEQ 2686,
US-09-422-978-6620
                                                                                                                                                                                                                                                                                                                                                         Gaps
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APPLICANT: McSwiggen, James
APPLICANT: Newton, Roger S.
APPLICANT: Newton, Roger S.
APPLICANT: Rambarack, Randy
TITLE OF INVENTION: REDOZYME TREATMENT OF DISEASES
TITLE OF INVENTION: OR CONDITIONS RELATED TO LEVELS OF
TITLE OF INVENTION: PLASMA LIPOPROTEIN (a) [LP(a)] BY
TITLE OF INVENTION: INHIBITING APOLIPOPROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16.2%; Score 11.8; I
ilarity 86.7%; Pred. No. 88;
Conservative 0; Mismatches
FILE REFERENCE: ISPH-0321
CURRENT APPLICATION NUMBER: US/09/167,109
CURRENT FILING DATE: 1998-10-06
NUMBER OF SEQ ID NOS: 228
SEQ ID NO 154
LENGTH: 18
                                                                                                                                                                                                                  ; OTHER INFORMATION: antisense sequence US-09-167-109-154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 77, Application US/08311760A, Patent No. 5599706, GENERAL INFORMATION:
                                                                                                                                                   TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                        909 TITCTTIGGICITIG 923
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               903 GGTCATTTTCTTTGG 917
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: Homo Sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 13; Conserv
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                                                                                                                                                                                                        FEATURE:
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US-09-061-769A-21/C
Sequence 21, Application US/09061769A
Sequence 21, Application US/09061769A
Sequence 21, Application US/09061769A
Sequence 21, Application US/09061769A
GENERAL INFORMATION:
TITLE OF INVENTION: Use for Same
TITLE OF INVENTION: use for Same
FILE REFERENCE: mea genes
CURRENT APPLICATION NUMBER: US/09/061,769A
CURRENT FILING DATE: 1998-04-16
PRIOR FILING DATE: 1998-04-16
NUMBER OF SEQ ID NOS: 21
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 21
LENGTH: 18
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CTHER INFORMATION: Description of Artificial Sequence: synthetic;
CTHER INFORMATION: primer
US-09-061-769A-21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 16.2%; Score 11.8; DB 1; Length 18; Best Local Similarity 86.7%; Pred. No. 88; Matches 13; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
16.2%; Score 11.8; DB 1; Length 18,
Best Local Similarity 86.7%; Pred. No. 88;
Matches 13; Conservative 0; Mismatches 2; Indels
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US-09-154/c
US-09-167-109-154/c
; Patent No. 6399297
; GENERAL INFORMATION:
; APPLICANT BAKET, Brenda F.
; APPLICANT: Monia, Brett P.
; APPLICANT: Wonla, Brett P.
; APPLICANT: XU, Xiaoxing S.
; APPLICANT: XI, Xiaoxing S.
; TITLE OF INVENTION: ANTISENSE MODULATION OF TRAF EXPRESSION
                                                                                            APPLICANT: Lex M. Cowestt
APPLICANT: Lex M. Cowestt
APPLICANT: Lex M. Cowestt
APPLICANT: Ser M. O'Malley
APPLICANT: Bert W. O'Malley
TITLE OF INVENTION: ANTISENSE MODULATION OF SRA EXPRESSION
FILE REPERENCE: RTS-0048
CURRENT APPLICATION NUMBER: US/09/280,409
CURRENT FILING DATE: 1999-03-29
NUMBER OF SEQ ID NOS: 146
SEQ ID NO 72
LENGTH: 18
                                                                                                                                                                                                                                                                                                                                                                                                                          ; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-280-409-72
                       US-09-280-409-72; Sequence 72, Application US/09280409; Patent No. 6107092
                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                935 TCCTCTTCATTGGTT 949
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              924 CCTTTTATCCCTCCT 938
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GENERAL INFORMATION:
APPLICANT: Stinchcomb, Daniel T.
APPLICANT: Stinchcomb, Daniel T.
APPLICANT: Stinchcomb, Daniel T.
APPLICANT: Stinchcomb, Daniel T.
APPLICANT: Newton, Roger S.
APPLICANT: Newton, Roger S.
APPLICANT: Newton, Roger S.
APPLICANT: Newton, Randarack, Randy
ITILE OF INVENTION: PLASWA LIPOPROTEIN (a) [LP(a)] BY
ITILE OF INVENTION: INHIBITING APOLIPOPROTEIN
ITILE OF INVENTION:
INTILE OF INVENTION:
INHIBITING APOLIPOPROTEIN
ADDRESSEE: Lyon & Lyon
STREET: Saite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 11.4; D
Pred. No. 86;
6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: 5.5" DISKETTE, 1.6"
COMPUTER: 18M COMpatible
OPERATING SYSTEM: 18M P.C. DOS 5.0
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA: US/08/774, 310
FILING DATE: December 23, 1996
PRIOR APPLICATION NUMBER: 08/311,760
FILING DATE: September 23, 1994
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 32,327
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION DATA:
FILING DATE: September 23, 1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 1994
PRIOR DATE: September 23, 1994
PRIOR DATE: REPLEMENTION:
APPLICATION NUMBER: 20, 32, 32
REFERENCE/DOCKET NUMBER: 32, 32, 32
REFERENCE/DOCKET NUMBER: 208/155
TELECHONE: (213) 955-0440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 77, Application US/08774310
Patent No. 5877022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 46.2%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 7
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                935 TCCTCTTCATTGG 947
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0.S.A.
90071
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TOPOLOGY:
US-08-311-760A-78
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US-08-311-760A-78
US-08-311-760A-78
Sequence 78, Application US/08311760A
Fatent No. 5599706
GENERAL INFORMATION:
GENERAL INFORMATION:
FAPPLICANT: Stinchcomb, Dan T.
APPLICANT: Newton, James
APPLICANT: Newton, Story
TITLE OF INVENTION: RIBOZYME TREATMENT OF DISEASES
TITLE OF INVENTION: RADAY
TITLE OF INVENTION: PLASMA LIPORROTEIN
TITLE OF INVENTION: INHIBITING APOLIPORROTEIN
TITLE OF INVENTION: INHIBITING APOLIPORROTEIN
TITLE OF INVENTION: INHIBITING APOLIPORROTEIN
TITLE OF INVENTION:
TITLE OF INVENTION: INHIBITING APOLIPORROTEIN
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION: SEQUENCES:
CORRESPONDENCE ADDRESS:
STREET: 633 West fifth Street
STREET: SUITE 4770
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 1; Length 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Indels
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15.6%; Score 11.4; L
Best Local Similarity 46.2%; Pred. No. 86;
Matches 6; Conservative 6; Mismatches
                                                                                                                                                                                                                    COMPUTER READBLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb MEDIUM TYPE: 3.5" Diskette, 1.44 Mb MEDIUM TYPE: 3 storage COMPUTER: 1BM Compatible OPERATING SYSTEM: IBM P.C. DOS 5.0 SOFTWARE: PARESEQ VERSION 1.5 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/311,760A FILING DATE: September 23, 1994
APPLICATION NUMBER: 23, 1994
APPLICATION NUMBER: APPLICATION DATA:
APPLICATION DATE: APPLICATION DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IEM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: WALCHEY, KICHARG
REGISTRATION WINBER: 32,327
REFERENCE/DOCKET NUMBER: 208/155
TELEPHONE: (213) 489-1600
TELEPHONE: (213) 955-0440
                                                           ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 77:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          933 CCTCCTCTTCATT 945
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 CAUCCUCCUCAUU 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: single
          NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                          STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                : Los Angeles
E: California
TRY: U.S.A.
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                                                                                                                                                                                                       ZIP: 90071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-311-760A-77
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PCT-US91-03680-96

Sequence 96, Application PC/TUS9103680

Sequence 96, Application PC/TUS9103680

BAPLICANT: Mattencci, Mark D.

APPLICANT: Mattencci, Mark D.

APPLICANT: Mattencci, Mark D.

TITLE OF INVENTION: SEQUENCE-SPECIFIC NONPHOTOACTIVATED

TITLE OF INVENTION: DUPLEX DNA

TITLE OF INVENTION: DUPLEX DNA

NUMBER OF SEQUENCES: 158

CORRESPONDENCE ADDRESS:

ADDRESSER: Mattison & Foerster

STREET: 545 Middlefield Road, Suite 200

CITY: Menlo Park
            Gaps
                                                                                                                                                                                                                        ASSUBLICATION OS OB 929-856

Sequence 57, Application US/08929856

Patent No. 6136584

Patent No. 6136584

Patent No. 6136584

APPLICANT: Hiatt, Andrew

APPLICANT: Rose, Floyd

TITLE OF INVENTION: DE NOVO POLYNUCLEOTIDE SYNTHESIS USING

TITLE OF INVENTION: ROLLING TEMPLATES

NUMBER OF SEQUENCES: 190

CORRESPONDENCE ADDRESS:

ADDRESSEE: LERNER, DAVID, LITTENBERG, KRUMHOLZ & ADDRESSEE: MENTILIK

STREET: 600 South, Avenue West

CITY: Westfield

STATE: Now Jersey

COUNTRY: USA
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            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: USA

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Ploppy disk
COMPUTER: THE PC-000/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURSENT APPLICATION DATA:
APPLICATION NUMBER: US/08/929,856
FILING DATE: 15-SEP-1997
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: FOLEY, Shawn P.
REGISTRATION NUMBER: 33,071
REGISTRATION NUMBER: 33,071
TELEPHONE: 908-654-5000
TELEPHONE: 908-654-5000
TELEPHONE: 908-654-5000
TELEFAX: 908-654-7866
INFORMATION FOR SEQ ID NO: 57:
FWATH. 15 base pairs
         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15.6%; Score 11.4; I 92.3%; Pred. No. 86; ative 0; Mismatches
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                                                                  935 TCCTCTTCATTGG 947
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                                                                                                2 UCCUCUUCAUUUG 14
         6; Conservative
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Best Local Similarity 92.3
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear MOLECULE TYPE: DNA
         Matches
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Sequence 78, Application US/08774310

Fatent No. 5877022

GENERAL INFORMATION:
APPLICANT: Stinchcomb, Daniel T.
APPLICANT: McSwiggen, James
APPLICANT: McSwiggen, James
APPLICANT: Newfor, Roger S.
TITLE OF INVENTION: RIBOZYME TREATMENT OF DISEASES
TITLE OF INVENTION: PLASMA LIPOPROTEIN
TITLE OF INVENTION: INHIBITING APOLIFOPROTEIN
TITLE OF INVENTION: INHIBITING APOLIFOPROTEIN
TITLE OF INVENTION: INHIBITING APOLIFOPROTEIN
MUMBER OF SEQUENCES: 392
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 470
CITY: Los Angeles
STREET: Suite 470
CITY: Los Angeles
STRIEE: California
COUNTRY: U.S.A.
ZIP: 90071

COMPUTER READABLE FORM:
MEDIUM TYPE: Storage
COMMITTED: Tab Compatible
                                                                                                                                                                                                                                                                                                                  15.6%; Score 11.4; DB 1; Length 15; 46.2%; Pred. No. 86; tive 6; Mismatches 1; Indel8
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Pred. No. 86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DCS S.0
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/774,310
FILING DATE: December 23, 1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/311,760
FILING DATE: September 23, 1994
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 223/229
TELEPHONE: (213) 489-1600
TELEPHONE: (213) 955-0440
TELEPHONE: (313) 955-0440
TELEPHONE: (213) 489-1600
TELEX: (7-3510
TELEX: (7-3510
INFORMATION FOR SEQ ID NO: 77:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
COS-074-310-77
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Best Local Similarity 46.2
Matches 6; Conservative
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Best Local Similarity
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15.3%; Score 11.2; DB 1; Length 16; 81.2%; Pred. No. 1e+02; rive 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                         15.3%; Score 11.2; DB 1; Length 16; 81.2%; Pred. No. 1e+02; ive 0; Mismatches 3; Indels
TITLE OF INVENTION: Therapy
FILE REPERENCE: 41984/78179
CURRENT APPLICATION NUMBER: US/09/270,542
CURRENT FILING DATE: 1999-03-17
EARLIER APPLICATION NUMBER: 09/221,222
SARLIER FILING DATE: 1999-12-23
NUMBER OF SEQ ID NOS: 207
SOFTWARE: Patentin Ver: 2.0
SCO ID NO 186
LENGTH: 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  937 CTCTTCATTGGTTTAA 952
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                                                                                                                                                                                                                        TYPE: DNA
CRGANISM: Rattus norvegicus
US-09-270-542-186
                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 81.2*
....hes 13, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: RNA
CORGANISM: Homo sapiens
US-09-479-005A-176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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US-09-270-542-186
US-09-270-542-186
; Sequence 186, Application US/09270542
; Patent No. 6322976
; GENERAL INFORMATION:
; APPLICANT: Altman, Timothy
; APPLICANT: Stanton, Lawrence
; APPLICANT: Stanton, Lawrence
; TITLE OF INVENTION: Compositions and Methods of Disease Diagnosis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .,
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                                                                                                                                             OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US91/03680
FILING DATE: 19910524
CLASSIFICATION: 435
ATTORNEY/AGRYT INFORMATION:
NAME: Muzashige, Kate H.
REGISTATION NUMBER: 29,959
REFRENCE/DOCKET NUMBER: 4610-0011.40
TELECHMONICATION INFORMATION:
TELEFAX: 415-327-2550
TELEFAX: 415-327-2550
TELEFAX: 415-327-2551
TELEFAX: 415-327-2551
TELEFAX: 416-327-2551
TELEFAX: 415-327-2550
TELEFAX: 415-327-2550
TELEFAX: 415-327-2551
TELEFAX: AUS-MARCHERISTICS:
LENGTH: 16 base pairs
TYPE: MUCLEIC ACID
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCATION: 3
OTHER INFORMATION: /mod base= OTHER
OTHER INFORMATION: /note= "5-methylcytosine"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /mod_base= OTHER
/note= "5-methylcytosine"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15.6%; Score 11.4; D
80.0%; Pred. No. 92;
tive 1; Mismatches
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OTHER INFORMATION: /mod_base= OTHER
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /mod_base= OTHER
                                              ZIP: 94025
COMPUTER REALABLE FORM:
MEDIUM TYPE: Floppy disk
CMEDUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 918 TCTTTGCCTTTTATC 932
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
NAME/KEY: modified_base
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: modified_base
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: modified base
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LOCATION: 14
OTHER INFORMATION:
OTHER INFORMATION:
      California
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Matches 12; Conserv
         STATE:
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US-08-299-48)C

Sequence 48, Application US/08299849B

Sequence 48, Application US/08299849B

Sequence 48, Application

Sequence 5612201

Patent No. 5612201

APPLICANT: De Plaen, Etienne; Boon-Falleur, Thierry;

APPLICANT: Leth, Bernard; Szikora, Jean-Pierre; De Smet, Charles;

APPLICANT: Leth, Bernard; Szikora, Jean-Pierre; De Smet, Charles;

TITLE OF INVENTION: Determining Expression Of A Tumor Antigen Precursor NUMBER OF SEQUENCES: 48

CORRESPONDENCE ADDRESS:

ADDRESSEE: Felfe & Lynch

STREET: 805 Third Avenue

CITY: New York City
                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-479-005A-176/c
US-09-479-005A-176/c
US-09-479-005A-176, Application US/09479005A

Patent No. 6656731
GENERAL INFORMATION
TITLE OF INVENTION: Nucleic Acid Catalysts with Endonuclease Activity
TITLE OF INVENTION: Nucleic Acid Catalysts with Endonuclease Activity
TITLE OF INVENTION: Nucleic Acid Catalysts with Endonuclease Activity
TITLE OF INVENTION: Nucleic Acid Catalysts with Endonuclease Activity
CURRENT PILING DATE: 2000-01-07
PRIOR APPLICATION NUMBER: US/09/44,209
PRIOR APPLICATION NUMBER: US 09/159,274
PRIOR FILING DATE: 1999-11-19
PRIOR APPLICATION NUMBER: US 60/059,473
PRIOR FILING DATE: 1998-09-22
NUMBER OF SEQ ID NOS: 1208
SOFTWARE: PatentIn version 3.0
SEQ ID NO 176
INSTERN 106

Gaps
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US-08-373-124A-1012

Sequence 1012, Application US/08373124A

Pareent No. 5646042.

APPLICANT: Stinchcomb, Dan T.
APPLICANT: Draper, Kenneth
APPLICANT: Draper, Kenneth
APPLICANT: Jarvis, Thale
TITLE OF INVENTION: TREATHEND COMPOSITIONS FOR
TITLE OF INVENTION: TREATHEND COMPOSITIONS FOR
TITLE OF INVENTION: CANCER USING RIBOZYMES
ITILE OF INVENTION: CANCER USING RIBOZYMES
NUMBER OF SEQUENCES: 2627
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 613 West Fifth Street
STREET: 613 West Fifth Street
STREET: Galifectia
COUNTRY: California
COUNTRY: Los Angeles
STREET: California
COUNTRY: U.S.A.

MEDIUM TYPE: Storage
COMPUTER READABLE FORM:
MEDIUM TYPE: Storage
COMPUTER: IBM COMPACIAL
COMPUTER: IBM COMPACIAL
COMPUTER: IBM COMPACIAL
CORRESTING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION NUMBER: US/08/373,124A
FILING DATE: January 13, 1995
PRIOR APPLICATION DATA:
                MEDIUM TYPE: storage
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/373,124A
FILING DATE: January 13, 1995
PRIOR APPLICATION NUMBER: 08/192,943
FILING DATE: May 18, 1994
APPLICATION NUMBER: 08/192,943
FILING DATE: December 7, 1994
APPLICATION NUMBER: 07/936,132
FILING DATE: December 7, 1992
APPLICATION NUMBER: 07/936,132
FILING DATE: PAUSER: 07/936,422
FILING DATE: AUGUST: 209/035
FILING DATE: AUGUST: AUGUST: 209/035
FILING DAT
         MEDIUM TYPE: 3.5" Diskette, 1.44 Mb MEDIUM TYPE: storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        948 TITAATGTATCGCTAC 963
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16 rracardraacecrac 1
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US-08-373-124A-366
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COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage COMPUTER: IBM OPERATING SYSTEM:
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: U5/08/299,849B
FILING DATE: 1-SEPTEMBER-1994
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: 08/037,230
FILING DATE: 26-MARCH-1993
PRIOR APPLICATION NUMBER: PCT/US92/04354
FILING DATE: 22-MAY-1992
PRIOR APPLICATION NUMBER: PCT/US92/04354
FILING DATE: 12-EDCEMBER-1991
PRIOR APPLICATION NUMBER: 07/764,364
FILING DATE: 23-SEPTEMBER-1991
PRIOR APPLICATION NUMBER: 9-JULY-1991
ATPOLNEY/AGENT INFORWATION:
NAME: Hanson NO. 5612201man D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTOWNEY THE MATTOWN NAMES:

NAME: Hanson, No. 5612201man D. REGISTRATION NUMBER: 30,946

REFERENCE/DOCKET NUMBER: LUD 5355

TELEPHONE: (212) 688-9200

TELEPHONE: (212) 688-9200

TELEPHONE: (212) 838-3884

INFORMATION FOR SEQ ID NO: 48:

SEQUENCE CHARACTERISTICS:

LENGTH: 17 base pairs

TYPE: nucleic acid

STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     927 TTTATCCCTCTTTC 942
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US-08-299-849B-48
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Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15.3%; Score 11.2; DB 1; Length 17; 81.2%; Pred. No. 1.1e+02; tive 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1012, Application US/08435628
; Patent No. 181796
; GENERAL INFORMATION:
APPLICANT: Stinchcomb, Dan T.
APPLICANT: Draper, Kenneth
APPLICANT: Draper, Kenneth
APPLICANT: Jarvis, Tames
APPLICANT: Jarvis, Tames
TITLE OF INVENTION: TREATMENT OF RESTENOSIS AND
TITLE OF INVENTION: TREATMENT OF RESTENOSIS AND
TITLE OF INVENTION: CANCER USING RIBOZYMES
NUMBER OF SEQUENCES: 2627
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: 5.5" DISKETTE, 1.00 S.0.
SOFTWARE: 100 Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 08/043,628
FILING DATE: 05-MAY-1995
CLASSIFTCATION DATA:
APPLICATION NUMBER: 08/193,124
FILING DATE: Manuary 13, 1995
APPLICATION NUMBER: 08/192,943
FILING DATE: Manuary 7, 1994
APPLICATION NUMBER: 07/987,132
FILING DATE: December 7, 1992
APPLICATION NUMBER: 07/987,132
FILING DATE: AUGUST 7, 1992
APPLICATION NUMBER: 07/986,132
FILING DATE: AUGUST 7, 1992
APPLICATION NUMBER: 07/986,132
FILING DATE: AUGUST 7, 1992
APPLICATION NUMBER: 07/986,132
RECERENCE/DOCKET NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 32,327
                                                                                                       NAME: Warburg, Richard
REGISTRATION UNMBER: 32,327
REFERENCE/DOCKET NUMBER: 209/035
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEPAK: (213) 955-0440
TELEPAK: (213) 955-0440
TELEPAK: (213) 955-0440
TELEPAK: (213) 955-0440
TELEPAK: (7-3510
TELEPAK: (7-3510
TELEPAK: 7-3510
TELEPAK: 7-3510
TELENTH: 17 base pairs
TYPE: nucleic acid
STRANDENNESS: single
TYPE: nucleic acid
STRANDENNESS: single
US-08-435-628-366
                         07/936,422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               948 TITAAIGIAICGCIAC 963
                                                FILING DATE: August 26, ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16 rracardraddcrac 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13; Conservative
                      APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-435-628-1012
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 36. Application US/08435628

Patent No. 5817796

GENERAL INFORMATION:
APPLICANT: Stinchcomb, Dan T.
APPLICANT: Stinchcomb, Dan T.
APPLICANT: McSwiggen, James
APPLICANT: Jarvis, Thale
ITILE OF INVENTION: TREATMENT OF RESTENOSIS AND
ITILE OF INVENTION: TREATMENT OF RESTENOSIS AND
ITILE OF SEQUENCES: 2627

CORRESPONDENCE ADDRESS:
APPLICATION NUMBER: Us, 1994
APPLICATION NUMBER: Us, 1994
APPLICATION NUMBER: 08192,943
FILING DATE: February 7, 1994
APPLICATION NUMBER: 07/987,132
FILING DATE: December 7, 1992
APPLICATION NUMBER: 07/987,132
FILING DATE: August 26, 1992
APTONENY AGENT INFORMATION:
NAME: Warburg, Richard
REGISTRATION NUMBER: 32,327
REFERENCE/BOCKET NUMBER: 209/035
TELEPHONE: (213) 955-0440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READBLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb MEDIUM TYPE: storage
COMPUTER: 1BM Compatible
OPERATING SYSTEM: 1BM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/435,628
FILING DATE: 05-MAY-1995
CLASSIFICATION S.14
PRIOR APPLICATION NUMBER: 08/373,124
FILING DATE: Annuary: 13, 1995
APPLICATION NUMBER: 08/245,466
FILING DATE: MAY 18, 1994
APPLICATION NUMBER: 08/192,943
FILING DATE: Pebruary 7, 1994
APPLICATION NUMBER: 08/192,943
FILING DATE: Pebruary 7, 1994
APPLICATION NUMBER: 07/981,132
FILING DATE: December 7, 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   913 TTTGGTCTTTGCCTTT 928
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 81
US-08-435-628-366/c
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                                                                                                                                                                                                                          15.3%; Score 11.2; DB 1; Length 17;
81.2%; Pred. No. 1.1e+02;
tive 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE: New York
COUNTRY: U.S.A.
ZIP: 10112-3801
COMPUTER READBLE FORM:
MEDIUM TYPE: Diskette - 3.50 inch, 720 Kb storage.
COMPUTER: IBM PS/V
COMPU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 47, Application US/08606505B
| Sequence 47, Application US/08606505B
| Patent No. 6114601
| GENERAL INFORMATION:
| APPLICANT: KINCHI, Yasuhiro
| APPLICANT: KINCHI, Yasuhiro
| APPLICANT: KINCHI, Yasuhiro
| APPLICANT: SHIMADA, Yukihisa
| APPLICANT: SHIMADA, Ritsuko
| APPLICANT: SHIMADA, Ritsuko
| APPLICANT: SHIMADA, Ritsuko
| APPLICANT: OKNINKA, Yasushi
| TITLE OF INVENTION: NOVEL PLANT GENES
| NUMBER OF SEQUENCES: 67
| CORRESPONDENCE ADDRESS:
| STREET: 30 ROCKEfeller Plaza
| CITY: New York
| CITY: New York
| CITY: New York
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Sequence 47, Application US/09616990
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                                                                                                                                                                                                                     Query Match
Best Local Similarity 81.2'
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 76.5
Matches 13; Conservative
TYPE: nucleic acid
STRANDEDNESS: singl
; TOPOLOGY: linear
US-08-967-727-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
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US-08-606-505B-47
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US-09-616-990-47
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US-08-967-727-28/C

i Sequence 28, Application US/08967727

i Patent No. 6025474

i GENERAL INFORMATION:

APPLICANT: Gaugler, B atrice; Van den Bynde, Beno t;

APPLICANT: Van der Bruggen, Pierre; Boon-Falleur, Thierry

APPLICANT: Van der Bruggen, Pierre; Boon-Falleur, Thierry

TITLE OF INVENTION: Tumor Rejection Antigen Precursor Mage-3 And Uses Thereof

NUMBER OF SEQUENCES: 30

CORRESPONDENCE ADDRESS:

ADDRESSEE: Felfe & Lynch

STREET: 805 Third Avenue

CITY: New York City

STATE: New York

STATE: New York

CITY: New York

MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage

COMPUTER: IBM

COMPUTER: IBM

COMPUTER: IBM

COMPUTER: IBM

COMPUTER: IBM

COMPUTER: IBM

COMPUTER: COMPUTER: IBM

COMPUTER: COMPUTER: DISKETTE AVENUE

COMPUTER: COMPUTER: COMPUTER: DISKETTE AVENUE

COMPUTER: COMPUTER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IEM
CORRUTER: IEM
COPERATING SYSTEM: PC-DOS
SOFRATING SYSTEM: PC-DOS
SOFRATING SYSTEM: PC-DOS
SOFRATING SYSTEM: Wordperfect
CURRENT APPLICATION DATA:
FILING DATE: CLASSIFICATION NUMBER: US/08/967,727
FILING DATE: 26-MARCH-1993
APPLICATION NUMBER: PCT/US92/04354
FILING DATE: 26-MARCH-1993
APPLICATION NUMBER: O7/807,043
FILING DATE: 12-DECRHER-1991
PRIOR APPLICATION DATA: 7764,365
FILING DATE: 23-SEPTEMBER-1991
PRIOR APPLICATION DATA: 7728,838
FILING DATE: 3-UCLX-1991
PRIOR APPLICATION DATA: 7728,838
FILING DATE: 23-SEPTEMBER-1991
PRIOR APPLICATION DATA: 7728,838
FILING DATE: 23-SEPTEMBER-1991
PRIOR APPLICATION NUMBER: 07/705,702
FILING DATE: 23-MAX-1991
APPLICATION NUMBER: 23-MAX-1991
APPLICATION NUMBER: 23-MAX-1991
APPLICATION NUMBER: 23-MAX-1991
ATTORNEY AGENT NUMBER: 23-MAX-1991
ATTORNEY AGENT NUMBER: 23-MAX-1991
ATTORNEY AGENT NUMBER: 23-MAX-1991
ATTORNEY AGENT NUMBER: 23-MAX-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Hanson, NO. 6025474man D. REGISTRATION NUMBER: 30,946
REPERENCE/DOCKET NUMBER: LUD 5353
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEPAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 nucleotides
                                          | TELEPHONE: (213) 489-1600
| TELEAX: (213) 955-0440
| TELEX: 67-3510
| INFORMATION FOR SEQ ID NO: 1012:
| SEQUENCE CHRACATERISTICS:
| LENGTH: 17 base pairs
| TYPE: nucleic acid
| TYPE: nucleic acid
| TOPOLOGY: linear
| US-08-435-628-1012
         TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               913 TTTGGTCTTTGCCTTT 928
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Gaps
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; Sequence 1574, Application US/08584040
; Patent No. 6346308
; GENERAL INFORMATION.
    APPLICANT: Pavco, Pamela
    APPLICANT: APPLICANT: APPLICANT: Stinchcomb, Dan T.
    APPLICANT: Stinchcomb, Dan T.
    APPLICANT: Stinchcomb, Dan T.
    APPLICANT: Escobedo, Jame
    TITLE OF INVENTION: METHOD AND REAGENT FOR THE
    TITLE OF INVENTION: CONDITIONS RELATED TO LEVELS;
    TITLE OF INVENTION: GROWTH FACTOR
    TITLE OF INVENTION: GROWTH FACTOR
    NUMBER OF SEQUENCES: 8502
    CORRESPONDENCE ADDRESS:
    ADDRESSEE: Lyon & Iven
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15.3%; Score 11.2; DB 1;
81.2%; Pred. No. 1.1e+02;
tive 0; Mismatches 3;
                               CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/037,230D
FILING DATE: 26-MARCH-1993
CLASSIFICATION NUMBER: US/08/037,230D
FILING DATE: 26-MARCH-1993
APPLICATION NUMBER: PCT/US92/04354
FILING DATE: 22-MAY-1992
FILING DATE: 22-MAY-1992
FILING DATE: 12-DECEMBER-1991
FILING DATE: 12-DECEMBER-1991
FILING DATE: 23-SEPTEMBER-1991
FILING DATE: 23-SEPTEMBER-1991
FILING DATE: 29-UGLY-1991
FILING DATE: 9-UGLY-1991
FILING DATE: 3-MAY-1991
APPLICATION NUMBER: 07/705,702
FILING DATE: 23-MAY-1991
ATTORNEY AGENT INFORMATION:
AMANUE VARGENEY NUMBER: 37-MAY-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM COMPATIBLE OPERATING SYSTEM: IBM P.C. DOS 5.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Hanson, No. 6235525man D.
REGISTRATION NUMBER: 30,946
REGISTRATION NUMBER: 30,946
REPERRENCE/DOCKET NUMBER: LUD 5353
TELECOMMUTICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEPAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 nucleotides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AUNKESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 927 TITATCCCTCCTCTTC 942
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 81.27
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STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TOPOLOGY:
US-08-037-230D-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ઠ
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US-08-037-28D-28/c
; Sequence 28, Application US/08037230D
; Sequence 28, Application US/08037230D
; Patent No. 6235525
; GENERAL INFORMATION:
; APPLICANT: Gaugler, B atrice; Van den Eynde, Beno t;
; APPLICANT: van der Bruggen, Pierre; Boon-Falleur, Thierry
; TITLE OF INVENTION: Isolated Nucleic Acid Molecules Coding For
; TITLE OF INVENTION: Tumor Rejection Antigen Precursor Mage-3 And Uses Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                              STATE: New York
COUNTRY: U.S.A.
ZIP: 10112-3801
COMPUTER READABLE PORM:
MEDIUM TYPE: Diskette - 3.50 inch, 720 Kb storage.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 15.3%; Score 11.2; DB 1; Length 17; Best Local Similarity 76.5%; Pred. No. 1.1e+02; Matches 13; Conservative 0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                  ADDRESSE: FITZPATRICK, CELLA, HARPER & SCINTO STREET: 30 Rockefeller Plaza CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
COMPUTER: IBM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PS/V
OPERATING SYSTEM: MS-DOS Ver3.30
SOFTWARE: PATENT AID Ver1.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/616,990
FILING DATE: 14-Jul-2000
PRIOR APPLICATION DATA:
FILING DATE: 02-MAR-1992
                                                                                                           OHBAYASHI, Masaya
SHIMADA, Ritsuko
OKINAKA, Yasushi
TITLE OF INVENTION: NOVEL PLANT GENES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 )

DESCRIPTION: SYNTHETIC DNA

SEQUENCE DESCRIPTION: SEQ ID NO: 47
US-09-616-990-47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear MOLECULE TYPE: Other nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Perry, Lawrence S. REGISTRATION NUMBER: 31865
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-218-2100
, Patent No. 6232109
, GENERAL INFORMATION:
, APPLICANT: KIKUCHI, Yasuhiro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 ccneeccararrerred 17
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Felfe & Lynch
STREET: 805 Third Avenue
CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 47
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: ACW Y STATE: New Y 10022
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RESULT 89

US 09-583-80-28/C
Sequence 28.48pplcation US/09583850
PERSONAL NEW PORTAL NEW PRINCE:
PRINCE OF INVENTION: Included New Prince: Van den Evnde, BenoEt;
PRINCE OF INVENTION: Included New Prince: Soon Fallace Coding Por ITLE OF INVENTION: Included New Prince: Soon Fallace Mage-3 And Uses Thereof CORRESPONDENCES: DATE ADDRESS:
CORRESPONDENCES: Pales & Lynch CTTY: New York CLTY
CORRESPONDENCES: Pales & Lynch CTTY: Normal C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 25.0%; Pred. No. 1.1e+02;
Matches 4; Conservative 9; Mismatches 3;
                                                                               FELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          907 ATTITCTITGGICTIT 922
                                                                                                             TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: (5-3510
INFORMATION FOR SEQ ID NO: 28: SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 AUAUUCUCUGCUCUUU 17
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US-08-584-040-2874
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INCORMATION:
APPLICANT: Pavco, Pamela
APPLICANT: Stinchcomb, Dan T.
APPLICANT: Stinchcomb, Dan T.
APPLICANT: Escobedo, Jaime
ITILE OF INVENTION: METHOD AND REAGENT FOR THE
ITILE OF INVENTION: CONDITIONS RELATED TO LEVELS
ITILE OF INVENTION: OF VASCULAR ENDOTHELIAL
ITILE OF INVENTION: GROWTH FACTOR
NUMBER OF SEQUENCES: 8502
CORRESPONDENCE ADDRESS:
ADDRESSE: Lyon & Lyon
STREET: SAW WEST Fifth Street
STREET: SAW EST Fifth Street
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/584,040
FILING DATE: January 11, 1996
CLASSIFICATION: 514
PRIOR APPLICATION NAMER: 60/005,974
APPLICATION NUMBER: 60/005,974
FILING DATE: October 26, 1995
ATTORNEY AGENT INPORMATION:
NAME: WARDING, RIChard J.
NAME: WARDING, RIChard J.
FREIERRACE/DOCKET NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 218/064
TELECOMMUNICATION INFORMATION:
FELERAK: (213) 955-0440
FELEX: 67-3510
FELE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Los Angeles
COUNTY: Los Angeles
COUNTY: U.S.A.
ZIP: 9001-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: Storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/584,040
FILING DATE: January 11, 1996
CLASSIPICATION BATA:
PREJICATION NUMBER: 60/005,974
FILING DATE: October 26, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 218/064
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2874, Application US/08584040 Patent No. 6346398
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Sequence 28, Application US/09404026
Patent No. 656587
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Van der Bruggen, Pierre; Boon-Falleur, Thierry
APPLICANT: van der Bruggen, Pierre; Boon-Falleur, Thierry
TITE OF INVENTION: Isolated Nucleic Acid Molecules Coding For
TITE OF INVENTION: Tumor Rejection Antigen Precursor Mage-3 And Uses Thereof
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
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                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage COMPUTER: IBM
OPERATING SYSTEM: PC-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRICE APPLICATION DATA:
APPLICATION NUMBER: US/08/037,230
FILING DATE: 26-MARCH-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/04354
FILING DATE: 22-MAY-1992
PRIOR APPLICATION DATA: 12-MAY-1992
PRIOR APPLICATION DATA: 07/807,043
FILING DATE: 12-DECEMBER-1991
PRIOR APPLICATION DATA: 07/764,364
FILING DATE: 23-SEPTEMBER-1991
PRIOR APPLICATION NUMBER: 07/728,838
FILING DATE: 9-JULY-1991
PRIOR APPLICATION DATA: MAPLICATION NUMBER: 07/705,702
PRIOR APPLICATION NUMBER: 07/705,702
PRIOR PRIOR PATTON: NUMBER: 07/705,702
PREGISTRATION NUMBER: 30,946
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LUD 5353
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US-09-311-772B-119/c
; Sequence 119, Application US/09371772B
; Patent No. 6566127
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    927 TITAICCTCCTCTTC 942
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/
FILING DATE: 23-SEPT-1999
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                   SSEE: Felfe & Lynch
F: 805 Third Avenue
New York City
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (212) 838-3884 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16 rrescececrerere
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           nucleic acid
EDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
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Matches 13; Conserv
                                                                                                                                                                                                                                                                                                                                                                              STATE: New York
ZIP: 10022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS:
                                         RESULT 91
US-09-404-026-28/c
                                                                                                                                                                                                                                                                                                         ADDRESSEE:
STREET: 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
TOPOLOGY:
US-09-404-026-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    à
                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Gaugler, Beatrice; Van den Eynde, Benoit;
.van der Bruggen, Pierre; Boon-Falleur, Thierry
.van der Bruggen, Pierre; Boon-Falleur, Thierry
TITLE OF INVENTION: Isolated Nucleic Acid Molecules Coding
For Tumor Rejection Antigen Precursor Mage-3 And Uses There
                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .
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                                                                                                                 15.3%; Score 11.2; DB 1; Length 17; 81.2%; Pred. No. 1.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
                                                                                                                                                                  3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IEM
OPERATING SYSTEM: PC-DOS
SOSTEMARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/579,197
FILING DATE: 26-May-2000
CLASSIPICATION NUMBER: 08/037,230
FILING DATE: CINKNOWN-
APPLICATION NUMBER: 08/037,230
FILING DATE: CINKNOWN-
APPLICATION NUMBER: 07/04,364
FILING DATE: 23-SEPTEMBER-1991
APPLICATION NUMBER: 07/764,364
FILING DATE: 23-SEPTEMBER-1991
APPLICATION NUMBER: 07/764,364
FILING DATE: 3-SEPTEMBER-1991
APPLICATION NUMBER: 07/728,838
FILING DATE: 23-SEPTEMBER-1991
APPLICATION NUMBER: 07/728,838
FILING DATE: 23-MAY-1991
APPLICATION NUMBER: 07/728,838
FILING DATE: 23-MAY-1991
APPLICATION NUMBER: 1091
APPLICATION NUMBER: 1090
TELEPHONE: HABBORNIN ON 9652180man D. REGISTRATION NUMBER: 1010 5353
TELEPHONE: (212) 688-3864
                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; SEQUENCE DESCRIPTION: SEQ ID NO: 28:
US-09-579-197-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESSE:
ADDRESSE: Felle & Lynch
STREFT: 805 Third Avenue
CITY: New York City
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                    Sequence 28, Application US/09579197
Patent No. 6552180
GENERAL INFORMATION:
                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 17 nucleotides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 28: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     927 TTTATCCCTCCTCTTC 942
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Best Local Similarity 81.2
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
                                                                                                                                                                     13; Conservative
TYPE: nucleic acid
STRANDEDNESS: sing
                                                                                                                                        Best Local Similarity
Matches 13; Conserva
                                              linear
                                                                                                                                                                                                                                                                                                                                                                    US-09-579-197-28/c
                                           TOPOLOGY:
US-09-583-850-28
                                                                                                                                                                                                                                                                  16
                                                                                                                      Query Match
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APPLICANT: MCSWiggen, Jim
APPLICANT: MCSWiggen, Jim
APPLICANT: Stinchcomb, Dan
APPLICANT: Stoched, Jaime
TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
TITLE OF INVENTION: Method and Reagent for the Treatment Pactor Receptor
TITLE OF INVENTION: MEVEL 1990-08-10
CURRENT PILING DATE: 1990-08-10
PRIOR PILING DATE: 1995-10-26
PRIOR PILING DATE: 1996-01-08
NUMBER OF SEQ ID NOS: 14225
SOFTWARE: Patentin version 3.0
FEMALE. 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-827-998-621/c

i Sequence 621, Application US/09827998

j Patent No. 6656700:

APPLICANT: GENERAL INFORMATION:

APPLICANT: Shannon, Mark

ITILE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E

FILE REFERENCE: MDHMORF-8

CURRENT FILING DATE: 2001-04-06

PRIOR APPLICATION NUMBER: US 60/207,456

PRIOR FILING DATE: 2000-09-27

NUMBER OF SEQ ID NOS: 1881

SOFTWARE: Aeomica Sequence Listing Engine

PROMINGENT NO 6256700

SEQ ID NOS: 1881
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Sequence 622, Application US/09827998

Factor No. 6656700

GENERAL INFORMATION:

APPLICANT: Shannon, Mark

TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E

FILE REFERENCE: MDHMORF-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15.3%; Score 11.2; DB 1; Length 17; 81.2%; Pred. No. 1.1e+02; ive 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 17;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ch 15.3%; Score 11.2; DB 1; Similarity 81.2%; Pred. No. 1.18+02; 13; Conservative 0; Mismatches 3;
     Ribozyme Pharmaceuticals, Inc.
Pavco, Pam
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        914 TIGGICTITGCCTTTT 929
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       922 IGCCITITATCCCICC 937
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 81.2
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17 rescriciárscric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: RNA; ORGANISM: Homo sapiens
US-09-371-772B-5149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; ORGANISM: Homo sapiens
US-09-827-998-621
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 13; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
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                                           APPLICANT: PACO, Pam
APPLICANT: McSwiggen, Jim
APPLICANT: McSwiggen, Jim
APPLICANT: McSwiggen, Jim
APPLICANT: Stinchcomb, Dan
APPLICANT: Stinchcomb, Dan
APPLICANT: Stinchcomb, Jam
APPLICANT: Escobedo, Jame
TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
TITLE OF INVENTION: 100/09/31/198)
CURRENT APPLICATION NUMBER: US/09/311,72B
CURRENT APPLICATION NUMBER: US 60/005,974
PRIOR PILING DATE: 1995-10-26
PRIOR FILING DATE: 1996-01-08
NUMBER OF SEQ ID NOS: 14225
SOFTWARE: Patentin Version 3.0
LENGTH: 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Structon, Jim
APPLICANT: Structcomb, Dan
APPLICANT: Escobedo, Jaime
TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
TITLE OF INVENTION WIMBER: US/09/371,772B
CURRENT FILING DATE: 1999-10-10
PRIOR APPLICATION NUMBER: US 60/005,974
PRIOR APPLICATION NUMBER: US 08/584,040
PRIOR FILING DATE: 1996-01-08
NUMBER OF SEQ ID NOS: 14225
SOFTWARE: Patentin version 3.0
SEQ ID NO 1398
LENGTH: 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 93
US-00-371-772B-1398
Sequence 1398, Application US/09371772B
Patent No. 6566127
GENERAL INFORMATION:
APPLICANT: Ribozywe Pharmaceuticals, Inc.;
APPLICANT: Pavco, Pam
                             APPLICANT: Ribozyme Pharmaceuticals, Inc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 94
US-09-371-772B-5149/c
; Sequence 5149, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
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Best Local Similarity 81.2
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: RNA
CRGANISM: Homo sapiens
US-09-371-772B-119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: RNA
CNGANISM: Homo sapiens
US-09-371-772B-1398
GENERAL INFORMATION:
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RESULT 98
US-09-866-108A-7084/c
; Sequence 7084, Application US/09866108A
· Patent No. 6686188
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                                     934 CICCICITCATIGGIT 949
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81.2%;
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HANZEL, David K.
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Best Local Similarity 81.29
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US-09-866-108A-7084
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 99
US-08-256-568B-34
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APPLICANT: 01, Yonggang
APPLICANT: 01, Yonggang
APPLICANT: PENN, Sharron G.
APPLICANT: PENN, Sharron G.
APPLICANT: RANK, David K.
APPLICANT: RANK, David R.
APPLICANT: CHEN, Wensheng
APPLICANT: CHEN, Wensheng
APPLICANT: SHANNON, Mark
TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
THE REPERENCE: ABOMICAT:
CURRENT APPLICATION NUMBER: US/09/866,108A
CURRENT FILING DATE: 2001-05-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT PILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR PILING DATE: 2000-06-26
PRIOR FILING DATE: 2000-10-46
PRIOR FILING DATE: 2000-10-04
PRIOR PELING DATE: 2000-10-04
PRIOR PELING DATE: 2001-01-30
PRIOR PELING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR PELING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
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PRIOR FILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
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CURRENT APPLICATION NUMBER: US/09/827,998;
CURRENT FILING DATE: 2001-04-06;
PRIOR APPLICATION NUMBER: US 60/207,456;
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 60/236,359;
PRIOR FILING DATE: 2000-09-27;
NUMBER OF SEQ ID NOS: 1881;
SEQ ID NOS: 1881;
SEQ ID NO 622;
SEQ ID NO 622
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-866-108A-7083/c
; Sequence 7083, Application US/09866108A
; Patent No. 6686188
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Best Local Similarity 81.2%;
Matches 13; Conservative
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COGANISM: Homo sapiens
US-09-827-998-622
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US-09-866-108A-7083
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APPLICANT: RANK, Wensheng
APPLICANT: RANK, Wensheng
APPLICANT: CHEN, Wensheng
APPLICANT: CHEN, Wensheng
APPLICANT: CHEN, Wensheng
APPLICANT: SHANNON, MARK
ITILE OF INVENTION: WYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
FILE REPERBNCE: ABOMICA-7
CURRENT APPLICATION NUMBER: 105/02/04/05
FRIOR PILING DATE: 2000-05-26
FRIOR APPLICATION NUMBER: GB 24263.6
FRIOR APPLICATION NUMBER: GB 24263.6
FRIOR APPLICATION NUMBER: PCT/US01/00666
FRIOR APPLICATION NUMBER: PCT/US01/00666
FRIOR FILING DATE: 2001-01-30
FRIOR FILING DATE: 2001-01-30
FRIOR PLING DATE: 2001-01-30
FRIOR APPLICATION NUMBER: PCT/US01/00669
FRIOR APPLICATION NUMBER: 
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Fatent No. 5846704
Fatent No. 5846704
FAPLICANT: MAERTENS, GEERT; STUTVER, LIEVEN;
APPLICANT: MAERTENS, GEERT; STUTVER, HUGO
TITLE OF INVENTION: PROCESS FOR TYPING OF HCV
TITLE OF INVENTION: ISOLATES
NUMBER OF SEQUENCES: 97
CORRESSONDENCE ADDRESS:
ADDRESSEE: BIERMAN & MUSERLIAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 11.2; DB 1;
Pred, No. 1.1e+02;
0; Mismatches 3;
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Gaps
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15.1%; Score 11; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 11; Conservative 0; Mismatches 0; Indels
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US-09-378-900A-34
; Sequence 34, Application US/09378900A
; Patent No. 6495670
; GENERAL INFORMATION:
APPLICANT: MAERTENS, GERRT; STUYVER, LIEVEN;
APPLICANT: ROSSAU, RUDI; VAN HEUVERSWIN, HUGO
TITLE OF INVENTION: ISOLATES
TITLE OF INVENTION: STOLATES
CORRESPONDENCES: 97
CORRESPONDENCES: 97
CORRESPONDENCES: DIERMAN & MUSERLIAN
STREET: 600 THIRD AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
                             FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION NUMBER:
APPLICATION NUMBER:
PRIOR APPLICATION NUMBER:
PRIOR APPLICATION NUMBER:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FORTING DATE: 36-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP/93/402,129.6
FILING DATE: 31-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP/92/403,222.0
FILING DATE: 27-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: CHARLES A: MUSELLIAN
REGISTRATION NUMBER: 19.683
REFERENCE/DOCKET NUMBER: 410.004
TELEPHONE: (212) 661-8000
TELEPAX: (212) 661-8000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/378,900A
FILING DATE:
CLASSIPICATION:
PRIOR APPLICATION NUMBER: 08/256,568
FILING DATE: 18-JUL-1994
APPLICATION NUMBER: PCI/EP93/03325
FILING DATE: 26-NOV-1993
PRIOR APPLICATION NUMBER: PCI/EP93/03325
FILING DATE: 26-NOV-1993
                     APPLICATION NUMBER: US/09/038,369B
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15.1%; Score 11; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 11; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 100
US-038-369B-34

i Sequence 34, Application US/09038369B

j Patent No. 6171784

GENERAL INFORMATION:
APPLICANT: MAEMPENS, GERT; STUXVER, LIEVEN;
APPLICANT: ROSSAU, NUD1; VAN HEUVERSWYN, HUGO
ITILE OF INVENTION: ISOLATES
NUMBER OF SEQUENCES: 97

CORRESPONDENCE ADDRESS:
ADDRESSEE BIERMAN & MUSERLIAN
STARE: NEW YORK
COUNTRY: USA

ITILE OF THE OF THE AVENUE

CITY: NEW YORK
COUNTRY: USA

ISTATE: NEW YORK
COUNTRY: USA

CIP: 10016

CIP: NEW YORK

COMPUTER: Floppy disk

COMPUTER: Floppy disk

COMPUTER: BIAN PC compatible

COMPUTER: BIAN PC compatible

COMPUTER: SYSTEM: PC-DOS/MS-DOS
STREET: 600 THIRD AVENUE
CITY: NEW YORK
STATE: NEW YORK
CCUNTRY: USA
ZIP: 10016
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ISM PC COMPALIBLE
COMPUTER: ISM PC COMPALIBLE
COMPUTER: ISM PC COMPALIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/256,568B
FILING DATE: 18-JUL-1994
CLASSIFICATION NUMBER: PC/PEP3/03325
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP/92/403,222.0
FILING DATE: 31-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP/92/403,222.0
FILING DATE: 27-NOV-1992
ATTORNEY/AGENT INFORMATION:
APPLICATION NUMBER: 19,683
FILING DATE: (212) 661-8000
TELEFRAX: LENGER SEQ ID NO: 34:
SURPRINGENESS: SINGIE
TYPER: NUCLEIC SINGIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 / ANTI-SENSE: NO US-08-256-568B-34
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CURRENT APPLICATION DATA:
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GENERAL INFORMATION:
APPLICANT: Gaynor, Richard B.
APPLICANT: Li, Ching
APPLICANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 15;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 16;
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STATE: Tex.

COUNTRY: USA

COUNTRY: USA

ZIP: 77210

ZIP: 77210

COMPUTER READABLE FORM:

MEDIUM TYPE: Ploppy disk

COMPUTER: Ploppy disk

COMPUTER: Ploppy disk

COMPUTER: Ploppy disk

SOFTWARE: Patentin Release #1.0, Version #1.30

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION NUMBER: US/07/906,930E

FILING DATE: 30-UNN-1992

CLASSIFICATION NUMBER: 34,430

REFERENCE/DOCKET NUMBER: 34,430

REFEREN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 85.7%; Pred. No. 1.1e+02;
Matches 12; Conservative 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15.1%; Score 11; DB 1; Le
100.0%; Pred. No. 1.1e+02;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                          TOPOLOGY: linear MOLECULE TYPE: genomic DNA HYPOTHETICAL: NO ARTH. SENSE: NO SEQUENCE DESCRIPTION: SEQ ID NO: 34:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SSEE: Arnold, White & Durkee I: P. O. Box 4433 Houston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DESCRIPTION: /desc = "DNA"
                TELEFAX: (212) 661-8002
                                                       INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 base pairs
                                                                                                                                                                              TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             934 CICCICITCATIGG 947
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INFORMATION FOR SEQ ID NO: 8
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 100.
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   900 CCTGGTCATTT 910
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Pred. No. 1.1e+02;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 34, Application US/09899044

Patent No. 6548244

GENERAL INFORMATION:
APPLICANT: MAERTENS, GERT; STUYVER, LIEVEN;
ROSSAU, RUDI; VAN HEUVERSWYN, HUGO
TITLE OF INVENTION: PROCESS FOR TYPING OF HCV
NUMBER OF SEQUENCES: 97

CORRESPONDENCE ADDRESS:
ADDRESSEE: BIERMAN & MUSERLIAN
STREET: 600 THIRD AVENUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/899,044
FILING DATE: 06-011-2001
CLASSIFICATION: UNKNOWN-
PRIOR APPLICATION TO BATA:
APPLICATION DATA:
APPLICATION NUMBER: 09/378,900
FILING DATE: <0/0000000
FILING DATE: 26-NOV-1993
APPLICATION NUMBER: PCT/EP93/0325
FILING DATE: 31-AUG-1993
APPLICATION NUMBER: EP/92/403,222.0
FILING DATE: 37-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: CHARLES A. MUSERLIAN
REGISTRATION NUMBER: 19,683
REFERENCE/DOCKET NUMBER: 410.004
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
APPLICATION NUMBER: EP/93/402,129.6
FILING DATE: 31-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP/92/403,222.0
FILING DATE: 27-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: CHARLES A. MUSERLIAN
REGISTRATION NUMBER: 19,683
REFERENCE/DOCKET NUMBER: 410.004
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 base pairs
INFOR: NUCLEIC ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 10016
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15.1%; Scc.
100.0%; Pre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: genomic DNA HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          900 CCTGGTCATTT 910
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 cérédrécktrr 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; ANTI-SENSE:
US-09-378-900A-34
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 106
US-08-317-432A-2/c

### Sequence 2, Application US/08317432A

### Sequence 3, Application US/08/317432A
NUMBER OF SEQUENCES: 909
CORRESPONDENCE ADDRESS:
ADDRESSE: Lyon & Lyon
STREET: 633 Weet Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: Los Angeles
STATE: U.S.A.
ZIP: 900.71-2066
COMPUTEN READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: 15" Diskette, 1.44 Mb
MEDIUM TYPE: 10" DISKETE, 10" DISKETE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Watching, Kichard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 209/032
TELEPHONE: (213) 499-1600
TELEPHONE: (213) 955-0440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (4.2.)
TELEX: 67-510
INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     944 TIGGITTAATGTAT 957
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14 TTAGTTAAATGTAT 1
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Best Local Similarity 85.77
Matches 12; Conservative
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY:
US-08-334-847-46
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Pred. No. 1.1e+02;
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                                                                                                                                                                                                                          PAPELICANT: DESCRIPTION:
APPLICANT: DESCRIPTION:
APPLICANT: DESCRIPTION:
APPLICANT: PAVCO, PAM
TITLE OF INVENTION: INHIBITING RESPIRATORY
TITLE OF INVENTION: SYNCYTIAL VIRUS
NUMBER OF SEQUENCES: 909
CORRESCONDENCE ADDRESS:
ADDRESSE: Lyon & Lyon
STREET: 631 West Fifth Street
STREET: 631 West Fifth Street
STREET: 631 West Pifth Street
COMPUTER REPARABLE FORM:
MEDIUM TYPE: Storage
COMPUTER REPARABLE FORM:
MEDIUM TYPE: Storage
COMPUTER: BENCATION NUMBER: US/08/334,847
FILING DATE: NO. 5693532ember 4, 1994
PRIOR APPLICATION NUMBER: 32,327
REGISTRATION FOR SEQ ID NO: 45:
SEQUENCE CHARACTERISTICS:
LEEFPAN: (213) 955-0440
TELLERA (7-3510
TELLERA (7-3510
TELLERA (7-3510
TELLERA (7-3510
TELLERA (7-3510
TELLERA (7-3510
TYPE: nucleic acid
STRANDENNESS: single
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Patent No. 5693520:
GNESAL IMPORMATION:
APPLICANT: McSwiggen, James
APPLICANT: Draper, Kenneth
APPLICANT: Pavco, Pam
APPLICANT: Poolf, Tod
TITLE OF INVENTION: INHIBITING RESPIRATORY
TITLE OF INVENTION: SYNCYTIAL VIRUS
TITLE OF INVENTION: SYNCYTIAL VIRUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                        Sequence 45, Application US/08334847
Patent No. 5693532
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Best Local Similarity 85.7%;
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           944 TIGGITIAAIGIAT 957
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          14 CTCTCCTTCATTGG
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US-08-334-847-45
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US-08-334-847-46/c
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US-08-334-847-45/c
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                                                                                         Score 10.8; DB 1; Length 15;
Pred. No. 1.1e+02;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 15;
                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Stinchcomb, Daniel T.
APPLICANT: Stinchcomb, Daniel T.
APPLICANT: McSwigen, James
APPLICANT: McSwigen, James
TITLE OF INVENTION: METHOD AND REAGENT FOR THE
TITLE OF INVENTION: INDUCTION OF GRAFT TOLERANCE
TITLE OF INVENTION: AND REVERSAL OF IMMUNE RESPONSES
NUMBER OF SEQUENCES: 2751
CORRESPONDENCE ADDRESS:
ADDRESSE: Lyon & Lyon
STREET: Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 10.8; DB 1;
Pred. No. 1.1e+02;
6; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FEASESW Oversion 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/585,684B
FILING DATE: January 16, 1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/000,951
FILING DATE: July 7, 1995
ATTORNEY/AGENT INFORMATION:
NAME: WATDLIER: RICHARD
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 218/078
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECHARD: (213) 955-0440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
                                                                                                                                                                                                                                                                                     US-08-585-684B-271
; Sequence 271, Application US/08585684B
; Patent No. 5877021
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Match
Local Similarity 42.9%; Process 6; Conservative 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 271:
SEQUENCE CHARACTERISTICS:
                                                                                             Query Match
Best Local Similarity 85.7%;
Matches 12; Conservative
                                                                                                                                                                          924 CCTTTTATCCCTCC 937
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          943 ATTGGTTTAATGTA 956
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 15 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071
                    ; TOPOLOGY: linear; MOLECULE TYPE: DNA US-08-894-922A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
    STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TOPOLOGY:
US-08-585-684B-271
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US-08-959-853-7/c
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Matches
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US-08-894-922A-1/C
Sequence 1, Application US/08894922A
Patent No. 5863765
GENERAL INFORMATION:
APPLICANT: BERRY, Mark John
APPLICANT: DAND BR LOGT, Cornelius P.E.
APPLICANT: WAN DER LOGT, Cornelius P.E.
APPLICANT: WHITELAM, Garry Clark
TITLE OF INVENTION: PRODUCTION IN YEASTS OF STABLE ANTIBODY
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                   Query Match 14.8%; Score 10.8; DB 1; Length 15; Best Local Similarity 85.7%; Pred. No. 1.1e+02; Matches 12; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSE: Pillsbury Madison & Sutro, L.L.P. STREET: 1100 New York Avenue, N.W. CITY: Washington STREET: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               60113/241261
APPLICATION NUMBER: 08/919,872
FILING DATE: 27-Jul-92
APPLICATION NUMBER: 08/084,505
FILING DATE: 1-Jul-93
ATTORNEY/AGENT INFORMATION:
NAME: Friedman, Mark M.
REGISTRATION NUMBER: 33,883
REGISTRATION NUMBER: 128/7
TELEPHONE: 972-3-5625553
TELEPHONE: 972-3-5625554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 6011
TELECOMMUNICATION INFORMATION:
TELEFRAX: (202) -861-3503
TELEFRAX: (202) -822-0944
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    911 TCTTTGGTCTTTGC 924
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                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15 base pairs
                                                                                                                                                                                                                                                                     LENGTH: 15
TYPE: nucleic acid
STRANDEDNESS: single
TYPE: TOPOLOGY: linear
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 10.8; DB 1; Length 15;
Pred. No. 1.1e+02;
6; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Dempcy, Robert O.
APPLICANT: Gall, Alexander A.
APPLICANT: Incheov, Sergey G.
APPLICANT: Lokhov, Sergey G.
APPLICANT: Singer, Michael J.
APPLICANT: Singer, Michael J.
APPLICANT: Kutyavin, Igor V.
APPLICANT: Vermeulen, Nicolass M.J.
APPLICANT: Vermeulen, Nicolass M.J.
APPLICANT: PEoch Biosciences, Inc.
TITLE OF INVENTION: T.m. Leveling Methods
FILE REFERENCE: 17682A-003630US
CURRENT FILING DATE: 2001-12-21
PRIOR APPLICATION NUMBER: US 09/054,830
PRIOR FILING DATE: 1998-04-03
PRIOR APPLICATION NUMBER: US 09/054,832
PRIOR APPLICATION NUMBER: US 09/054,832
PRIOR PILING DATE: 1999-11-01
PRIOR APPLICATION NUMBER: US 09/640,953
PRIOR FILING DATE: 2000-03-01
PRIOR PILING DATE: 2000-01-06
PRIOR PILING DATE: 2000-01-16
PRIOR PILING DATE: 2000-01-16
PRIOR APPLICATION NUMBER: US 09/796,988
PRIOR FILING DATE: 2000-01-16
PRIOR PILING DATE: 2000-01-16
PRIOR PILING DATE: 2000-01-16
PRIOR APPLICATION NUMBER: US 09/796,988
PRIOR PILING DATE: 2000-01-16
PRIOR PILING DATE: 2000-01-16
PRIOR PILING DATE: 2000-01-16
PRIOR PILING DATE: 2000-01-16
PRIOR APPLICATION NUMBER: US 09/796,988
PRIOR PILING DATE: 2000-01-16
PRIOR PILING DATE: 2000-01-16
PRIOR PILING DATE: 2000-01-16
PRIOR APPLICATION NUMBER: US 09/796,988
PRIOR PILING DATE: 2000-01-16
PRIOR PILING DATE: 2001-02-28
CURRENT APPLICATION DATA:

PRING DATE:
FILING DATE:
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/58,684
FILING DATE:
FILING TOWN INFORMATION:
FILING FILING TOWN INFORMATION:
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FILING FILI
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Patent No. 6683173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 42.9%;
Matches 6; Conservative 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          943 ATTGGTTTAATGTA 956
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Patent No. 619410

GENERAL INFORMATION:
APPLICANT: Stinchcomb, Daniel T.
APPLICANT: Stinchcomb, Daniel T.
APPLICANT: McSwiggen, James
TITLE OF INVENTION: METHOD AND REAGENT FOR THE
TITLE OF INVENTION: MCSWIGGEN, TITLE OF INVENTION: MCSWIGGEN, TITLE OF INVENTION: AND REVERSAL OF INMUNE RESPONSES
NUMBER OF SEQUENCES: 2751
CORRESPONDENCES ADDRESS:
ADDRESSEE: Lyon & Lyon
                                                                                                                            PREEDL NO. 6090553

GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: USE OF URACIL-DNA GIYCOSYLASE
TITLE OF INVENTION: USE OF URALIL-DNA GIYCOSYLASE
TITLE OF INVENTION: UN GENETIC ANALYSIS
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSE:
STREET: 2500 Harbor Boulevard
CITY: Fullerton
STATE: ADSALE: Beckman
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage
COMPUTER: IBM compatible
OMBUTH TYPE: Diskette, 3.50 inch, 1.44 Mb storage
COMPUTER: IBM compatible
OMBUTH TYPE: Diskette, 3.50 inch, 1.44 Mb storage
COMPUTER: IBM compatible
OMBUTH TYPE: Diskette, 3.50 inch, 1.44 Mb storage
COMPUTER: IBM COMPATION:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage
COMPUTER: IBM WINDOWS S. - WORDPERFECT 7.0
SOFTWARE: ASCIT (DOS) TEXT
APPLICATION NUMBER: 20,022
REFERENCE/DOCKET NUMBER: 450-1566
TELEGOMMUNICATION INFORMATION:
NAME: P.R. HARGER
TELEFAX: (714) 773-7936
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH TYPE: NUCLEIC acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 30171
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FASTSEQ Version 1.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ALUNESSEE: Lyon & Lyon STREET: G13 West Fifth Street STREET: Suite 4700 CITY: Los Angeles STATE: California COUNTRY: U.S.A
                                                                    Sequence 7, Application US/08959853
Patent No. 6090553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        911 TCTTTGGTCTTTGC 924
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US-09-038-073-271
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Score 10.4, DB 1; Length 12;
Pred. No. 1e+02;
0; Mismatches 1; Indels
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-hes 1; Indels
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1S-09-475-947A-286/C

Sequence 286, Application US/09475947A

Patent No. 6472154

GENERAL INFORMATION:
APPLICANT: Garner, Harold R.
APPLICANT: Winna, John D.
APPLICANT: Winna, John D.
TITLE OF INVENTION: Folymorphic Repeats in Human Genes
FILE REFERENCY: US-09475,947A

CURRENT APPLICATION NUMBER: US/09/475,947A

CURRENT FILNG DATE: 1999-12-31

NUMBER OF SEQ IN NOS: 346

SOFTWARE: PATENTIN Ver. 2.1

FENCINE OF 286

SOFTWARE: PATENTIN Ver. 2.1
              85 : FROM 1 TO 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 10.4; DB 1;
Pred. No. 1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
RELEVANT RESIDUES IN SEQ ID NO:
US-08-173-489C-85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 91.7%;
Matches 11; Conservative (
                                                                                                                 Query Match
Best Local Similarity 91.7%;
Matches 11; Conservative
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Best Local Similarity 91.7
Matches 11; Conservative
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ORGANISM: Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TYPE: DNA
; ORGANISM: human
US-09-475-947A-286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-487-799-87
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ORGANISM: BOUNCE:
ORGANISM: Homo sapiens
POSITION IN GENOME:
CHROWOSOME/SEGMENT: chromosome 13
MAP POSITION: 13q14.2
PUBLICATION INFORMATION:
AUTHORS: Friend, S H, Horowitz, J M, Gerber, M R, AUTHORS: Wang X F, Bogenmann, E, Li, F P, Weinberg, AUTHORS: R A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: Genomic DNA
DESCRIPTION: retinoblastoma gene (Accession #
DESCRIPTION: M33647, J02994) nucleotides 2236 to 2247
                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Deletions of a DNA sequence in retinoblastomas and mesenchymal tumors: Organization of the sequence and its encoded
                                                                                                                                                                                                                                                                                  RESULT 112
US-08-173-489C-85/c
US-08-173-489C-85/c
Sequence 85, Application US/08173489C
Patent No. 5861244
GENERAL INFORMATION:
APPLICANT: WANG, C. -G.
TITLE OF INVENTION: GENETIC SEQUENCE ASSAY USING DNA TITLE OF INVENTION: TRIPLE-STRAND FORMATION.
NUMBER OF SEQUENCES: 365
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Proceedings of the National Academy of Sciences, USA
              Best Local Similarity 85.7%; Pred. No. 1.1e+02;
Matches 12; Conservative 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SSEE: PROFILE DIAGNOSTIC SCIENCES, INC.,
P. 5.10 EAST 73RD STREET,
NEW YORK
NEW YORK
XY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APELICATION DAILS

PELING DATE: 22 DEC 1993

CLASSIFICATION TO THE 435

PULDED DATE: 22 DEC 1993

CLASSIFICATION DATE: 435

PRICE APPLICATION DATE: 435

PRICE APPLICATION DATE: 436

FILING DATE: 29 OCT 1992

ATTORNEY AGENT INFORMATION:
NAME: Handelman, Joseph H.
REFERENCE/DOCKET NUMBER: 456,179

REGISTRATION NUMBER: 456,179

REFERENCE/COCKET NUMBER: 19518-6

TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION INFOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 10021
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44Mb storage
COMPUTER: IBM PC/XI/AT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM: MS-DOS version 6.2 SOFTWARE: Wordperfect Version 5.1 CURRENT APPLICATION DATA:
                                                                                                                     940 TICATIGGITIAAT 953
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9059-9063
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE: NI
COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    JOURNAL:
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Sequence 87, Application US/08487799C

Sequence 87, Application US/08487799C

Sequence 87, Application US/08487799C

Seteration No. 6010908

APPLICANT: Kunzelmann, Karl

TITLE OF INVENTION: GENEE THERAPY BY SMALL FRAGMENTS HOMOLOGOUS REPLACEMENT

TITLE OF INVENTION: GENEE THERAPY BY SMALL FRAGMENTS HOMOLOGOUS REPLACEMENT

FILE REFERENCE: 480.18-1(HV)

CURRENT APPLICATION NUMBER: US/08/487,799C

CURRENT FILING DATE: 1995-06-07

EARLIER PILING DATE: 1995-06-21

EARLIER FILING DATE: 1995-03-24

NUMBER OF SEQ ID NOS: 87

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 87
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 10.4; DB 1; Length 14;
Pred. No. 1.2e+02;
0; Mismatches 1; Indels
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US-08-319-492B-439

Sequence 439, Application US/08319492B

Sequence 439, Application

APPLICANT: Bullivan, Sean M.
APPLICANT: Bullivan, Sean M.
APPLICANT: Stinchoomb, Dan T.

ITILE OF INVENTION: REDOZYME TREATMENT OF DISEASES

ITILE OF INVENTION: OR CONDITIONS RELATED TO LEVELS

ITILE OF INVENTION: OP IL-5

NUMBER OF SEQUENCES: 751

CORRESPONDENCE ADDRESS:

ADDRESSE: Lyon & Lyon

STREET: Suite 4700
         CUUNTKIE U.S.C.

ZIPE 90071

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

MEDIUM TYPE: BECOMPATHE

COMPUTER: IEM COMPATHE

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/319,492B

FILING DATE: October 7, 1994

PRIOR APPLICATION DATA: including application

PRIOR APPLICATION NUMBER: 08/008/895

FILING DATE: December 7, 1992

ATTORNEY/AGENT INFORMATION:

NAME: Warburg, Richard

NEFERROCF/DOCKET NUMBER: 209/276

TELEFAX: (213) 955-0440

TELEFAX: (213) 955-0440

TELEFAX: (213) 489-1600

TELEFAX: (210) 480-1600

TELEFAX: (210) 480-1600

TELEFAX: (2
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STATE: California
COUNTRY: U.S.A.
ZIP: 90071
COMPUTER READBLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM Compatible OPERATING SYSTEM: IBM P.C. DOS 5.0 SOFTWARE: Word Perfect 5.1 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/319,492B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  935 TCCTCTTCATTG 946
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
TOPOLOGY:
US-08-319-492B-438
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 116
US-08-319-492B-438

| Sequence 438, Application US/08319492B
| Patent No. 5616488
| GENERAL INFORMATION:
| APPLICANT: Sullivan, Sean M. APPLICANT: Sullivan, James
| APPLICANT: Stinchcomb, Dan T. TILLE OF INVENTION: RIBOZYME TREATMENT OF DISEASES
| TILLE OF INVENTION: OF IL-5
| TILLE OF INVENTION: OF IL-5
| NUMBER OF SEQUENCES: 751
| CORRESPONDENCE ADDRESS:
| ADDRESSEE: Lyon & Lyon STREET: 633 West Fifth Street
| STREET: 633 West Fifth Street
| STREET: Sulte 4700
| CITY: Los Angeles
                                                                                                     Sequence 245, Application US/08105483

Patent No. 5494807

GENERAL INFORMATION:
TITLE OF INVENTION: GENETICALLY ENGINEERED VACCINE
TITLE OF INVENTION: STRAIN
NUMBER OF SEQUENCES: 462

CORRESPONDENCE ADDRESS:
ADDRESSES: c/o William S. Frommer
STREET: 530 Fifth Avenue
CITY: New York
STATE: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

MEDIUM TYPE: MEDIUM TYPE

MEDIUM MEDRE: US/08/105,483

MEDIUM TYPE

MEDIUM NUMBER: US 07/847,951

MAME: Frommer, William S.

MAME: Frommer, William S.

MAME: Frommer, William S.

MAME: Frommer, WINDER: 25,506

MEDIUM TELEPHONE: (212) 840-9712

MEDIUM TELEPAX: (212) 840-9713

MEDERATION FR SEQ ID NO: 245:

MEDRATION FR SEQ I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    945 TGGTTTAATGTA 956
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US-08-105-483-245
                                RESULT 115
US-08-105-483-245
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                                                          Query Match 14.2%; Score 10.4; DB 1; Length 15; Best Local Similarity 91.7%; Pred. No. 1.3e+02; Matches 11; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14.2%; Score 10.4; DB 1; Length 15; 91.7%; Pred. No. 1.3e+02; ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                              US-08-396-945-19
Sequence 19, Application US/08398945
Patent No. 5639872
GENERAL NECRMATION:
TITLE OF INVENTION: Human VEGF-Specific
TITLE OF INVENTION: Oligonucleotides
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/398,945
FILING DATE:
CLASSIFICATION: 435
ATTONEY/AGENT INFORMATION:
NAME: Kerner, Ann-Louise
REGISTRATION NUMBER: 33,523
REPERECAMUNICATION INFORMATION:
TELECHONE: 617-330-1300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 19, Application US/08501779
Patent No. 5661135
GENERAL INFORMATION:
APPLICANT: RObinson, Gregory S.
TITLE OF INVENTION: Human VEGF-Specific
TITLE OF INVENTION: Oligonucleotides
NUMBER OF SEQUENCES: 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Lappin & Kusmer
STREET: 200 State Street
CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 617-330-1311
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
                                                                                                                                               934 CTCCTCTTCATT 945
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         934 CTCCTCTTCATT 945
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Best Local Similarity 91.7
Matches 11; Conservative
                                                                                                                                                                                       3 CICCICITICATI 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Boston
STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRATION TO TO THE THE TO THE T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: US
; ANTI-SENSE:
US-08-502-185-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 120
US-08-501-779-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-398-945-19
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Pred. No. 1.3e+02;
6; Mismatches 1; Indels
                                        including application described below:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 19, Application US/08502185
| Patent No. 5639736
| CENERAL INFORMATION:
| TITLE OF INVENTION: Human VEGF-Specific TITLE OF INVENTION: 01igonucleotides
| TITLE OF INVENTION: 01igonucleotides
| TORRESPONDENCES: 53
| CORRESPONDENCE ADDRESS:
| ADDRESSEE: Lappin & Kusmer STREET: 200 State Street
| CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HYZ-031CPDV1
                 PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: 06/08,895
FILING DATE: January 19, 1993
APPLICATION NUMBER: 07/989,849
FILING DATE: December 7, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 209/276
TELECOMMUNICATION INFORMATION:
TELECHORE: (213) 955-0440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/502,185
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: KETERATION NUMBER: 33.523
REFERENCE/DOCKET NUMBER: HYZ-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-330-1300
INFORMATION FOR SEQ ID NO: 19: SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 439:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
    October 7, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14.28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                935 TCCTCTTCATTG 946
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Best Local Similarity 41.7
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 uccucuuccuug 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                linear
    FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
TOPOLOGY: 1
US-08-319-492B-439
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US-08-502-185-19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-38 - 18-260-19
Sequence 19, Application US/08378860
Sequence 19, Application US/08378860
Sequence 19, Application US/08378860
SEGNERAL INFORMATION:
APPLICANT: Robinson, Gregory S. APPLICANT: Smith, Lois E.H.
TITLE OF INVENTION: Neovascularization Using TITLE OF INVENTION: WGF-Specific TITLE OF INVENTION: USGF-Specific TITLE OF INVENTION: Oligonuclectides NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSES: Lappin & Kusmer STREET: 200 State Street
STREET: 200 State Street
STREET: 200 State Street
STREET: WASSACHUSELTS
STATE: MASSACHUSELTS
STATE: MASSACHUSELTS
STATE: WASSACHUSELTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 10.4; DB 1;
Pred. No. 1.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/378,860
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: KENTER: Ann-Louise
REGISTRATION NUMBER: 33,523
REFERENCE/DOCKET NUMBER: HYZ-031
TELECHONES: 617-330-1310
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
ITYPE: nucleic acid
STRANDEDNESS: single
TOPPLOGGY: linear
TOPPLOGGY: linear
TOPPLINEAR TYPE: CDNA
                                                          HYZ-031DV2
                                               REFERENCE DOCKET NUMBER: HYZ-
TELECOMUNICATION INFORMATION:
TELEPHONE: 617-330-1310
TELEFEX: 617-330-1311
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
STRANDEDNESS: single
                         REGISTRATION NUMBER: 33,523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     934 CICCICITCATT 945
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                                                                                                                                                                                                                                                                                                                                                                     linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                     ; TOPOLOGY: linea; MOLECULE TYPE: CE; HYPOTHETICAL: NO; ANTI-SENSE: YES US-08-501-713-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-378-860-19
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14.2%; Score 10.4; DB 1; Length 15;
Best Local Similarity 91.7%; Pred. No. 1.3e+02;
Matches 11; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-501-713-19;
Sequence 19, Application US/08501713
Patent No. 5710136;
GENERAL INFORMATION:
APPLICANT: Robinson, Gregory S.
APPLICANT: Smith, Lois B.H.
ITLE OF INVENTION: Inhibition of
TITLE OF INVENTION: USER-Specific
TITLE OF INVENTION: VEGF-Specific
TITLE OF INVENTION: VEGF-Specific
TITLE OF INVENTION: Oldgonuclectides
UNDMER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSE: Lappin & Kusmer
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: EMPROAGHE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HYZ-031CPDV2
                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/501,779
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Kerner, Ann-Louise
REGISTRATION NUMBER: 33,523
REFERENCE/DOCKET NUMBER: HYZ-031CPDV:
TELEPHONE: 617-330-1310
TELEPHONE: 617-330-1311
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGRATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERI
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lappin & Kusmer
STREET: 200 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFFWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/501,713
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
CLASSIPICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Kerner, Ann-Louise
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            934 CTCCTCTTCATT 945
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; MOLECULE TYPE: CDNA

; HYPOTHETICAL: NO

; ANTI-SENSE: YES

US-08-501-779-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-501-713-19
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Gaps
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Pred. No. 1.3e+02;
0; Mismatches 1; Indels
ue Taisne, Charles
...rulCANT: Limbach, Keith J.
APPLICANT: Johnson, Gerard P.
APPLICANT: Johnson, Steven E.
APPLICANT: Cox, William I.
APPLICANT: Audonnet, Jean-Christophe Francis
APPLICANT: Audonnet, Jean-Christophe Francis
APPLICANT: Audonnet, Jean-Christophe Francis
APPLICANT: Gettig, Russell Robert
TITLE OF INVENTION: GENETICALLY ENGINEERED VACCINE
TITLE OF INVENTION: STRAIN
NUMBER OF SEQUENCES: 467
CORRESPONDENCE ADDRESS:
ADDRESSEE: Curtis, Morris & Safford
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: DEAD PC Compatible
COMPUTER: DEAD PC COMPATIONS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/458,101
FILING DATE: 01-JUN-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Frommer, William S.
REGISTRATION NUMBER: 25,506
REBERENCE/POCKET UNMBER: 25,506
REBERENCE/POCKET UNDBER: 25,506
REBERENCE CALORETION:
INFORMATION FOR SEO ID NO: 245:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 19, Application US/08501626
Patent No. 5801156
GENERAL INFORMATION
APPLICANT: Robinson, Gregory S.
APPLICANT: Smith, Lois E.H.
TITLE OF INVENTION: Inhibition of
TITLE OF INVENTION: VEGF-Specific
TITLE OF INVENTION: Oligonucleotides
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lappin & Kusmer
STREET: 200 State Street
CITY: BOSTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIF: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 91.7
Marches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           945 TGGTTTAATGTA 956
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                rccrrraarcca 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 10036
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: Massachusetts
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       02109
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US-08-501-626-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
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                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: USA

ZIP: 10036

ZIP: 10036

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/709, 209

FILING DATE: 21-AUG-1996

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

PRIOR APPLICATION DATA:

PRIOR APPLICATION NUMBER: US 08/105, 483

FILING DATE: 12-AUG-1993

APPLICATION NUMBER: US 08/105, 483

FILING DATE: 12-AUG-1993

APPLICATION NUMBER: US 08/105, 483

FILING DATE: 06-MAR-1992

ATTONEY/AGENT INPORMATION:

NAME: RECOMMENTION:

NAME: RECOMMENT NOW WITHOUS: WITHOUS W
                                                                                                                                                                                                                                                                                                                                                                       RESULT 123
US-08-709-209-245
Sequence 245, Application US/08709209
Patent No. 5762938
GENERAL INFORMATION:
APPLICANT: Paoletti, Enzo
TITLE OF INVENTION: GENETICALLY ENGINEERED VACCINE
TITLE OF INVENTION: STRAIN
NUMBER OF SEQUENCES: 462
CORRESPONDENCE ADDRESS:
                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tartaglia, James
No. 5766599ton, Elizabeth K.
Riviere, Michel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Frommer, William S.
REGISTRATION NUMBER: 25.506
REFERENCE/DOCKET NUMBER: 454310-2400
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Curtis, Morris & Safford
ADDRESSEE: c/o William S. Frommer
STREET: 530 Fifth Avenue
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 124
US-08-458-101-245
Sequence 245, Application US/08458101
Setence 245, Application US/08458101
PAPELICANT: Paoletti, Enzo
APPLICANT: Paoletti, Marion E.
APPLICANT: Taylor, Jill
APPLICANT: Taylor, Jill
APPLICANT: Tartaglia, James
APPLICANT: Na. 5766599con, Elizabeth
APPLICANT: No. 5766599con, Elizabeth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (212) 840-3333
TELEFAX: (212) 840-0712
INFORMATION FOR SEQ ID NO: 245:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 945 TGGTTTAATGTA 956
                                                                                                                                                                                           934 CICCICITCATT 945
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                                                                                                                      11; Conservative
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TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                3 crccrcrrccrr 14
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
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14.2%; Score 10.4; DB 1; Length 15;
Best Local Similarity 91.7%; Pred. No. 1.3e+02;
Matches 11; Conservative 0; Mismatches 1; Indels
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Best Local Similarity 41.7%; Pred. No. 1.3e+02;
Matches 5; Conservative 6; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 8458, Application US/08584040
| Sequence 8458, Application US/08584040
| Patent No. 6346398
| Patent No. 6346398
| GENERAL INFORMATION:
| APPLICANT: Bavco, Pamela APPLICANT: Stinchcomb, Dan T. APPLICANT: Stinchcomb, Dan T. APPLICANT: Stinchcomb, Dan T. APPLICANT: Stinchcomb, Dan T. TITLE OF INVENTION: TREATMENT OF DISEASES OR TITLE OF INVENTION: CONDITIONS RELATED TO LEVELS ITILE OF INVENTION: OF VASCULAR ENDOTHELIAL TITLE OF INVENTION: OF VASCULAR ENDOTHELIAL ITILE OF INVENTION: GROWTH FACTOR NUMBER OF SEQUENCES: 8502
| CORRESPONDENCE ADDRESS:
| STREET: 633 West Fifth Street STREET: SILE 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/584,040
FILING DATE: January 11, 1996
CLASSIFICATION: 514
PRICR APPLICATION DATA:
APPLICATION NUMBER: 60/005,974
FILING DATE: October 26, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 218/064
TELECOMMUNICATION INFORMATION:
TELESCOMMUNICATION INFORMATION:
TELEBRONE: (213) 955-0440
TELEBRAX: (213) 955-0440
TELEBRAX: 67-3510
SEQUENCE CHARACTERISTICS:
TENGTH: 15 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
                                                                                                                                                                                                                                                                          934 CICCICITCAIL 945
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              922 TGCCTTTTATCC 933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: nucleic acid
STRANDEDNESS: single
                linear
                                                                                        YES
                              MOLECULE TYPE:
HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TOPOLOGY: ...
US-08-584-040-8458
                TOPOLOGY:
                                                                                        ; ANTI-SENSE:
US-08-501-356-19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-501-356-19

Sequence 19, Application US/08501356

Patent No. 5814620

GENERAL INFORMATION:
APPLICANT: Robinson, Gregory S.
APPLICANT: Smith, Lois E.H.
TITLE OF INVENTION: Inhibition of
TITLE OF INVENTION: VEGF-Specific
TITLE OF INVENTION: VEGF-Specific
TITLE OF INVENTION: Oligonuclectides
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Lappin & Kusmer STREET: 200 State Street
CITY: Boston
STRAET: Boston
STRAE: Boston
STRAET: Boston
STRAET: Boston
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: GONETIER: US/08/501,356
FILING DATE:
CLASSIFICATION NUMBER: US/08/501,356
FILING DATE: Ann-Louise
REGISTRATION NUMBER: A3,523
REFERENCE/DOCKET NUMBER: HYZ-031DV3
TELECOMMUNICATION: TELECOMMUNICATION:
TELECOMMUNICATION: TELECOMMUNICATION:
TELECOMMUNICATION INPORMATION:
                   SOFTWARE:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/501,626
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Kerner, Ann-Louise
REGISTRATION NUMBER: 33,523
REFRENCE/DOCKET NUMBER: HYZ-031DV4
FELECOMMUNICATION INFORMATION:
TELEFAX: 617-330-1310
FILEPAX: 617-330-1311
INFORMATION FOR SEQ ID NO: 19:
ELENGATION SEQ ID NO: 19:
LENGATION E CARACTERISTICS:
LENGATION E DASE PAIRS
TYPE: MOLECIC acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ANTT-SENSE: YES
OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELERAX: 617-330-1311
INFORMATION FOR SEQ ID NO: 15
SEQUENCE CHRACKTERISTICS:
LENGTH: 15 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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US-928-465-9/C
Sequence 9, Application US/08928465
Sequence 9, Application US/08928465
Patent No. 6204024
GENERAL INFORMATION:
APPLICANT: Lee, Eum Mi
TITLE OF INVENTION: ACRS RNA Transcription Based
TITLE OF INVENTION: Amplification Assay
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSE: AACO NO. 6204024el Patent Department
STREET: 1300 Piccard Drive
CITY: Rockville
STREET: Waryland
COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hepatitis B virus genome (subtype ayw) cloned in E coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RELEVANT RESIDUES IN SEQ ID NO: 167 :FROM 1 TO 16 US-08-173-489C-167
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MEDIUM TYPE: Floppy disk
GOMPUTER: IBM FO Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/928,465
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 10.4; DB 1;
Pred. No. 1.4e+02;
0; Mismatches 1;
                                                                                                                                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: genomic DNA
DESCRIPTION: heparitis B virus ayw isolate,
DESCRIPTION: nucleotides 2771 to 2786
HYPOTHETICAL: no
ANTI-SENSE: no
ORIGINAL SOURCE:
(attorney) (212) 708-1880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PUBLICATION INFORMATION:
AUTHORS: Galibert, F, Mandart, E, AUTHORS: Tiollais, P, Charnay, P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nucleotide sequence of the
                                                                                                                                                           TYPE: nucleic acid
STRANDEDNESS: double stranded
                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Hepatitis B virus INDIVIDUAL ISOLATE: ayw
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY AGENT INFORMATION:
NAME: Gormley, Mary B.
REGISTRATION NUMBER: 34,409
TELECOMMUNICATION INFORMATION:
TELEPHONE: 301-948-7400
                                  (212)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14.2%;
91.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 933 CCTCCTCTTCAT 944
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Best Local Similarity 91.7
Matches 11; Conservative
                               TELEFAX: (attorney) (2
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                   LENGTH: 16 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      646-650
   TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        JOURNAL:
VOLUME: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        à
                                                                                                                                                                                                                                                                                              APPLICANT: McSwiggen, Jim
APPLICANT: McSwiggen, Jim
APPLICANT: Bavco, Pam
APPLICANT: Stinchroub, Dan
TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
CURRENT APPLICATION NUMBER: US/09/371,772B
PRIOR APPLICATION NUMBER: US 60/005,974
PRIOR APPLICATION NUMBER: US 60/005,974
PRIOR FILING DATE: 1996-01-08
NUMBER OF SEQ ID NOS: 14225
SOFTWARE: Patentin version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
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Pred. No. 1.3e+02;
6; Mismatches 1; Indels
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US-08-173-489C-167/C
US-08-173-489C-167/C
Sequence 167, Application US/08173489C
Sequence 167, Application US/08173489C
Sequence 167, Application US/08173489C
Sequence 167, Application US/08173489C
Sequence 167, Application Constant Normalion Constant Name Constant Constant Side Constant Name Constant C
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COMPUTER READABLE FORM:
MEDIUM TYPER: 3.5 inch, 1.44Mb storage
COMPUTER: 18M PC/XT/AT
OPERATING SYSTEM: MS-DOS version 6.2
SOFTWARE: MORDER-fect Version 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/173,489C
CLASSIFICATION DATA:
PRING DATE: 2 DEC 1993
CLASSIFICATION DATA:
APPLICATION NUMBER: US 07/968,436
FILING DATE: 29 OCT 1992
ATTORNEY AGBRY INFORMATION:
NAME: Handelman, Joseph H.
REFERENCE/DOCKET NUMBER: U9518-6
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
                                                                                                                                                                         Sequence 4114, Application US/09371772B Patent No. 6566127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 41.7%;
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              922 TGCCTTTTATCC 933
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             3 UUCCUUUUAUCC 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-371-772B-4114
                                                                                                                                                US-09-371-772B-4114
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LENGTH: 15
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Gaps

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Indels

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; OTHER INFORMATION: Description of Artificial Sequence: synthetic; OTHER INFORMATION: oligonucleotide
US-09-813-781-57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DANIEL A.

TITLE OF INVENTION: PROCEDURES AND REGULATORY DNA SEQUENCES
FOR GENERICALLY ENGINEERING DISEASE RESISTANCE AND OTHER
FINDUCIBLE TRAITS IN PLANTS
OUNBER OF SEQUENCES: 9
CURRENT APPLICATION DATA:
REPLICATION NUMBER: US/07/393,301
FILING DATE: 13-JUN-1989
SEQ ID NO:9:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Indels
   TITLE OF INVENTION: AND A SINGLE-CHAIN T-CELL RECEPTOR FILE REFRENCE: 46/45(1758)
CURRENT APPLICATION DATE: US/09/813,781
CURRENT FILING DATE: 2001-03-22
NUMBER OF SEQ ID NOS: 130
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 57
LENGTH: 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5312912-9/c; Patent No. 5312912 | Patent No. 5312912 | Patent No. 5312912 | Patent No. 5312912 | Patent No. 540ROVITZ, STAPLICANT: HADWIGER, LEE A.; CHIANG, CHIN C.; HOROVITZ, STAPLICANT HADWIGER, LEE A.; CHIANG, CHIN C.; HOROVITZ, STAPLICANT STAPLICANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 10.4; DB 1;
Pred. No. 1.4e+02;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
14.2%; Score 10.4; DB 1;
Best Local Similarity 91.7%; Pred, No. 1.4e+02;
Matches 11; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 47, Application US/08334847
Fatent No. 5693532
GENERAL INFORMATION:
MCSWiggen, James
APPLICANT: Draper, Kenneth
APPLICANT: Pavoo, Pam
APPLICANT: Pavoo, Pam
APPLICANT: Pavoo, Pam
APPLICANT: Poolf, Tod
ITLE OF INVENTION: METHOD AND REAGENT FOR
ITLE OF INVENTION: MITBITING RESPIRATORY
ITLE OF INVENTION: SYNCYTIAL VIRUS
NUMBER OF SEQUENCES: 909
CORRESPONDENCES 1900 & Lyon
STREET: Suite 4700
STREET: Suite 4700
STREET: Suite 4700
                                                                                                                                                                                                                                                    TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 91.7%;
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                917 GICTITGCCTIT 928
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         940 TICATIGGITTA 951
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13 TTCAATGGTTTA 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Di
MEDIUM TYPE: storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: U.S.A. ZIP: 90071-2066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 134
US-08-334-847-47/c
                                                                                                                                                                                                                                                                                                                     FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    셤
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Sequence 101, Application US/0866341A

Sequence 101, Application US/0866341A

Patent No. 6365345

GENERAL INFORMATION:

APPLICANT:

TITLE OF INVENTION: Antisense nucleic Acids for the

TITLE OF INVENTION: Of c-exbB plays a role

NUMBER OF SEQUENCES: 106

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                  ö
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Patent No. 6405989
GENERAL INFORMATION:
APPLICANT: WEIDANZ, JON A.
APPLICANT: CARD, KIMBERLYN F.
APPLICANT: WONG, HING C.
TITLE OF INVENTION: FUSION PROTEINS COMPRISING BACTERIOPHAGE COAT PROTEIN
                                                                                                                                                                                                                                                                                                                  o,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
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Pred. No. 1.4e+02;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                  1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Jacobson, Price, Holman and Stern, PLLC STREET: 400 Seventh street, N.W. STREET: Ashington STATE: D.C. COUNTRY: USA
                                                                                                                                                                                                                                             Query Match

14.2%; Score 10.4; DB 1;
Best Local Similarity 91.7%; Pred. No. 1.4e+02;
Matches 11; Conservative 0; Mismatches 1;
TYPE: nucleic acid
STRANDEDNESS: single
FOPOLOGY: not relevant
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "DNA Oligonulceotide"
US-08-928-465-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14.2%;
91.7%;
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Best Local Similarity 91.7
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                      13 TTTAATGTATGG 2
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US-09-813-781-57/c
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Length 16;

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ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: 1BM Compatible
COMPUTER: IBM Compatible
OPERATION TYPE: Word Perfect 5.1
CURRENT APPLICATION DATA: 1994
FILING DATE: September 23, 1994
CLASSIFICATION DATA: accribed below:
FILING DATE: September 23, 1994
CLASSIFICATION DATA: including application
FRIOR APPLICATION NUMBER: 09/089,849
FILING DATE: December 7, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 209/166
TELEFNOW: (213) 955-0440
TELEFNX: (213) 955-0440
INFORMATION ECHARACTER STICS:
LENGTH: 15 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 3.6 Application US/08311486C
Sequence 3.6 Application US/08311486C
SEQUENCE 5.8 Application US/08311486C
SENERAL INFORMATION:
APPLICANT: Sean Sullivan
APPLICANT: Kenneth Draper
APPLICANT: Mames McSwiggen
APPLICANT: Application Condition
APPLICANT: Application Condition
APPLICANT: Revin Kisich
APPLICANT: Application
APPLICANT: NEWINION: RIBOZYME TREATMENT OF
TITLE OF INVENTION: BISEASES OR CONDITIONS
TITLE OF INVENTION: RELATED TO LEVELS OF
TITLE OF INVENTION: TNF.
CORRESPONDENCE ADDRESS:
ADDRESSE:
ADDR
                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match

14.0%; Sc
Best Local Similarity 80.0%; Pr
Matches 12; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      944 TIGGITTAATGIATC 958
    TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 5
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15 rrgarrgrardrard 1
         (213) 955-0440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS: Sin
                                                                                                                                                                                                                                                                                                                       linear
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TOPOLOGY:
US-08-334-847-53
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US-08-311-486C-36
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Patent No. 569532
GENERAL INFORMATION:
APPLICANT: McSwigen, James
APPLICANT: Draper, Kenneth
APPLICANT: Pavco, Pam
APPLICANT: Povco, Pam
APPLICANT: Povco, Pam
APPLICANT: Woolf, Tod
TITLE OF INVENTION: INHIBITING RESPIRATORY
TITLE OF INVENTION: SYNCYTIAL VIRUS
NUMBER OF SEQUENCES: 909
CORRESPONDENCE ADDRESS:
COMPUTER: IBM Compatible
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/334,847
FILING DATE: No. 569353cmber 4, 1994
PRIOR APPLICATION DATA:
APPLICATION DATA:
FILING DATE: No. 569353cmber 4, 1994
PRIOR APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REGRENCE/DOCKET NUMBER: 39/032
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFACE: (213) 955-0440
INFORMATION FOR SEQ ID NO: 47:
CENTRY OF SEQ ID NO: 47:
CEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IEM COMPATIBLE
OPERATING SYSTEM: IEM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
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APPLICATION NUMBER: US/08/334,847
FILING DATE: No. 563532ember 4, 1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: Callfornia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REPRENCE/DOCKET NUMBER: 209/
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                942 CATTGGTTTAATGTA 956
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15 CGTTAGTTAATGTA 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TOPOLOGY: linear
US-08-334-847-47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 135
US-08-334-847-53/c
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219-228
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US-08-585-684B-272
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DESCRIPTION: dystrophin gene (Accession # M18533,
DESCRIPTION: dystrophin gene (Accession # M18533,
DESCRIPTION: M17154, M18026) mucleotides 13280 to 13294
HYPOTHETICAL: No
ANTI-SENSE: No
ORGANISM: Homo sapiens
POSITION IN GENOME:
CHROMSOME-SENBENT: A-chromosome
MAP POSITION: X521.3-p1.1
PUBLICATION INFORMATION: AP21.3-p21.1
PUBLICATION INFORMATION: AP21.3-p1.1
AUTHORS: Koenig, M, Hoffman, E P, Bertelson, C J,
AUTHORS: Monaco, A P, Feener, C, Kunkel, L M.
TITLE: Complete cloning of the
TITLE: preliminary genomic organization of the DMD
TITLE: gene in normal and affected individuals
JOURNAL: SO
PAGES: 509-517
                                                  Query Match
14.0%; Score 10.2; DB 1; Length 15;
Best Local Similarity 46.7%; Pred. No. 1.4e+02;
Matches 7; Conservative 5; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                    RESULT 137
US-08-173-489C-45
is Sequence 45, Application US/08173489C
is Berent No. 5861244
is GENERAL INFORMATION:
is APPLICANT: HEPBURN, A. G.
is TITLE OF INVENTION: GENETIC SEQUENCE ASSAY USING DNA.
ITLE OF INVENTION: TRIPLE-STRAND FORMATION.
is NUMBER OF SEQUENCES: 365
is CORRESPONDENCE ADDRESS:
is ADDRESSED: PROFILE DIAGNOSTIC SCIENCES, INC.,
is STREET: 510 EAST 73RD STREET,
is STREET: NEW YORK
is STATE: NEW YORK
is STATE: NEW YORK
is SCUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: USAS
ZIP: USAS
ZIP: USAS
ZIP: USAS
ZIP: USADDABLE FORM:
MEDLUM TYPE: 3.5 inch, 1.44Mb storage
COMPUTER: IBM PC/XT/AT
OPERATING SYSTEM: MS-DOS version 6.2
SOFTWARE: WORDER-FECT VERSIOn 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/173,489C
TILING DATE: 22 DEC 1993
CLASSIFICATION DATA:
APPLICATION NUMBER: US/08/173,489C
FILING DATE: 29 OCT 1992
ATTORNEY/AGENT INFORMATION:
NAME: Handelman, Joseph H.
REGISTRATION NUMBER: US-6179
REFERENCE/DOCKET UNDRER: US-18-6
TELECOMMUNICATION INFORMATION:
TELEFHONE: (attorney) (212) 246-8959
INFORMATION FOR SEQ ID NO: 45:
ENGTH: 15 base pairs
TYPE: NUCLEIC Acid
STRANDEDNESS: double stranded
TOPLOGY: Linear TOPE: USA
                                                                                                                                                        923 GCCTTTTATCCCTCC 937
                                                                                                                                                                                          1 GCCUCCUCCCUCC 15
US-08-311-486C-36
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AUTHORS: Kunkel, 1.W.

AUTHORS: Kunkel, 1.W.

TITLE: Conservation of the Duckense

TITLE: Conservation of the Duckense

TITLE: Conservation of the Duckense

DATE: 1386

DATE: 1386

TITLE: Operation of the Duckense

PROCESS 347-350

DATE: 1386

TITLE: The complete grapance of

TITLE: The complete
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                                                               Score 10.2; DB 1; Length 15;
Pred. No. 1.4e+02;
6; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Stinchcomb, Daniel T.
APPLICANT: Jarvis, Thale
APPLICANT: McSwiggen, James
TITLE OF INVENTION: METHOD AND REAGENT FOR THE
TITLE OF INVENTION: INDUCTION OF GRAFT TOLERANCE
TITLE OF INVENTION: AND REVERSAL OF IMMUNE RESPONSES
NUMBER OF SEQUENCES: 2751
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: U.S.A.
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: SLORAGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
OPERATING SYSTEM: IBM P.C. DOS 5.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/038,073
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  218/078
                                                                                                                                                                                                                                                         Sequence 272, Application US/09038073
Patent No. 6194150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/585,684
                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Warburg, Richard
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 216
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
                                                                   14.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14.0%;
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                                                                                                                                                           UUGCUUAAUGUAAC 15
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                                                    Query Match
Best Local Similarity 40.vv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEX: 67.3510
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 40.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: nucleic acid
STRANDEDNESS: single
   single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Los Angeles
STRANDEDNESS: sin
TOPOLOGY: linear
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                    ; TOPOLOGY: 1
US-08-585-684B-272
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
US-09-038-073-272
                                                                                                                                                                                                                          RESULT 139
US-09-038-073-272
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RESULT 14.
US-09-479-770A-15
; Sequence 15, Application US/09479770A
; Sequence 15, Application US/09479770A
; Patent NO: 6391555
; GENERAL INFORMATION:
APPLICANT: Johnson, Eric S.
; APPLICANT: Johnson, Exic S.
; TITLE OF INVENTION: Assay for the Detection of Avian Leukosis/Sarcoma
; TITLE OF INVENTION: Assay for the Detection of Avian Leukosis/Sarcoma
; ITLE OF INVENTION: Assay for the Detection of Avian Leukosis/Sarcoma
Patent No. 6391555
GENERAL INFORMATION:
APPLICANT: Johnson, Eric S.
TITLE OF INVENTION: Assay for the Detection of Avian Leukosis/Sarcoma
TITLE OF INVENTION: Assay for the Detection of Avian Leukosis/Sarcoma
Viruses (ALSV) in DNA from Human and Animal Biological Speci
                                                                                                                                                   NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSE: GARVEY, SMITH, NEHRBASS & DOODY, L.L.C.
STREET: Three Lakeway Center, Suite 3290 3838 No. 6391555th Causeway
BOUlevard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: GARVEY, SMITH, NEHRBASS & DOODY, L.L.C.
STREET: Three Lakeway Center, Suite 3290 3838 No. 6391555th Causeway
Boulevard
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COMPUTEX: USA
COMPUTEX ESADABLE-FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage
COMPUTEN: Dell Diamension XPS D300
OPERATING SYSTEM: Windows 98
SOFTWARE: Microsoft Word 2000
                                                                                                                                                                                                                                                                                                                                                              ZIP: 70002-1767
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage
COMPUTER: Dell Dimension XPS D300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                               OCHRATING STATEM WINDOWS SOFTWARE: MICROSOFT WINDOWS SOFTWARE: MICROSOFT WORD 2000
CURRENT APPLICATION DATA: US/09/479,770A
APPLICATION NUMBER: US/09/479,770A
FILING DATE: 07-0ct-2000
CLASSIFICATION DATA:
APPLICATION NUMBER: 60/115,087
FILING DATE: 07-JAN-1999
ATTORREY/AGENT INFORMATION:
NAME: Nehrbass, Seth M.
REGISTRATION NUMBER: 31,281
REFERENCE/DOCKET NUMBER: A98146US (88126.1)
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 10.2; DB 1;
Pred. No. 1.4e+02;
0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE DESCRIPTION: SEQ ID NO: 13:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (504) 835-2000
TELEFAX: (504) 835-2070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGIH: 15 nucleotides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (504) 835-2
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14.0%;
80.0%;
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Best Local Similarity 80.03
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Metairie
                                                                                                                                                                                                                                                                                      CITY: Metairie
                                                                                                                                                                                                                                                                                                               STATE: LA
COUNTRY: USA
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FILING DATE:
CLASSIFICATION: 435
RICA APPLICATION DATA:
APPLICATION NUMBER: US/07/882,713
         Sequence 254, Application US/09475947A
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linear
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STRANDEDNESS: singl
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
ORGANISM: human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-475-947A-254
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US-09-031-952-8/C

US-09-031-952-8/C

Sequence 8, Application US/09031952A

Patent No. 6395476

GENERAL INFORMATION:
APPLICANT: Thomas, Howard C.
APPLICANT: Summerfield, John A.
APPLICANT: Summerfield, John A.
TITLE OF INVENTION: METHODS OF PREDICTING THE OUTCOME OF INFECTION
FILE REFERENCE: Thomas
CURRENT FILING DATE: 1998-01-27
CURRENT FILING DATE: 1998-01-27
EARLIER APPLICATION NUMBER: 951539-8
EARLIER FILING DATE: 1995-07-09
EARLIER APPLICATION NUMBER: 9614414.2
EARLIER PILING DATE: 1996-07-09
EARLIER PILING DATE: 1996-07-05
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 8
LENGTH: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 80.0%; Pred. No. 1.4e+02;
Matches 12; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
14.0%; Score 10.2; DB 1; Length 15;
Best Local Similarity 80.0%; Pred. No. 1.4e+02;
Matches 12; Conservative 0; Mismatches 3; Indels
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/479,770A
FILING DATE: 07-Oct-2000
CLASSIFCATION: 435
FRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: 60/115,087
FILING DATE: 07-JAN-1999
ATTORNY/AGENT INFORMATION:
REGISTRATION NUMBER: 31,281
REPERENCE/DOCKET NUMBER: 498146US (88126.1)
TELECOMMUNICATION INFORMATION:
TELECHONE: (504) 835-2070
INFORMATION FOR SEQ. ID NO: 15:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; increase incledides; incledides; incledides; incledides; incledid stranceDNESS: single; sequence description: Sequence description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        930 ATCCCTCCTCTTCAT 944
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 AGCCATCCGCTTCAT 15
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US-09-475-947A-254/c
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ö Query Match 14.0%; Score 10.2; DB 1; Length 15; Best Local Similarity 80.0%; Pred. No. 1.4e+02; Matches 12; Conservative 0; Mismatches 3; Indels Length 10; PATENT NO. 647-2154
GENERAL INFORMATION:
PAPPLICANT: Garner, Harold R.
APPLICANT: Wren, Jonathan D.
TITLE OF INVENTION: Polymorphic Repeats in Human Genes
FILE REFERENCE: USD0667;
CURRENT APPLICATION NUMBER: US/09/475,947A;
CURRENT FILING DATE: 1999-12-31
NUMBER OF SEQ ID NOS: 346
SOFTWARE: PATENTIN VET. 2.1
SEQ ID NO 254 DB 1; 13.7%; Score 10; FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 197/294
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:

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Gaps
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0
APPLICANT: HEPBURN, A. G.
TITLE OF INVENTION: GENETIC SEQUENCE ASSAY USING DNA
TITLE OF INVENTION: TRIPLE-STRAND FORMATION.
NUMBER OF SEQUENCES: 365
CORRESPONDENCE ADDRESS:
ADDRESSEE: PROFILE DIAGNOSTIC SCIENCES, INC.,
STREET: 510 EAST 73RD STREET,
CITY: NEW YORK
STATE: NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Hepatitis B virus
INDIVIDUAL ISOLATE: adw2
INDIVIDUAL ISOLATE: adw2
PUBLICATION INFORMATION:
AUTHORS: Valenzuela, P, Quiroga, M, Zaldivar, J, AUTHORS: Gray, P, Ruter, W J.
TITLE: The nucleotide sequence of
TITLE: the Hepatitis B viral genome and the
TITLE: identification of the major viral genes
JONENAL: In "Animal Virus Genetics", Fields, B N, JONENAL: Jaenisch, R, Fox C F eds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Quiroga, M, Zaldivar, J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; RELEVANT RESIDUES IN SEQ ID NO: 185 :FRCM 1 TO 14 US-08-173-499C-185
                                                                                                                                                                                                              ZIP: 10021.

COMPUTER READABLE FORM:
MEDIUW TYPE: 3.5 inch, 1.44Mb storage
COMPUTER: IBM PC/XT/AT
OPERATING SYSTEM: MS-DOS version 6.2
SOFFWARE: Wordperfect Version 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/173,489C
FILING DATE: 22 DEC 1993
CLASSIFICATION DATA:
APPLICATION NUMBER: US 07/968,436
FILING DATE: 29 OCT 1992
ATTORNEY/AGENT INFORMATION:
NAME: Handelman, JOSeph H.
REGISTRATION NUMBER: 26,179
REFERENCE/DOCKET NUMBER: 26,179
REFERENCE/DOCKET NUMBER: 26,179
TELEPHONE: (attorney) (212) 708-1880
TELECOMUNICATION INFORMATION:
TELEPHONE: (attorney) (212) 246-8959
INFORMATION FOR SEQ ID NO: 185:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 base pairs
TYPE: nucleic acid
TYPE: TYPE: genomic DNA
DESCRIPTION: nucleotides 1810 to 1823
HYPOTHETICAL: no
ANTI-SENSE: A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13.7%; Score 10; DB 1; Le
100.0%; Pred. No. 1.4e+02;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-173-489C-197; Sequence 197, Application US/08173489C; Patent No. 5861244; PARERAL INPORMATION: APPLICANT: WANG, C. -G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ANTI-SENSE: no
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         57-70
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                                           Gaps
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                                                                                                                                                                                           RESULT 145
US-08-363-233B-13/C
US-08-363-233B-13/C
Sequence 13, Application US/08363233B.
Patent No. 5714383
GENERAL INFORMATION:
APPLICANT: Thompson, James D.
TITLE OF INVENTION: MELOGENOUS LEUKEMIA
ITLE OF INVENTION: MYELOGENOUS LEUKEMIA
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSE: Lyon & Lyon
                Pred. No. 1e+02;
6; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 12;
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s 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: December 23, 1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA: including application
PRIOR APPLICATION DATA: including application
PRIOR APPLICATION DATA: described below:
APPLICATION NUMBER: 07/882,822
FILING DATE: FEbruary 7, 1994
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 23,327
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
13.7%; Score 10; DB 1;
Best Local Similarity 100.0%; Pred. No. 1.2e+0
Matches 10; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSEQ for Windows 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/363,233B
FILING DATE: December 23, 1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: 209/165
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAS: (213) 955-0440
TELEX: 67-3-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 146
US-08-173-489C-185
Sequence 185, Application US/08173489C
Patent No. 5861244
GENERAL INFORMATION:
APPLICANT: WANG, C.-G.
                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Lyon & Lyon STREET: 633 West Fifth Street STREET: 801te 4700 CITY: Los Angeles CITY: Los Angeles COUNTRY: U.S.A. ZIATE: 90071-2066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
                Best Local Similarity 40.0%;
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: nucleic acid
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                   902 TGGTCATTTT 911
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1 UGGUCAUTUT 10
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US-08-363-233B-13
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                                                                               TITLE OF INVENTION: METHOD AND REAGENT FOR THE
TITLE OF INVENTION: INDUCTION OF GRAFT TOLERANCE
TITLE OF INVENTION: AND REVERSAL OF IMMUNE RESPONSES
NUMBER: OF SEQUENCES: 2751
CORRESPONDENCE ADDRESS:
ADDRESSER: Lyon & Lyon
STREET: 631 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STREET: Galdeles
STREE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-555-684B-2258

Sequence 2258, Application US/08585684B
Sequence 2258, Application US/08585684B
Sequence 2258, Application US/08585684B
Sequence 2258, Application US/08585684B
Sequence 2258, Application
Sequence 2258, Application
TOTOMERATION
TOTO
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13.7%; Score 10; DB 1; I
Best Local Similarity 50.0%; Pred. No. 1.5e+02;
Matches 5; Conservative 5; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEX: 67-310

INFORMATION FOR ESQ ID NO: 2257:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
TYPE: nucleic acid
STRANDENESS: single
;
TOPOLOGY: linear
US-08-585-6848-2257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      917 GTCTTTGCCT 926
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STATE: California
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX:
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APPLICANT: HERBURN, A. G.
TITLE OF INVENTION: GENETIC SEQUENCE ASSAY USING DNA
TITLE OF INVENTION: TAIPLE-STRAND FORMATION.
NUMBER OF GENETIC STRAND FORMATION.
NUMBER OF GENETIC STRAND FORMED INC.,
STREET: S.O. BRAY 73RD STREET,
CONFRICTION.
STREET: NEW YORK
CONFIT NEW FOLK NEW SOON
SOOTHARE: WON YORK
STATE: 23 DGC 1993
FILING APPLICATION HARBER: US 08/173,489C
FILING DATE: 29 DGC 1993
FILING DATE: 20 DGC 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DATE: 1983
; RELEVANT RESIDUES IN SEQ ID NO: 197 :FROM 1 TO 14
US-08-173-489C-197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 148
US-08-565-684B-2257
Sequence 2257, Application US/08585684B
Patent No. 5877021
GENERAL INFORMATION:
APPLICANT: Stinchcomb, Daniel T.
APPLICANT: McSwiggen, James
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 100.
Matches 10, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     935 TCCTCTTCAT 944
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                                                                                                                                                                                                          13.7%; Score 10; DB 1; Length 15; 50.0%; Pred. No. 1.5e+02; tive 5; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-038-073-2258

Sequence 2258, Application US/09038073

Sequence 2258, Application US/09038073

GENERAL INFORMATION:
APPLICANT: Stinchcomb, Daniel T.
APPLICANT: OF UNCENTION: METHOD AND REAGENT FOR THE TITLE OF INVENTION: INDUCTION OF GRAFT TOLERANCE TITLE OF INVENTION: INDUCTION OF GRAFT TOLERANCE TITLE OF INVENTION: AND REVERSAL OF IMMUNE RESPONSES NUMBER OF SEQUENCES: 2751

CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: Saite 4700

STREET: Saite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13.7%; Score 10; DB 1; I 50.0%; Pred. No. 1.5e+02; tive 5; Mismatches 0;
                                                                                                                                                                                                                                                         5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Fast-SEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/038,073
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Kichard
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 218/078
TELEPHONE: (213) 489-4600
TELEPHONE: (213) 489-4600
TELEPHONE: (213) 955-0440
TELEPHONE: (213) 955-0440
INFORMATION FOR SEQ ID NO: 2258:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/585,684
FILING DATE:
                          INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
TYPE: nucleic acid
STRANIEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                               Best Local Similarity 50.0 Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    : 15 base pairs
nucleic acid
EDNESS: single
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Matches 5; Conservative
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                                                                                                                                                                                                                                                                                                       917 GTCTTTGCCT 926
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4 GUCUUUGCCU 13
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                                                                                                                                            TOPOLOGY: JUS-09-038-073-2257
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                                                                                                                                                                                                                 Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Stinchcomb, Daniel T.
APPLICANT: Stinchcomb, Daniel T.
APPLICANT: Jarvis, Thale
APPLICANT: Jarvis, Thale
TITLE OF INVENTION: METHOD AND REAGENT FOR THE
TITLE OF INVENTION: INDUCTION OF GRAFT TOLERANCE
TITLE OF INVENTION: AND REVERSAL OF INMUNE RESPONSES
NUMBER OF SQUENCES: 2751
CORRESPONDENCE ADDRESS:
ADDRESSE: Lyon & Lyon
STREET: Suite 4700
STREET: Suite 4700
SOFTWATER FESTENCY OF S.O.
SOFTWATER: FASTENCY VERSION 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/585,684B
FILING DATE: January 16, 1996
FILING DATE: JANUARY, 1995
PHIOR DATE: JULY 7, 1995
FILING DATE: JULY 7, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard
REGISTRATION NUMBER: 218/078
FEFERENCE/DOCKET NUMBER: 218/078
TELEFRAMINICATION INFORMATION:
TELEFRAM: (213) 955-0440
TELEFRAMINICATION FOR SEQ ID NO: 2258:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
TYPE: ULINGTH: SINGLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READBLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FARSENG VERSION 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/038,073
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTLING DATA

ATTORNEY/AGENT

NAME: Warburg, Richard

REGISTRATION NUMBER: 32,327

REFERENCE/DOCKET NUMBER: 218/078

TELECOMMUNICATION INFORMATION:
TELEPRINE: (213) 955-0440

TELERAX: 67.3510
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Patent No. 6194150
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/585,684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         917 GTCTTTGCCT 926
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4 GUCUTUGCCU 13
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STATE: California
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 150
US-09-038-073-2257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING
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13.4%; Score 9.8; DB 1; Length 13; llarity 84.6%; Pred. No. 1.4e+02; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Cronin, Maureen T.
APPLICANT: Miyada, Charles Garrett
APPLICANT: Hubbell, Earl A.
APPLICANT: Hubbell, Earl A.
APPLICANT: Fodor, Stephen P.A.
APPLICANT: Hondy, Xiachua C.
APPLICANT: Hobban, Peter E.
APPLICANT: Morris, Macdonald S.
APPLICANT: Morris, Detecting Cystic Fibrosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: other nucleic acid
DESCRIPTION: third strand derived from HER-2
DESCRIPTION: sequence region in Seq ID No. 586124455
HYPOTHETICAL: Yes
       GENETIC SEQUENCE ASSAY USING DNA TRIPLE-STRAND FORMATION. 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PUBLICATION INFORMATION:
RELEVANT RESIDUES IN SEQ ID NO: 56 :FROM 1 TO 13
TITLE OF INVENTION: GENETIC SEQUENCE ASSAY USING TITLE OF INVENTION: TRIPLE-STRAND FORMATION. NUMBER OF SEQUENCES: 365
CORRESPONDENCE ADDRESS: ADDRESSE: PROFILE DIAGNOSTIC SCIENCES, INC., STREET: 510 EAST 73RD STREET, CITY: NEW YORK STATE: NEW YORK COUNTRY: USA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Townsend and Townsend and Crew LLP
                                                                                                                                                              STATE: NEW YORK
COUNTRY: USA

ZATE: 10021.
COMPUTER READABLE FORM:
NEDIUM TYPE: 3.5 inch, 1.44Mb storage
COMPUTER. IBM PO/XT/AT
COMPUTER: IBM PO/XT/AT
OPERATING SYSTEM: MS-DOS version 6.2
SOFTWARE: Wordperfect Version 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/173,489C
FLING DATE: 22 DEC 1993
CLASSIFICATION DATA:
APPLICATION NUMBER: US 07/968,436
FLING DATE: 29 OCT 1992
ATTORNEY/AGENT INFORMATION:
NAME: Handelman, Joseph H.
REGISTRATION NUMBER: 26,179
REPERENCE/DOCKET WIMBER: US518-6
TELEFAX: (attorney) (212) 246-8959
INFORMATION FOR ESQ ID NO: 56;
SEQUENCE CHARACTERISTICS:
LENGTH: 13 bases
TYPE Nucleic Acid
STRANDENESS: single stranded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-544-381B-29
; Sequence 29, Application US/08544381B
; Patent No. 6027880
; GENERAL INFORMATION:
; APPLICANT: Cronin, Mauxeen T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      924 CCTTTTATCCCTC 936
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 11; Conserval
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                                                                                                                                            APPLICANT: Cree, Mark
APPLICANT: Croin, Maureen T.
APPLICANT: Croin, Maureen T.
APPLICANT: Fodor, Stephen P.A.
APPLICANT: Hubbell, Barl A.
APPLICANT: Lipshutz, Robert J.
APPLICANT: Lipshutz, Robert J.
APPLICANT: Lipshutz, Robert J.
APPLICANT: Sheldon, Edward L.
TITLE OF INVENTION: Macdonald S.
APPLICANT: Sheldon, Edward L.
TITLE OF INVENTION: Biological Chips
NUMBER OF SEQUENCES: 360
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcedero Center, 8th Floor
CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER TRADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER TRADABLE FORM:
SOFTWARE: PRECENTINE PC-DOS/MS-DOS
SOFTWARE: PRECENTINE APPLICATION DATA:
FILING DATE: 16-NAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/143,312
FILING DATE: 26-OCT-1993
CLASSIFICATION NUMBER: US 08/082,937
FILING DATE: 25-JUN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Liebeschuetz, JOSEPH O.
REGISTRATION NUMBER: 37,505
RELEBENDUM: 650-326-2400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 9.8; DB 1;
Pred. No. 1.4e+02;
0; Mismatches 2;
                                               US-08-441-887A-268/c
; Sequence 268, Application US/08441887A
; Patent No. 5837832
; Patent No. 5837832
; APPLICANT: Chee, Mark
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 56, Application US/08173489C
Patent No. 5861244
GENERAL INFORMATION
APPLICANT: HEPBURN, A. G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFRMATION FOR SEQ ID NO: 268: SEQUENCE CHARACTERISTICS: LENGTH: 13 base pairs TYPE: nucleic acid STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 84.6%;
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
HOLECULE TYPE: DNA (probe)
US-08-441-887A-268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            910 TICTITIGGICTT 922
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US-08-173-489C-56
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13.4%; Score 9.8; DB 1; Length 13; 84.6%; Pred. No. 1.4e+02; ive 0; Mismatches 2; Indels
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MEDIUM TYPE: Diskette COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette COMPATIBLE COMPUTER: DISKETTE COMPATIBLE COMPATIBLE COMPATIBLE COMPATIBLE COMPATIBLE COMPATIBLE COMPATIBLE COMPATIBLE COMPATIBLE CONTINUED DATA:

APPLICATION NUMBER: US/08/778,794A
FILING DATE: 03-JAN-1997
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/143,312
FILING DATE: 26-OCT-1993
APPLICATION NUMBER: US 08/284,064
FILING DATE: 26-OCT-1994
APPLICATION NUMBER: US 08/284,064
FILING DATE: 26-OCT-1994
APPLICATION NUMBER: US 08/510,521
FILING DATE: 02-AUG-1995
APPLICATION NUMBER: US 08/544,381
FILING DATE: 10-OCT-1995
APPLICATION NUMBER: US 08/544,381
FILING DATE: 10-OCT-1995
APPLICATION NUMBER: US 08/544,381
FILING DATE: 10-OCT-1995
APPLICATION NUMBER: US 08/544,381
FILING DATE: LAGBESCHUEZ, UGE
REGISTRATION NUMBER: 37,505
REFERRENCE/DOCKET NUMBER: 37,505
REFERRENCE/DOCKET NUMBER: 016547-015700US
TELECOMMUTCATION INFORMATION:
FURLEDCOMMUTCATION INFORMATION:
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MEDIUM TYPE: 3.5 inch 1.44Mb
COMPUTER: IBM PC compatible
OPERATING SYSTEM. PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/242,664
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TELEFAX: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            915 TGGTCTTTGCCTT 927
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 84.6
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 13 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE: New York COUNTRY: U.S.A. ZIP: 10112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-778-794A-87
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Patent No. 6309823

GENERAL INFORMATION:
APPLICANT: Miyada, Charles Garrett
APPLICANT: Hubbell, Earl A.
APPLICANT: Hubbell, Earl A.
APPLICANT: Fodor, Mark
APPLICANT: Fodor, Stephen P.A.
APPLICANT: Injohutz, Robert J.
APPLICANT: Lipshutz, Robert J.
APPLICANT: Lipshutz, Robert J.
APPLICANT: Lipshutz, Robert J.
APPLICANT: Lipshutz, Robert J.
APPLICANT: Loban, Peter E.
APPLICANT: Sheldon, Edward L.
TITLE OF INVENTION: Arrays of Nucleic Acid Probes
TITLE OF INVENTION: for Analyzing Biotransformation Genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13.4%; Score 9.8; DB 1; Length 13; 84.6%; Pred. No. 1.4e+02; trive 0; Mismatches 2; Indels
                                                                                                                       COMPUTER: PALLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN ENGLASE #1.0, Version #1.25
CURSENT APPLICATION DATA:
APPLICATION NUMBER: US/08/544,381B
FILING DATE: 10-OCT-1995
CLASSIFFCATION: A35
PRIOR APPLICATION: A35
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/510,521
FILING DATE: 02-AUG-1995
FILING DATE: 26-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/284,064
FILING DATE: 26-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/143,312
FILING DATE: 26-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: Liebeschuetz, Joe
REGISTRATION NUMBER: 37,505
REFERENCE/DOCKET NUMBER: 018847-004130US
TELEDEHONE: A15-56-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3: Townsend and Townsend and Crew LLP
Two Embarcadero Center, Eighth Floor
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TOPOLOGY: linear , MOLECULE TYPE: DNA (oligonucleotide) US-08-544-381B-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 415-576-0300 INFORMATION FOR SEQ ID NO: 29:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         915 TGGTCTTTGCCTT 927
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Best Local Similarity 84.6
Matches 11; Conservative
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nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: Two Embarcac
CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS:
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US-08-778-794A-87
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Sequence 29, Application US/08535249
Patent No. 645569
GENERAL INFORMATION:
APPLICANT: Schlingensiepen, Georg-Ferdinand
APPLICANT: Schlingensiepen, Karl-Hermann
APPLICANT: Schlingensiepen, Reimar
APPLICANT: Schlingensiepen, Reimar
APPLICANT: Schlingensiepen, Reimar
APPLICANT: Schlingensiepen, Reimar
APPLICANT: International Schlingensiepen, Reimar
APPLICANT: Schlingensiepen, Reimar
APPLICANT: Schlingensiepen, Reimar
APPLICANT: Schlingensiepen, Reimar
APPLICANT: Schlingensiepen, Reimann
APPLICA
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Pred. No. 1.6e+02;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/535,249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDESSEE: Jacobson, Price, Holman & Stern STREET: 400 Seventh St. N.W.
CITY: Washington D.C.
COUNTRY: U.S.A.
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 93 107 089.0
FILING DATE: 30-APR-1993
PRIOR APPLICATION NUMBER: EP 93 107 849.7
FILING DATE: 13-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: Player, William E.
REGISTRATION NUMBER: 31,409
REFERENCE/DOCKET NUMBER: 10577/P58418
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
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Patent No. 6632057
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    unknown
E: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (202) 393-5350
TELEFAX: RCA 248593 IDEA UR
INFORMATION FOR SEQ ID NO: 299
SEQUENCE CHARACTERISTICS:
LENGTH: 14 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 84.6%;
Matches 11; Conservative
                               919 CTTTGCCTTTTAT 931
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               928 TTATCCCTCCTCT 940
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APPLICANT: LEWIN, ALFRED S.
APPLICANT: SHAW, LYNN C.
                                                                                               13 CTTTTCCTTTTT 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
STRANDEDNESS: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: ur
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-874-601-110/c
                                                                                                                                                                                          RESULT 158
US-08-535-249-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-535-249-29
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0
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13.4%; Score 9.8; DB 1; Length 14
84.6%; Pred. No. 1.6e+02;
tive 0; Mismatches 2; Indels
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Sequence 15, Application US/08484138

Patent No. 565230

APPLICANT: Watanabe, Kyoichi A. APPLICANT: Watanabe, Kyoichi A. APPLICANT: Weil, Rogentlementary DNA and Toxins ITILE OF INVENTION: Complementary DNA and Toxins NUMBER OF SEQUENCES: 43

CORRESPONDENCES: 43

CORRESPONDENCES: 63

ADDRESSER: Cooper & Dunham LLP

STREET: 1185 Avenue of the Americas

COUNTRY: U.S.A.

ZITY: New York

STATE: New York

COUNTRY: U.S.A.

ZIP: 10036

COMPUTER: SABALE FORM:

MEDIUM TYPE: 3.5 inch 1.44Mb

COMPUTER: IBM PC

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARR: PatentIn Release #1.24

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/484,138

FILING BATE: June 7, 1995

FILING BATE: June 7, 1995

FILING BATE: June 7, 1995

FILING BATE: June 7, 1995
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                                                                                                                NAME: White, John P.
REGISTRATION UNUMBER: 28,678
REFERENCE/DOCKET UNMBER:
TELECOMMUNICATION INFORMATION:
TELEFAN: 212-64-0525
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 base pairs
TYPE: nucleic acid
STRANDENNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REPERENCE/DOCKET NUMBER: 4468
TELEPHONE: 212-977-9550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 212-664-0525
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
CLASSIFICATION: 514
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: White. 7ct-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: DNA (genomic) US-08-484-138-15
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Best Local Similarity 84.6
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-242-664-15
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) Patent No. 5521300

) GENERAL INFORMATION:

APPLICANT: Shah, Jyotsna S.

APPLICANT: Natupski, Raymond M.

APPLICANT: Iniu, Jing

TITLE OF INVENTION: Oligonuclectides Complementary to

TITLE OF INVENTION: Mycobacterial Nucleic Acids

NUMBER OF SEQUENCES: 127

CORRESPONDENCE ADDRESS:

ADDRESSEE: Kevin M. Farrell, P.C.

STREET: P.O. BOX 999

CONTY: York Harbor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 9.8; DB 1; Length 14; pred. No. 1.6e+02; 0; Mismatches 2; Indels
                          Sequence 15, Application PC/TUS9506379
GENERAL INFORMATION:
APPLICANT: Watenabe, Kyoichi A.
APPLICANT: Wen, Wu-Yun
APPLICANT: Weil, Roger
TITLE OF INVENTION: Complementary DNA and Toxins
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATUR: SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                            CORFESTOR COOPER & Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STREET: New York
STREET: New York
COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch 1.44Mb
COMPUTER: IBM PC
COMPUTER: IBM PC
COMPUTER: IBM PC
COMPUTER: BATCHIN Release #1.24
CURRENT APPLICATION DATA:
RPLIATION NUMBER: PCT/US95/06379
FILLING DATE: May 13, 1994
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFRENCE/DOCKET NUMBER: 4466:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-278-0400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 212-391-0526
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 84.6%;
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              919 CTTTGCCTTTAT 931
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13 crirrccrirrr 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         USA
               PCT-US95-06379-15/c
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US-07-744-282C-123
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US-09-874-601-111/c
; Sequence 111, Application US/09874601
; Patent No. 6632057
; GENERAL INFORMATION:
; APPLICANT: LEWIN, ALRED S.
; APPLICANT: SHAW, LYRN C.
; APPLICANT: SHAW, LYRN C.
; TITLE OF INVENTION: THE TREATMENT OF RETINAL DISEASES
; TITLE OF INVENTION: THE TREATMENT OF RETINAL DISEASES
; TILE REFERENCE: 4300.014100
; TITLE OF INVENTION: THE TREATMENT OF RETINAL DISEASES
; FILE REFERENCE: 4300.014100
; CURRENT APPLICATION NUMBER: 09/063,67
; PRIOR APPLICATION NUMBER: 60/046,147
; PRIOR PILING DATE: 1997-04-21
; PRIOR APPLICATION NUMBER: 60/046,147
; PRIOR PELING DATE: 1997-04-21
; NUMBER OF SEQ ID NOS: 182
; SOFTWARE: PATENTIN VERSION 3.0
TITLE OF INVENTION: ADELLY DELIVERED RIBOZYME COMPOSITIONS AND METHOD TITLE OF INVENTION: THE TREATMENT OF RETINAL DISEASES FILE OF INVENTION: THE TREATMENT OF RETINAL DISEASES FILE OF INVENTION: THE TREATMENT OF RETINAL DISEASES FILE REFERENCE: 4300.014100

CURRENT FILING DATE: 2001-05-01

PRIOR APPLICATION NUMBER: 09/063,667

PRIOR APPLICATION NUMBER: 60/046,147

PRIOR APPLICATION NUMBER: 60/046,147

PRIOR PAPLICATION NUMBER: 60/044,492

PRIOR FILING DATE: 1997-04-21

NUMBER OF SEQ ID NOS: 182

SEQ ID NOS: 182

SEQ ID NO 110

LENGTH: 14
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13.4%; Score 9.8; DB 1; Length 14;
Best Local Similarity 84.6%; Pred. No. 1.6e+02;
Matches 11; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 9.8; DB 1; Length 14;
Pred. No. 1.6e+02;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: misc feature LOCATION: ()...() orher information: synthetic oligonucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: misc_feature
| LOCATION: () ...()
| THER INFORMATION: SYNTHETIC OLIGONUCLEOTIDE
US-09-874-601-110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: RNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: RNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 84.6%;
Matches 11; Conservative
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LENGTH: 14
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Gaps
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              Best Local Similarity 73.3%; Pred. No. 1.7e+02;
Matches 11; Conservative 1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                             Sequence 64, Application US/08319492B
Patent No. 561648B
GENERAL INFORMATION:
APPLICANT: Sullivan, Sean M.
APPLICANT: Draper, Kenneth G.
APPLICANT: McSwiggen, James
TITLE OF INVENTION: RIBOZYNE TREATMENT OF DISEASES
TITLE OF INVENTION: OR CONDITIONS RELATED TO LEVELS
TITLE OF INVENTION: OF IL-5
NUMBER OF SEQUENCES: 751
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Joyon & Lyon
STREET: 613 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 30071
COMPUTER READABLE FORM:
MEDIUM TYPE: 31. Diskette, 1.44 Mb
MEDIUM TYPE: 32. Diskette, 1.44 Mb
MEDIUM TYPE: 32. Diskette, 1.44 Mb
MEDIUM TYPE: Storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US 08/08/19, 492B
FILING DATE: October 7, 1994
PRIOR APPLICATION DATA: including application
PRIOR APPLICATION DATA: including application
PRIOR APPLICATION DATA: 1993
APPLICATION NUMBER: 08/008/895
FILING DATE: December 7, 1992
APPLICATION NUMBER: 07/899/849
FILING DATE: December 7, 1992
APPLICATION NUMBER: 32,327
RESERVENCE/DOCKET NUMBER: 32,327
RESER
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US-08-319-492B-73
; Sequence 73, Application US/08319492B
                                                                                                                     920 TITGCCITITATCCC 934
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 13.4
Best Local Similarity 84.6
Matches 11; Conservative
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TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15 ATTGGTTTACTCT 3
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US-08-319-492B-64/C
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13.4%; Score 9.8; DB 1; Length 15;
Best Local Similarity 73.3%; Pred. No. 1.7e+02;
Matches 11; Conservative 1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Shah, Jyotsna S.
APPLICANT: Mietupski, Raymond M.
APPLICANT: Nietupski, Raymond M.
APPLICANT: Liu, Jing
TITLE OF LIVENTION: Oligonucleotides Complementary to
TITLE OF INVENTION: Mycobacterial Nucleic Acids
TITLE OF INVENTION: Mycobacterial Nucleic Acids
TUMBER OF SEQUENCES: 127
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kevin M. Farrell, P.C.
STREET: P.O. Box 999
CITY: York Harbor
STATE: ME
COUNTRY: USA
ZIP: 03911
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 1; Length 15;
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COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER LIBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/744,282C

FILING DATE: August 13, 1991

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Kevin M. Farrell

REGISTRATION NUMBER: GTR90-05

REFERENCE/DOCKET NUMBER: GTR90-05

TELEPAN: (207) 363-0558

TELEPAN: (207) 363-0558

INFORMATION FOR SEQ ID NO: 125:

SEQUENCE CHARACTERISTICS:

LENGTH: 15 base pairs

TYPE: nucleic acid

STRANBEDNESS: double

TYPE: NOPOLOGY: linear

MOLECULE TYPE: DNA (Genomic)

US-07-744-282C-125
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/744,282C
FILING DATE: Adgust 13, 1991
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Kevin M. Farrall
REFERENCE/DOCKET NUMBER: 35.505
REFERENCE/DOCKET NUMBER: GTR90-05
TELEPHONE: (207) 363-0528
TELEPHONE: (207) 363-0528
TELEPHONE: (207) 363-0528
INFORMATION FOR SEQ ID NO: 123:
SEQUENCE CHARACTER/STICS:
LENGRATION FOR SEQ ID NO: 123:
SEQUENCE CHARACTER/STICS:
LENGRATION FOR SEQ ID NO: 123:
SEQUENCE CHARACTER/STICS:
TYPE: NUCLEIC acid
STRANDENESS; double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13.4%; Score 9.8;
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US-07-744-282C-125
US-07-744-2155, Application US/07744282C
; Patent No. 5521300
) GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-07-744-282C-123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      920 TITGCCITITATCCC 934
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; Sequence 170, Application US/08319492B
; Patent No. 561448B
; GENERAL INFORMATION:
    APPLICANT: Sullivan, Sean M.
    APPLICANT: Braper, Kenneth G.
    APPLICANT: McSwiggen, James
    TITLE OF INVENTION: RIBOZYME TREATMENT OF DISEASES
    TITLE OF INVENTION: OR CONDITIONS RELATED TO LEVELS
    TITLE OF INVENTION: OF IL-5
    NUMBER OF SEQUENCES: 751
    CORRESPONDENCE ADDRESS:
    ADDRESSEE: 1937 West Fifth Street
    STREET: 633 West Fifth Street
    STREET: 633 West Fifth Street
    COUTRY: Los Angeles
    COUTRY: U.S.A.
    ZIP: 90071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13.4%; Score 9.8; DB 1; Length 15; 30.8%; Pred. No. 1.7e+02; tive 7; Mismatches 2; Indels
                                                                                                                                                               COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

MEDIUM TYPE: stcrage
COMPUTER: IBM COMPAIDLE
OPERATING SYSTEM: IBM P.C. DOS 5.0

SOFTWARE: Word Perfect 5.1

CURRENT APPLICATION DATA:
APPLICATION DATA:
PRIOR APPLICATION DATA: including application
PRIOR APPLICATION NUMBER: 08/008/895
FILING DATE: December 7, 1992
APPLICATION NUMBER: 07/989,849
FILING DATE: December 7, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 209/276
TELECOMMUNICATION INFORMATION:
TELECHONE: (21) 489-1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 MD
MEDIUM TYPE: STORAGE
COMPUTER: IBM Compatible
                      Fifth Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 169:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           943 ATTGGTTTAATGT 955
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Best Local Similarity 30.83
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2 AUUUAUUUAAUGU 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: nucleic acid
STRANDEDNESS: single
                                                    LIY: Los Angeles
STATE: California
COUNTRY: U.S.
                   : 633 West F
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US-08-319-492B-169
ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ð
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                                                       APPLICANT: Sullivan, Sean M.
APPLICANT: Sullivan, Kenneth G.
APPLICANT: Draper, Kenneth G.
APPLICANT: McSwiggen, James
TITLE OF INVENTION: RIBOZYME TREATMENT OF DISEASES
TITLE OF INVENTION: OR CONDITIONS RELATED TO LEVELS
TITLE OF INVENTION: OF IL-5
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Sullivan, Sean M.
APPLICANT: Draper, Kenneth G.
APPLICANT: McSwiggen, James
APPLICANT: Stinchcomb, Dan T.
TITLE OF INVENTION: REBOZYME TREATMENT OF DISEASES
TITLE OF INVENTION: OR CONDITIONS RELATED TO LEVELS
TITLE OF INVENTION: OF IL-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: 5.5" Diskette, 1.44 Mb
MEDIUM TYPE: 1.5" Diskette, 1.44 Mb
MEDIUM TYPE: 5.5" Diskette, 1.44 Mb
MEDIUM TYPE: 1.5" Diskette, 1.44 Mb
MEDIUM TYPE: 1.5" Diskette, 1.44 Mb
SOFTWARE: 1.5" Diskette, 1.44 Mb
SOFTWARE: 1.5" Diskette, 1.44 Mb
SOFTWARE: 1.5" DISKET 1.
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US-08-319-492B-169
; Sequence 169, Application US/08319492B
; Patent No. 5616488
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             944 TTGGTTTAATGTA 956
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 13.4
Best Local Similarity 46.2
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SS: single
linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
US-08-319-492B-73
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; Sequence 437, Application US/08319492B
; Patent No. 561648B
; GENERAL INFORMATION:
APPLICANT: Sullivan, Sean M.
APPLICANT: Draper, Kenneth G.
APPLICANT: Braper, Kenneth G.
APPLICANT: Brinchcomb, Dan T.
TITLE OF INVENTION: RIBOZYME TREATMENT OF DISEASES
TITLE OF INVENTION: OF LL-5
NUMBER OF SEQUENCES: 751
CORRESPONDENCE ADDRESS:
ADDRESSEE: Suite 4700
CITY: Los Angeles
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNNEY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 13.4%; Score 9.8; DB 1; Length 15; Best Local Similarity 61.5%; Pred. No. 1.7e+02; Matches 8; Conservative 3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IFE: SECTORGE
COMPUTER: IFE: SECTORGE
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/319,492B
FILING DATE: OCCODER 7, 1994
PRIOR APPLICATION DATA: including application
PRIOR APPLICATION DATA: 108008,895
FILING DATE: January 19, 1993
APPLICATION NUMBER: 08/008,895
FILING DATE: December 7, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard
REGIERRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 32,327
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION THE SECTION T
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COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
                                                         FILING DATE: December 7, 1992

ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard
REGISTRATION NUMBER: 32,327
REPERBORE/DOCKET NUMBER: 209/276
FELEPHONE: (213) 489-1600
FELEFAX: (213) 955-0440
FELEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     931 TCCCTCCTCTTCA 943
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13.4%; Score 9.8; DB 1; Length 15;
Best Local Similarity 30.8%; Pred. No. 1.7e+02;
Matches 4; Conservative 7; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-319-492B-436

US-08-319-492B-436

Sequence 436, Application US/08319492B

Patent No. 561648B

JEGNERAL INFORMATION:
APPLICANT: Sullivan, Sean M.
APPLICANT: Draper. Kenneth G.
APPLICANT: Stinchcomb, Dam T.
TILE OF INVENTION: RECONDITIONS RELATED TO LEVELS
TITLE OF INVENTION: OF IL-5
TITLE OF INVENTION: OF IL-5
TITLE OF SEQUENCES: 751
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: Salle 4700

CITY: Los Angeles
STREET: Galifornia
COMPUTER: Raddles
STREET: Sulle 4700

COMPUTER: B.S. Diskette, 1.44 Mb
MEDIUM TYBE: Storage
COMPUTER: IBM P.C. DOS 5.0

COMPUTER: IBM P.C. DOS 5.0

COMPUTER: IBM COMPATION DATA:
APPLICATION DATA: including application
PRIOR APPLICATION DATA: including application
PRIOR APPLICATION DATA: including application
PRIOR APPLICATION DATA: described below:
APPLICATION NUMBER: 08/0895
FILING DATE: January 19, 1993
APPLICATION NUMBER: 07/989,849
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/319,492B
FILING DATE: Occober 7, 1994
PRIOR APPLICATION DATA: including application
PRIOR APPLICATION DATA: including application
PRIOR APPLICATION DATA: described below:
PRIOR APPLICATION DATA: described below:
APPLICATION NUMBER: 08/009,895
FILING DATE: January 19, 1993
APPLICATION NUMBER: 07/989,849
FILING DATE: December 7, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard
NAME: Warburg, Richard
NAME: Warburg, Richard
NAME: Warburg, Richard
NEFERENCE/DOCKET NUMBER: 209/276
TELEFAX: (213) 955-0440
TELEFAX: (213) 955-0440
TELEFAX: (213) 955-0440
TELEFAX: (213) 955-0440
TELEFAX: (213) 555-0440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         943 ATTGGTTTAATGT 955
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1 AUUUAUUUAAUGU 13
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US-08-319-492B-170
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915 TGGTCTTTGCCTT 927
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 15 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-363-240A-228
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                                  US-08-363-240A-228
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                                                                                                                      Length 15;
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                                                                                                                                                           2; Indels
                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Coulture, Larry
APPLICANT: Coulture, Larry
APPLICANT: Coulture, Larry
APPLICANT: Mcaugen, James
APPLICANT: Bisgaier, Charles
APPLICANT: Pape, Michael
TITLE OF INVENTION: MFEVENTION, INHIBITION OF
TITLE OF INVENTION: PROGRESSION AND REGRESSION
TITLE OF INVENTION: PROGRESSION AND REGRESSION
TITLE OF INVENTION: OF VASCULAR DISEASES
NUMBER OF SEQUENCES: 1243
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: Sailte 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071
                                                                                                                  Query Match 13.4%; Score 9.8; DB 1; Best Local Similarity 61.5%; Pred. No. 1.7e+02; Matches 8; Conservative 3; Mismatches 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: WOLD PETCECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/363,240A
FILING DATE: December 23, 1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  210/096
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Warburg, Richard
REGISTRATION NUMBER: 32,327
REFRENCE/DOCKET NUMBER: 210/
TELECOMMUNICATION INFORMATION:
TELEPAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 227:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  915 TGGTCTTTGCCTT 927
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                                                                                                                                                                                                                         3 UCCCUCCCCUCA 15
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Best Local Similarity 38.5
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 15 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
15 base pairs
          TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
US-08-363-240A-227
                                                          ;
TOPOLOGY: ]
US-08-319-492B-437
                                                                                                                                                                                                                                                                                                       RESULT 170
US-08-363-240A-227
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13.4%; Score 9.8; DB 1; Length 15;
Best Local Similarity 53.8%; Pred. No. 1.7e+02;
Matches 7; Conservative 4; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 174

US-08-311-486C-75

US-08-311-486C-75

i Sequence 75, Application US/08311486C

i Patent No. 5811300

GENERAL INFORMATION:
APPLICANT: Renneth Draper
APPLICANT: Renneth Danger
ITLE OF INVENTION: RIBGATED TO LEVELS OF
TITLE OF INVENTION: RELATED TO LEVELS OF
TITLE OF INVENTION: TUR-'
NUMBER OF SEQUENCES:
ITSTEET: 613 West Fifth Street
STREET: 613 West Fifth Street
STREET: Gaite 4700

CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: Storage
COMPUTER READABLE FORM:
MEDIUM TYPE: Storage
COMPUTER READABLE FORM:
MEDIUM TYPE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/311, 486C
FILING DATE: September 23, 1994
CLASSIFICATION DATA: ASE
PRIOR APPLICATION DATA: ASE
PRIOR APPLICATION DATA: APPLICATION DATA:
PRIOR APPLICATION NUMBER: 08/008,895
FILING DATE: January 19, 1993
APPLICATION NUMBER: 07/989,849
FILING DATE: September 23, 1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA: including application partor APPLICATION DATA: including application partor APPLICATION DATA: described below: APPLICATION NUMBER: 08/008,895
FILING DATE: Jannary 19, 1993
APPLICATION NUMBER: 07/989,849
FILING DATE: December 7, 1992
ATTORNEY AGENT INFORMATION: NAME: Warburg, Richard J. REFERNCE/DOCKET NUMBER: 32,327
REPERSENCE/DOCKET NUMBER: 32,327
REPERSENCE/DOCKET NUMBER: 32,327
FELECOMMUNICATION INFORMATION: TELEPAX: (213) 955-0440
ITELEFAX: (213) 955-0440
ITELEFAX: (213) 955-0440
INFORMATION FOR SEQ ID NO: 74: SEQUENCE CHARACTERISTICS: LENGTH: 15 base pairs
ILENGTH: 15 base pairs
TOPOLOGY: Linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       935 TCCTCTTCATTGG 947
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2 UCCUCUUCAAGGG 14
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US-08-311-486C-74
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
13.4%; Score 9.8; DB 1; Length 15;
Best Local Similarity 84.6%; Pred. No. 1.7e+02;
Matches 11; Conservative 0; Mismatches 2; Indels
STATE: Massachusetts

CCUNTRY: U.S.A.

ZIP: 02110-2804

ZIP: 0210-2804

COMPUTER: BADABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
COMPUTER: BAD MS/2 Model 502 or 555X

OPERATING SYSTEM: IBM P.C. DOS (Version 3.30)
SOFTWARE: WordPerfect (Version 5.0)
SOFTWARE: WordPerfect (Version 5.0)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/294,424

FILING DATE: CLASSIFICATION A35
FILING DATE: 16 JAN 1993
APPLICATION NUMBER: US/08/000,922
FILING DATE: 16 JAN 1993
APPLICATION NUMBER: US/07/629,601B
FILING DATE: 17-DEC-1990
ATTORNEY/AGENT INFORMATION:
NAMM: Freemen, US/DH W.
RECISTRATION NUMBER: 29,066
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION FOR SEQ ID NO: TELEX: 201154
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 173
US-08-311-486C-74
i Sequence 74 Application US/08311486C
j Patent No. 5811300
GENERAL INFORMATION:
APPLICANT: Kenneth Draper
APPLICANT: Kenneth Draper
APPLICANT: Kenneth Draper
APPLICANT: Manes McSwiggen
TITLE OF INVENTION: RIBOZYME TREATMENT OF
TITLE OF INVENTION: DISEASES OR CONDITIONS
TITLE OF INVENTION: RIBOZYME TREATMENT OF
TITLE OF INVENTION: RIBOZYME
CORRESPONDENCE ADDRESS:
ADDRESSE: LOS APPRESS:
ADDRESSE: LOS Appales
STREET: Suite 4700
CITY: LOS Appales
STREET: Suite 4700
CITY: LOS Appales
STREET: Suite 4700
CITY: LOS Appales
STREET: Suite 4700
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" DISKETTE, 1.44 Mb
MEDIUM TYPE: SCOTGAB
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COMPUTER: IBM COMPATA: MAD APPLICATION NUMBER: US/08/311,486C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               924 CCTTTTATCCTTC 936
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13 CCTTTCCTCCTC 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-294-424-48
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CLASSIFICATION: 435

PRIOR APPLICATION DATA:

PRIOR APPLICATION DATA:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/08,895

FILING DATE: January 19, 1993

FILING DATE: January 19, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Sean Sullivan
APPLICANT: Sean Sullivan
APPLICANT: Kenneth G. Draper
TITLE OF INVENTION: RIBOZYME OR CONDITIONS
TITLE OF INVENTION: BISABLES OR CONDITIONS
TITLE OF INVENTION: NITRACELLULAR ADHESION
TITLE OF INVENTION: MOLECULE-1 (I-CAM-1)
NUMBER OF INVENTION: MOLECULE-1 (I-CAM-1)
NUMBER OF SEQUENCES: 2390
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CARRESTEE LYON & LYON
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
CITY: Los Angeles
COUNTY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: Storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
FILING DATE: AUGUST 17, 1994
CLASSIFICATION: 435
APPLICATION NUMBER: WO PCT/FR85/00096
FILING DATE: 24-APR-1985
ATTORNEY/AGENT THORNATION:
NAME: Rea, Teresa Stanek
REGISTRATION NUMBER: 30,427
REFERENCE/DOCKET NUMBER: 017753-061
TELECHONE: (703) 836-620
TELECHONE: (703) 836-620
TELEFAX: (703) 836-620
TELEFAX: (703) 836-620
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                           "oligonucleotide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 176
US-08-292-620A-121/C
US-08-292-620A-121/C
; Patent No. 5837542
; GENERAL INFORMATION:
APPLICANT: Susan Grimn
; APPLICANT: Dan T. Stinchcomb
; APPLICANT: James McSwiggen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 208/149
                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: other nucleic acid

DESCRIPTION: /desc = "oligonucleic ucid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: 07/5
FILING DATE: December 7, ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          941 TCATTGGTTTAAT 953
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 84.6 Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13 rccrrccracarıı
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Petent No. 5830477
GENERAL INFORMATION
GENERAL INFORMATION
APPLICANT: KIENY, Marie-Paule
APPLICANT: KIENY, Marie-Paule
APPLICANT: DRILLIEN, Robert
APPLICANT: DRILLIEN, Robert
TITLE OF INVENTION: VACCINE AGAINST RABIES AND PROCESS FOR TITLE OF INVENTION: PREPARATION THEREOF
TITLE OF ENVENTION: PREPARATION THEREOF
TORRESPONDENCES: 12
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ouery Match
Best Local Similarity 53.8%; Pred. No. 1.7e+02;
Matches 7; Conservative 4; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:

APPLICATION NUMBER: PC-DOS/MG-DOS

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/480,736

FILING DATE: 07-JUN-1995

FILING APPLICATION DATA:

APPLICATION NUMBER: US 08/231,457

FILING DATE: 21-APR-1994

PRIOR APPLICATION NUMBER: US 08/038,052

FILING DATE: 29-MAR-1993

PRIOR APPLICATION NUMBER: US 07/759,138

FILING DATE: 19-MAR-1993

PRIOR APPLICATION NUMBER: US 07/759,138

FILING DATE: 11-SEP-1991

PRIOR APPLICATION NUMBER: US 07/378,801

FILING DATE: 11-UUL-1989

PRIOR APPLICATION NUMBER: US 06/829,144

FILING DATE: 24-DEC-1985

PRIOR APPLICATION NUMBER: US 06/829,144

FILING DATE: 25-APR-1984

PRIOR APPLICATION NUMBER: US 06/829,144

FILING DATE: 25-APR-1984

PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Burns, Doane, Swecker & Mathis STREET: P.O. Box 1404
CITY: Alexandria
     FILING DATE: December 7, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 209/166
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEPAX: (213) 955-0440
TELEPAX: 67-3510
INFORMATION FOR SEQ ID NO: 75:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
TYPE: MUCleic acid
STRANDENNES: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           935 TCCTCTTCATTGG 947
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 UCCUCUUCAAGGG 13
                                                                                                                                                                                                                                                                                                                                                                          ; TOPOLOGY: linear
US-08-311-486C-75
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US-08-480-736-4/c
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Score 9.8; DB 1; Length 15;
Pred. No. 1.7e+02;
0; Mismatches 2; Indels
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Sequence 289, Application US/08292620A

Patent No. 58375EA

GENERAL INFORMATION:
APPLICANT: Susan Grimm
APPLICANT: Dane MCGWiggen
APPLICANT: Sean Sullivan
APPLICANT: APPLICANTION: NURACELLULAR APHESION
TITLE OF INVENTION: INTRACELLULAR APHESION
TITLE OF INVENTION: MOLECULE-1 (I-CAM-1)
NUMBER OF SEQUENCES: 2390
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 631 West Fifth Street
STREET: Sulle 4700
CITY: Los Angeles
STREET: California
COUMTRY: U.S.A.
ZIP: 90071-2066
COMPUTER REDABLE FORM:
MEDUM TYPE: 3.5" Diskette, 1.44 Mb
MEDUM TYPE: 3.5" Diskette, 1.44 Mb
MEDUM TYPE: STOARSEE
                                                                                                                                               13.4%;
84.6%;
                                                                                                                                                                                                                                                             959 GCTACCAACGGTG 971
                                                                                                                                            Query Match
Best Local Similarity 84.6
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                       15 GCTAACAAAGGTG 3
; TYPE: nucleic acid
; STRANDEDNESS: singl
; TOPOLOGY: linear
US-08-292-620A-288
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US-08-292-620A-289
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13.4%; Score 9.8; DB 1; Length 15;
Best Local Similarity 84.6%; Pred. No. 1.7e+02;
Matches 11; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESSE:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: 633 West Fifth Street
STREET: Galifornia
CUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER: READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: 18 Compatible
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COMPUTER: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/29,620A
FILING DATE: August 17, 1994
CLASSIFTATION DATA: including application
PRIOR APPLICATION DATA: including application
PRIOR APPLICATION DATA: 1993
FILING DATE: January 19, 1993
APPLICATION NUMBER: 08/008,895
FILING DATE: January 19, 1993
APPLICATION NUMBER: 07/089,849
FILING DATE: January 19, 1993
APPLICATION NUMBER: 32,327
REGENERALE JOCKET NUMBER: 32,327
REPERSING JOCKET NUMBER: 32,327
REBERSING JOCKET NUMBER: 32,327
RELEXA: (213) 955-0440
TELLERA: 67-3510
INFORMATION FOR SEQ ID NO: 288:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-292-620A-288/C

Sequence 288, Application US/08292620A

Sequence 288, Application US/08292620A

Sequence 288, Application US/08292620A

Patent No. 583784710M:
APPLICANT: Susan Grimm
APPLICANT: James McSwiggen
APPLICANT: Sean Sullivan
APPLICANT: Sean Sullivan
APPLICANT: Memeth G. Draper
ITILE OF INVENTION: RIBOZNET REATMENT OF
ITILE OF INVENTION: RIBOZNET CONDITIONS
ITILE OF INVENTION: RELATED TO LEVELS OF
ITILE OF INVENTION: MCLECULE-1 (I-CAM-1)

NUMBER OF SEQUENCES: 2390

CORRESONDENCE ADDRESS:
                  TELEPANE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEFAX: 67-3510
INFORMATION FOR SEQ ID NO: 121:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-292-620A-121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 901 CTGGTCATTTTCT 913
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two Length 15; MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/29,620A
FILING DATE: August 17, 1994
CLASSIFFCATION: 435
PRIOR APPLICATION DATA: described below:
PRIOR APPLICATION DATA: described below:
APPLICATION NUMBER: 08/08/85
FILING DATE: January 19, 1993
APPLICATION NUMBER: 08/08/85
FILING DATE: December 7, 1992
APPLICATION NUMBER: 32,327
APPLICATION NUMBER: 208/149
FILIEFAN: (213) 955-0440
TELEFAX: (213) 955-0440
TELEFAX: (213) 955-0440
TELEFAX: 67-3510
INFORMATION FOR SEQ ID NO: 289:
CENGTH: 15 base pairs
TYPE: nucleic acid
STRANDENNESS: single Score 9.8; DB 1; Pred. No. 1.7e+02; 13.4%; 84.6%; Query Match Best Local Similarity

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TELECOMMUNICATION INFORMATION:

US-08-441-887A-16/c

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                                                                                                              APPLICANT: Cronin, Maureen T.
APPLICANT: Cronin, Maureen T.
APPLICANT: Fodor, Stephen P.A.
APPLICANT: Hubbell, Earl A.
APPLICANT: Lipshutz, Robert J.
APPLICANT: Lobban, Peter E.
APPLICANT: Lobban, Peter E.
APPLICANT: Sheldon, Edward L.
TITLE OF INVENTION: Arrays of Nucleic Acid Probes on TITLE OF INVENTION: Biological Chips
NUMBER OF SEQUENCES: 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPANIOS SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAtentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/41,887A
FILING DATE: 16-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/143,312
FILING DATE: 26-OCT-1993
CLASSIFICATION: 435
PRIOR APPLICATION: 435
PRIOR APPLICATION UMBER: US 08/082,937
FILING DATE: 25-JUN-1993
ATTORNEY/AGENTION: ATTORNEY/AGENTION: ATTORNEY/AGENTION: ATTORNEY/AGENTION: ATTORNEY/AGENTION: ATTORNEY/AGENTION: ATTORNEY/AGENTION: ATTORNEY/AGENTION: ATTORNEY/AGENTION: ATTORNEY/AGENTION ATTORNEY/AGENTION: ATTORNEY/AGENTAIN: ATTORNEY/AGENTAIN: ATTORNEY/AGENTAIN: ATTORNEY/AGENTAIN: ATTORNEY/AGENTAIN: ATTORNEY/AGENTAIN: ATTORNEY/AGENTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, 8th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Liebeschuetz, Joseph O.
REGISTRATION NUMBER: 37,505
REFERENCE/DOCKET NUMBER: 018547-004160US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 17, Application US/08441887A
Patent No. 5837832
GENERAL INFORMATION:
APPLICANT: Chee, Mark
APPLICANT: Cronin, Maureen T.
APPLICANT: Podor, Stephen P.A.
APPLICANT: Huang, Xiaohua X.
                    Application US/08441887A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-326-2400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 650-326-2422
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: DNA (probe)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       911 TCTTTGGTCTTTGC 924
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STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-441-887A-17/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE: CE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
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   Gaps
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Pred. No. 1.7e+02;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Chee, Mark
APPLICANT: Chee, Mark
APPLICANT: Codin, Maureen T.
APPLICANT: Fodor, Stephen P.A.
APPLICANT: Huang, Xiaohua X.
APPLICANT: Lipshutz, Robert J.
APPLICANT: Lipshutz, Robert J.
APPLICANT: Lobban, Peter E.
APPLICANT: Sheldon, Edward L.
TITLE OF INVENTION: Arrays of Nucleic Acid Probes on TITLE OF INVENTION: Biological Chips
NUMBER OF SEQUENCES: 360
CORRESPONDENCE ADDRESS:
2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       E: Townsend and Townsend and Crew LLP
Two Embarcadero Center, 8th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/441,887A
PTLING DATE: 16-MAY-1995
CLASSIFICATION 1335
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/143,312
FILING DATE: 26-OCT-1993
CLASSIFICATION NUMBER: US 08/082,937
FILING DATE: 25-UN-1993
ATTORNEY/AGENT INFORMATION:
NAME: 116-DESCHUEZ: JOSEPH O.
REFERENCE/DOCKET NUMBER: 37,505
REFERENCE/DOCKET NUMBER: 018547-004160US
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                             RESULT 179
US-08-441-887A-8/c
; Sequence 8, Application US/08441887A
; Patent No. 583/832
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13.4%;
84.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: DNA (probe)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          938 TCTTCATTGGTTT 950
                                                                 959 GCTACCAACGGTG 971
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 84.6
Matches 11; Conservative
   11; Conservative
                                                                                                                            14 GCTAACAAAGGTG 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14 rcarcarregrer 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Chee. N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET:
   Matches
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RESULT 180

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TYPE: nucleic acid srranded stranded stranded strandboxs: single stranded TOPOLOGY: linear DESCRIPTION: third strand derived from Hepatitis B DESCRIPTION: third strand derived from Hepatitis B DESCRIPTION: isolate adr sequence region in Seq ID No. 5861244141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 13.4%; Score 9.8; DB 1; Length 15; Best Local Similarity 84.6%; Pred. No. 1.7e+02; Matches 11; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; RELEVANT RESIDUES IN SEQ ID NO: 142 :FROM 1 TO 15 US-08-173-489C-142
MEDIUM TYPE: 3.5 inch, 1.44Mb storage COMPUTER: 1BM PC/XY/AT COMPUTER: 1BM PC/XY/AT CORPUTER: 1BM PC/XY/AT CORPUTER: 1BM PC/XY/AT CORRANGE: Wordperfect Version 6.2 SOFTWARE: Wordperfect Version 5.1 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/173,489C FILING DATE: 22 DEC 1993 APPLICATION DATA: APPLICATION NUMBER: US 07/968,436 FILING DATE: 29 OCT 1992 APPLICATION NUMBER: 26,179 REGISTRATION INFORMATION: TELEPHONE: (attorney) (212) 246-8959 INFORMATION FOR SEQ ID NO: 142: CHENTH: 15 DASES INFORMATICS: LENGTH: LENGTH: LENGTH: 15 DASES INFORMATICS: LENGTH: LENGTH:
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PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HYPOTHETICAL:
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13.4%; Score 9.8; DB 1; Length 15;
Best Local Similarity 78.6%; Pred. No. 1.7e+02;
Matches 11; Conservative 0; Mismatches 3; Indels
APPLICANT: Lipshutz, Robert J.
APPLICANT: Lipshutz, Robert J.
APPLICANT: Lobban, Peter B.
APPLICANT: Morris, Macdonald S.
APPLICANT: Sheldon, Edward L.
TITLE OF INVENTION: Arrays of Nucleic Acid Probes on TITLE OF INVENTION: Biological Chips
NUMBER OF SEQUENCES: 360
CORRESPED TOWNSEND 360
STREET: Two Embarcadero Center, 8th Floor CITY: San Francisco STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 182
US-08-173-489C-142
| Sequence 1142 Application US/08173489C
| Patent NO. 5861244
| GENERAL INFORMATION:
| APPLICANT: MEDBURN, A. G.
| TITLE OF INVENTION: GENETIC SEQUENCE ASSAY USING DNA
| TITLE OF INVENTION: TRIPLE-STRAND FORMATION.
| NUMBER OF SEQUENCES: 365
| CORRESPONDENCE ADDRESS:
| ADDRESSEE: PROFILE DIAGNOSTIC SCIENCES, INC.,
| STREET: SIO EAST 73RD STREET,
| CITY: NEW YORK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CONTEXT: USA
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/441,887A
FILING DATE: 16-MAY-1995
CLASSIFICATION DATA:
PRILING DATE: 26-OCT-1993
CLASSIFICATION NUMBER: US 08/143,312
FILING DATE: 26-OCT-1993
CLASSIFICATION NUMBER: US 08/082,937
FILING DATE: 26-OUT-1993
ATTORNEY/AGENT INFORMATION:
NAME: Liebeschuetz, Joseph O.
REGISTRATION NUMBER: 37,505
TELEPHONE: 650-326-2400
TELEPHONE: 650-326-2400
TELEPAX: 650-326-2422
INFORMATION FOR ERQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
CUMBER: MIGHER BASE
SEQUENCE CHARACTERISTICS:
CHARLOT INFORMATION:
TELEPHONE: 650-326-2422
INFORMATION FOR ERQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
CHARLOT INFORMATICS:
CHARLOT I
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US-08-441-887A-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              911 TCTTTGGTCTTTGC 924
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STRANDEDNESS: single
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COMPUTER READABLE FORM:

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Gaps

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US-08-585-684B-1748/C

Sequence 1748, Application US/08585684B

Fatent No. 5877021

GENERAL INCORMATION:
APPLICANT: Stinchcomb, Daniel T.
APPLICANT: Jarvis, Thale
APPLICANT: McSwiggen, James
TITLE OF INVENTION: INDUCTION OF GRAFT TOLERANCE
TITLE OF INVENTION: AND REVERSAL OF IMMUNE RESPONSES
NUMBER OF SEQUENCES: 2751
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: Storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/585,684B
FILING DATE: January 16, 1996
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STATE: NEW YORK COUNTRY: USA

Gaps

schultz1-899.rni

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Score 9.8; DB 1; Length 15;
Pred. No. 1.7e+02;
5; Mismatches 2; Indels
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COMPUTER REALABLE FORM:
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPANING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN PC-DOS/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/544,381B
FILING DATE: 10-OCT-1995
CLASSIFICATION 1435
PRIOR APPLICATION NUMBER: US/08/510,521
PRIOR APPLICATION NUMBER: US/08/510,521
PRIOR APPLICATION NUMBER: US/08/244,064
PRIOR APPLICATION NUMBER: US/08/284,064
PRIOR APPLICATION NUMBER: US/08/143,312
PRIOR APPLICATION NUMBER: US/08/143,312
PRIOR APPLICATION NUMBER: US/08/143,312
PRIOR APPLICATION NUMBER: US/08/143,312
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Two Embarcadero Center, 8th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Lipshutz, Robert J.
APPLICANT: Lobban, Peter E.
APPLICANT: Morris, Macdonald S.
APPLICANT: Shellon, Edward L.
TITLE OF INVENTION: Arrays of Nucleic Acid Pri
TITLE OF INVENTION: Detecting Cystic Fibrosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           018547-004130US
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                                                                                                                                                                                                                                                                                              Sequence 114, Application US/08544381B Patent No. 6027880 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                   Cronin, Maureen T.
Miyada, Charles Garrett
Hubbell, Earl A.
                                                                                                                                                                                                                                                                                                                                                                                                                                   Chee, Mark
Fodor, Stephen P.A.
Huang, Xiaohua C.
Lipshutz, Robert J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 415-576-0300 INFORMATION FOR SEQ ID NO: 114: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Liebeschuetz, Joe
REGISTRATION NUMBER: 37,505
REFERENCE, POCKET NUMBER: 01
TELECOMMUNICATION INFORMATION:
                                         13.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and
                                                                                                                                  934 CICCICITCATIG 946
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                                         Ouery Match
Best Local Similarity 46.2
Matches 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         nucleic acid
EDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     linear
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TOPOLOGY: li
                                                                                                                                                                                                                                                                             US-08-544-381B-114/c
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US-08-585-684B-1811
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-544-381B-114
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2; Indels
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APPLICANT: Stinchcomb, Daniel T.
APPLICANT: Stinchcomb, Daniel T.
APPLICANT: Jarvis, Thale
APPLICANT: McSwiggen, James
TITLE OF INVENTION: METHOD AND REAGENT FOR THE
TITLE OF INVENTION: INDUCTION OF GRAFT TOLERANCE
TITLE OF INVENTION: AND REVERSAL OF IMMUNE RESPONSES
NUMBER OF SEQUENCES: 2751
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                       Score 9.8; DB 1;
Pred. No. 1.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 13.4%; Score 9.8; DB Best Local Similarity 84.6%; Pred. No. 1.7e Matches 11; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: storage
COMPUTER: IBM COMPAIDED
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FRAECEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 60/000,951
FILING DATE: July 7, 1995
ATTORNEY,ACENT INPORMATION:
NAME: WARDING, Richard
REGISTRATION NUMBER: 32,327
REFERENCE POCKET NUMBER: 218/078
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELECOMMUNICATION INFORMATION:
TELEPHONE: (7-3510
INFORMATION FOR SEG ID NO: 1811:
SEGUENCE CHARACTERISTICS:
LENGTH: 15 base pairs

LENGTH: 15 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 MD
MEDIUM TYPE: storage
                   FILING DATE: JULY 7, 1995
ATTORNEY AGENT INFORMATION:
NAME: Warburg Richard
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 218/078
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: (213) 955-0440
TELEFAX: (57-3510
INFORMATION FOR SEQ ID NO: 1748:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
TYPE: nucleic acid
STANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 184
2.08-58-688-1811
; Sequence 1811, Application US/08585684B
; Patent No. 5877021
  APPLICATION NUMBER: 60/000,951
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            E: Lyon & Lyon
633 West Fifth Street
Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     938 TCTTCATTGGTTT 950
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                       linear
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US-08-585-684B-1748
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STREET: 63
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RESULT 187
US-09-071-845-288/c
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                                                                                      Gaps
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Pred. No. 1.7e+02;
0; Mismatches 2; Indels
Query Match 13.4%; Score 9.8; DB 1; Length 15; Best Local Similarity 84.6%; Pred. No. 1.7e+02; Matches 11; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                             RESULT 186
US-09-071-845-121/C
Sequence 121, Application US/09071845
Fatent No. 6132967
GENERAL INFORMATION:
APPLICANT: Susan Grimm
APPLICANT: James McSwiggen
APPLICANT: James McSwiggen
APPLICANT: Gens Sullivan
APPLICANT: REBATHENT OF
TITLE OF INVENTION: RELATED TO LEVELS OF
TITLE OF INVENTION: MOLECULE-1 (I-CAM-1)
NUMBER OF SEQUENCES: 2390
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPRESSER: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: Storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
PRICK APPLICATION NUMBER: US/09/071,845
FILING DATE: August 17, 1994
APPLICATION NUMBER: US/09/071,845
FILING DATE: January 19, 1993
APPLICATION NUMBER: 07/989,849
FILING DATE: January 19, 1993
APPLICATION NUMBER: 208/149
FILING DATE: MADAIN 1000
FILING DATE: M
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13.4%; Soc
Best Local Similarity 84.6%; Pro
Matches 11; Conservative 0;
                                                                                                                                                        938 TCTTCATTGGTTT 950
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US-09-071-845-121
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US-09-071-845-288/C

Sequence 289, Application US/09071845

Patent No. 613286/C

Sequence 280, Application US/09071845

Patent No. 613286/C

APPLICANT: Susan Grimm
APPLICANT: Sean SUlivan
APPLICANTON: NUMERE Sulivan
APPLICANTON: Seat Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: Solon-200
ANGURRY: U.S.A.
ANGURRY: U.S.A.
ANGURRY: U.S.A.
ANGURRY: U.S.A.
ANGURRY: US-A.
ANGURRY: US-A.
ANGURRY: US-A.
ANGURRY: US-A.
APPLICANTON NUMBER: US/09/071,845
FILING DATE: ANGURST 17, 1994
APPLICANTON NUMBER: US/08/29,620
FILING DATE: ANGURST 17, 1994
APPLICANTON NUMBER: US/08/29,620
FILING DATE: ANGURST 17, 1994
APPLICANTON NUMBER: US/08/29,639
FILING DATE: ANGURST 17, 1994
APPLICANTON NUMBER: US/08/29,639
FILING DATE: ANGURST 17, 1994
APPLICANTON NUMBER: US/09/071,845
FILING DATE: ANGURST 17, 1997
ATTORNEY/AGENT INPORMATION:
NAME: WARDEN PURCANTON NUMBER: 208/149
FILING DATE: AUGUST 17, 1994
APPLICANTON NUMBER: 208/149
FILING DATE: AUGUST 17, 1994
APPLICANTON NUMBER: 208/149
FILING DATE: AUGUST 21, 1993
ATTORNEY/AGENT INPORMATION:
NAME: WARDEN US/08/201
TELEPAN: (213) 955-0440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-071-845-289/c
; Sequence 289, Application US/09071845
; Patent No. 6132957
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 288:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPLOGY: linear
US-09-071-845-288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          959 GCTACCAACGGTG 971
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1811, Application US/09038073
; Sequence 1811, Application US/09038073
; Patent No. 6194150
; GENERAL INFORMATION:
; APPLICANT: Stinchcomb, Daniel T.
APPLICANT: McSwiggen, James
; TITLE OF INVENTION: METHOD AND REAGENT FOR THE
; TITLE OF INVENTION: INDUCTION OF GRAFT TOLERANCE
; TITLE OF INVENTION: ADDICTION OF GRAFT TOLERANCE
; TITLE OF INVENTION: ADDICTION OF GRAFT TOLERANCE
; TITLE OF INVENTION: ADDICTION OF GRAFT TOLERANCE
; CORRESPONDENCE ADDRESS:
; CORRESPONDENCE ADDRESS:
                                                                        CITY: Los Angeles
COUNTY: Los Angeles
STATE: California
COUNTY: U.S.A.
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: Storage
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COMPUTER: FASTESEQ VERSION 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/038,073
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Los Angeles
STATE: California
COUNTY: U.S.A.
ZIE: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: 8.5" Diskette, 1.44 Mb
MEDIUM TYPE: 8.5" DISKETTE, 1.00 DERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/038,073
                                                                                                                                                                                                                                                                                                                                    218/078
                                        fth Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fifth Street
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STREET: 633 West Fifth
STREET: Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 84.6
Matches 11, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
STRANDEDNESS: single
                       ADDRESSEE: Lyon & I
STREET: 633 West Fi
STREET: Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         METHOD AND REAGENT FOR THE INDUCTION OF GRAFT TOLERANCE AND REVERSAL OF IMMUNE RESPONSES
APPLICANT: Susan Grimm
APPLICANT: Dan T. Stinchcomb
APPLICANT: Dan Stinchcomb
APPLICANT: Jeans McSwiggen
APPLICANT: Sean Sullivan
APPLICANT: Kenneth G. Draper
TITLE OF INVENTION: RIBOZYME TREATMENT OF
TITLE OF INVENTION: RELATED TO LEVELS OF
TITLE OF INVENTION: RELATED TO LEVELS OF
TITLE OF INVENTION: NOLECULE. (I-CAM-1)
NUMBER OF INVENTION: MOLECULE. (I-CAM-1)
NUMBER OF SEQUENCES: 2390
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                           ADDRESSEE: Lyon & Lyon STREET: 813 West Fifth Street STREET: Suite 4700 CITY: Los Angeles STATE: California COUNTRY: U.S.A. ZIP: 90071-2066 COMPUTEN READABLE FORM: MEDIUM TYPE: 3.5" Diskette, 1.44 Mb MEDIUM TYPE: storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
CLASSIFICATION:
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/292,620
FILING DATE: Auguet 17, 1994
APPLICATION NUMBER: 08/008,895
FILING DATE: January 19, 1993
APPLICATION NUMBER: 07/892,849
FILING DATE: December 7, 1992
ATTORNEY/AGENT INFORWATION:
NAME: WATDLEY RICHARD U.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 208/149
TELECHONE: (213) 955-0440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SUGNARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/071,845
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 289:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     959 GCTACCAACGGTG 971
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 84.6
Matches 11, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 15 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14 GCTAACAAAGGTG 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
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OTHER INFORMATION: Description of Artificial Sequence: OTHER INFORMATION: nucleotide base recognition sequence substantially OTHER INFORMATION: complementary to SEQ ID No. 6361945. 1 and 3
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    CONDITIONS RELATED TO LEVELS
OF VASCULAR ENDOTHELIAL
GROWTH FACTOR
8502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-346-551-4

US-09-346-551-4

Sequence 4, Application US/09346551B

Patent No. 0.6361945

GENERAL INFORMATION:
APPLICANT: BECKER, Michael M.
APPLICANT: SCHENCH, GATY P.
TITLE OF INVENTION: WOLECULAR TORCHES
FILE REFERENCE: GP098-02.UT

CURRENT FILING DATE: 1999-07-01

EARLIER APPLICATION NUMBER: US 60/091,616

EARLIER FILING DATE: 1998-07-02

NUMBER OF SEQ ID NOS: 9

SOFTWARE: PatentIn Ver: 2.0

SEQ ID NO 4

LENGTH: 15

TUNDE DENGTH: 15
TITLE OF INVENTION: CONDITIONS RELATED TO TITLE OF INVENTION: OF VASCULAR ENDOTHEL.

TITLE OF INVENTION: OF VASCULAR ENDOTHEL.

TITLE OF INVENTION: GROWTH FACTOR
NUMBER OF SEQUENCES: 8502
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTEN FRADABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COMPATING SYSTEN: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/584,040
FILING DATE: January 11, 1996
CLASSIFFICATION DATA:
APPLICATION NUMBER: 60/05,974
FILING DATE: OCCODER 26, 1995
ATTORNEY/AGENT INFORMATION:
NAME: WAIDLING, RICHARD J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 218/064
TELECOMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        916 GGTCTTTGCCTTT 928
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               linear
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Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-584-040-8493
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Sequence 3, Application US/09081646

Setent No. 6333152

Sequence 1, Application US/09081646

Setent No. 6333152

APPLICANT: Kinzler, Kenneth

APPLICANT: Zhou, Wei

TITLE OF INVENTION: Gene Expression Profiles in No. 6333152mal and

TITLE OF INVENTION: Cancer Cells

TITLE OF INVENTION: Cancer Cells

TITLE REFRENCE: 0107.7466

CURRENT APPLICATION NUMBER: 60/047,352

EARLIER APPLICATION NUMBER: 60/047,352

BARLIER PILING DATE: 1997-05-21

NUMBER OF SEQ ID NOS: 871

SEQ ID NO 3: SEQ ID NOS: 871

LENGTH: 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13.4%; Score 9.8; DB 1; Length 15; 84.6%; Pred. No. 1.70+02; tive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 192
US-08-564-040-8493
Sequence 8493, Application US/08584040
Sequence 8493, Application US/08584040
Settler No. 6346398
GENBRAL INFORMATION:
APPLICANT: Pavco, Pamela
SAPLICANT: Stinchcomb, James
APPLICANT: Stinchcomb, Dan T.
APPLICANT: Scinchcomb, Dan T.
APPLICANT: Scinchcomb, Dan T.
APPLICANT: Scinchcomb, TREATMENT FOR THE
TITLE OF INVENTION: TREATMENT OF DISSASES OR
TITLE OF INVENTION: TREATMENT OF DISSASES OR
                                                                                                                                                                                                                                                                                    218/078
                                                                                                             FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Harburg, Richard
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 218/07
FELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-160
FELEFAX: (213) 955-0440
FELEFAX: (213) 955
                                              PRIOR APPLICATION DATA: APPLICATION NUMBER: 08/585,684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       934 CTCCTCTTCATTG 946
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             922 TGCCTTTTATCCC 934
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Best Local Similarity 84.6
Matches 11; Conservative
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ORGANISM: Homo sapiens
                FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 191
US-09-081-646-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-081-646-3
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13.4%;
84.6%;
                                                                                                                                                                                               ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  916 GGTCTTTGCCTTT 928
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ouery Match
Best Local Similarity 46.24
Best Local Similarity 6.24
Conservative
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                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 84.6
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; ORGANISM: Mus sp.
US-09-371-772B-4147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -09-371-772B-4147
                                                                                                                                                                                                                                                                                                US-10-001-344-4
                                                                                                                                                                            TYPE: DNA
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                                                                            Gaps
                                                                                                                                                                                                                                               Sequence 5, Application US/08461210;
Fatent No. 6395475;
GENERAL INFORMATION:
APPLICANT: Leggett, Carol G.
TITLE OF INVENTION: Semiautomated Method for Fingerprinting
TITLE OF INVENTION: Bacterial DNA
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ruden, Barnett, McClosky, Smith, Schuster & ADDRESSEE: Ruden, Barnett, McClosky, Smith, Schuster & CREET: 200 East Broward Boulevard
CITY: Fort Lauderdale
STATE: Florida
                                                                            ..
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0
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Pred. No. 1.7e+02;
0; Mismatches 2; Indels
                                 Score 9.8; DB 1; Length 15
Pred. No. 1.7e+02;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/461,210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
CLASSIPFICATION: 436
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/064,596
FILING DATE: 18-MX-1993
ATTORNEY/AGENT INFORMATION:
NAME: Manso, Peter J. 264
REFERENCE/DOCKET NUMBER: FL20979-20
TELECOMMUNICATION: INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             32,264
ER: FL20979-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 4, Application US/10001344
Patent No. 6534274
GENERAL INFORMATION:
APPLICANT: BECKER, Michael M.
APPLICANT: SCHROTH, Gary P.
TITLE OF INVENTION: MOLECULAR TORCHES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear _ MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                  908 TTTTCTTTGGTCT 920
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             904 GTCATTTTCTTTG 916
                                                                                                                                                        2 rrrrccrrdcrcr 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 84.6
Matches 11; Conservative
                                    Query Match 13.4
Best Local Similarity 84.6
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 15 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13 Grcaarrccrrrg 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE:
                                                                                                                                                                                                                    RESULT 194
US-08-461-210-5/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-10-001-344-4
US-09-346-551-4
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APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Bavco, Pam
APPLICANT: Binchcomb, Jam
APPLICANT: Stinchcomb, Jam
APPLICANT: Stinchcomb, Jam
APPLICANT: Scobedo, Jaime
APPLICANT: Bacobedo, Jaime
APPLICANT: Brochedo, Jaime
APPLICANT: Brochedo, Jaime
APPLICANT: Brochedo, Jaime
TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Rel
TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
TITLE OF INVENTION: MHBRE: US/09/371,772B
CURRENT FILING DATE: 1999-08-10
PRIOR FILING DATE: 1999-10-26
PRIOR FILING DATE: 1995-01-08
NUMBER OF SEQ ID NOS: 14225
SOFTWARE: Patentin version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
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                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: Description of Artificial Sequence: OTHER INFORMATION: nucleotide base recognition sequence substantially OTHER INFORMATION: complementary to SEQ ID No. 6534274. 1 and 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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FILE REFERENCE: GP098-02.UT
CURRENT APPLICATION NUMBER: US/10/001,344
CURRENT FILING DATE: 2001-10-31
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/346,551
PRIOR FILING DATE: EARLIER FILING DATE: 1999-07-01
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PATENT VET. 2.0
SEQ ID NO 4
LENGTH: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 9.8; DB 1; Length 15;
Pred. No. 1.7e+02;
5; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 9.8; DB 1; Length 15;
Pred. No. 1.7e+02;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PCT-US92-06821A-129
; Sequence 129, Application PC/TUS9206821A
; GENERAL INFORMATION:
    APPLICANT: Shah, Jyotsna S.
    APPLICANT: Nietupski, Raymond M.
    TITLE OF INVENTION: Oligonucleotides Complementary to
    TITLE OF INVENTION: Mycobacterial Nucleic Acids
    NUMBER OF SEQUENCES: 133
    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 4147, Application US/09371772B Patent No. 6566127 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 13.4%; Score 9.8; DB 1; Length 15; Best Local Similarity 73.3%; Pred. No. 1.7e+02; Matches 11; Conservative 1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER KEALALALE FORM:
COMPUTER KEALALALE FORM:
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC COMPATION
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/259,148A
FILING DATE: 13-JUN 1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 822,335
FILING DATE: 17-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 505,888
FILING DATE: 05-APR-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 367,486
FILING DATE: 13-OCT-1989
PRIOR APPLICATION DATA:
APPLICATION DATE: US 36,672
PRIOR APPLICATION DATE: US 36,672
PRIOR APPLICATION DATE: US 386,672
PRIOR APPLICATION NUMBER: US 208,997
APPLICATION NUMBER: US 208,997
ATTORNEY/AGENT INFORMATION:
NAME: SAOLEZ, CHATLES K.
RAME: SAOLEZ, CHATLES R.
RAME: REPERPROPERTY NUMBER: US 386,672
REPERPROPERTY NUMBER: US 386,672
PRIORESTATION NUMBER: US 386,672
PRIORESTATION NUMBER: US 386,672
REPERPROPERTY NUMBER: US 386,672
PRIORESTATION NUMBER: US 386,672
PRIORESTATION NUMBER: US 386,672
REPERPROPERTY NUMBER: US 386,672
PRIORESTATION NUMBER: US 386,672
REPERPROPERTY NUMBER: US 386,672
REPUBLING NUMBER: US 386
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REFERENCE/DOCKET NUMBER: 4600-0093.20
                                                                                             131;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            920 TITGCCTTTTATCCC 934
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 rraccmrrrcaccc 15
                                              TELEFAX: 312-856-4972
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                           linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 350 Camb
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       USA
                                                                                                                                                                                                                                                                                       ; TOPOLOGY: li
; MOLECULE TYPE:
PCT-US92-06821A-131
            TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 199
US-08-259-148A-39
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FCT-US92-06821A-131

Sequence 131, Application PC/TUS9206821A

GENERAL INFORMATION:

APPLICANT: Nietupski, Raymond M.

APPLICANT: Liu, Jing

TITLE OF INVENTION: Mycobacterial Nucleic Acids

NUMBER OF SEQUENCES: 133

CORRESPONDENCE ADDRESS:

ADDRESSEE: Anacco Corporation

STREET: 200 East Randolph Drive, P.O. Box 87703

CITY: Chicago

STATE: 111inois

COUNTRY: U.S.A.

ZIP: 60680

COMPUTER: EADABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: BEN PC-DOS/NS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: BCT/US92/06821A

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/744,282

FILING DATE: 13-AUG-1991

ATTORNEY/AGENT INFORMATION:

NAME: GALloway, NOTVAL B.

REGESTRATION NUMBER: CN 5851

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
13.4%; Score 9.8; DB 1; Length 15;
Best Local Similarity 73.3%; Pred. No. 1.7e+02;
Matches 11; Conservative 1; Mismatches 3; Indels
                                                                                                                                                                             ADDRESSEE: Amoco Corporation
STREET: 200 East Randolph Drive, P.O. Box 87703
CITY: Chicago
STATE: 111inois
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             920 ITIGCCTTTTATCCC 934
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 TTAGCMTTTCACCCC 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: DNA PCT-US92-06821A-129
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Gaps
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; Sequence 55, Application US/07876941A
; Patent No. 5883768
; GENERAL INFORMATION:
    APPLICANT: Bradley, Daniel W.
    APPLICANT: Tam, Albert W.
    APPLICANT: Antichell, Carl
    TITLE OF INVENTION: Hepatitis E Virus Peptide Antigen and
    TITLE OF INVENTION: Antibodies
    NUMBER: OF SEQUENCES: 76
    CORRESPONDENCE ADDRESS:
    ADDRESSEE: Dealinger & Associates
    STREET: 350 Cambridge Avenue, Suite 250
    CITY: Palo Alto
. scanl, D A, Urbance, J W.

The division between fast-
and slow-growing species corresponds to natural
relationships among the mycobacteria
1. Journal of Bacteriology
570-574
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 9.4; DB 1; Length 11;
Pred. No. 1.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDLING TYPE: FIOPPY disk
COMPUTER: READABLE FORM:
MEDLING TYPE: FIOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM:
OFFIGATION BY PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/876,941A
FILING DATE: U1-MAY-1992
CLASSIFICATION NUMBER: US/07/876,941A
FILING DATE: 17-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 505,888
FILING DATE: 05-APRIL-1990
PRIOR APPLICATION NUMBER: US 36,7486
FILING DATE: 13-OCTOBER-1989
PRIOR APPLICATION NUMBER: US 36,7486
FILING DATE: 16-JUNE-1989
PRIOR APPLICATION NUMBER: US 36,7486
FILING DATE: 11-APRIL-1989
PRIOR APPLICATION NUMBER: US 320,997
FILING DATE: 11-APRIL-1989
PRIOR APPLICATION NUMBER: US 208,997
FILING DATE: 11-APRIL-1989
PRIOR APPLICATION NUMBER: US 208,997
FILING DATE: 17-JUNE-1988
ATTOMNEY/AGENT INPOMMER: US 208,997
FILING DATE: NUMBER: US 208,997
                                                                                                                                                                                                                                                                                                                    DATE: 1986 ... 

**RELEVANT RESIDUES IN SEQ ID NO: 307 :FROM 1 TO 11 US-08-173-489C-307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4600-0093.33
       ORGANISM: Corynebacterium renale PUBLICATION INFORMATION: AUTHORS: Stahl, D A, Urbance, J TITLE: The division between fast-TITLE: and slow-growing species C TITLE: relationships among the my
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REGISTRATION NUMBER: 38,615
REFERENCE/DOCKET NUMBER: 460
TELECOMMUNICATION: INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 12.9
Best Local Similarity 90.9
Matches 10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 201
US-07-876-941A-55
                                                                                                                                                                                                                                         JOURNAL:
VOLUME: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
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DESCRIPTION: 16s rRNA gene from Corynebacterium
DESCRIPTION: renale (Accession # M29553) nucleotides 997 to
DESCRIPTION: 1007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12.9%; Score 9.4; DB 1; Length 11; 90.9%; Pred. No. 1.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 307, Application US/08173489C
Patent No. 5861244
GENERAL INFORMATION:
APPLICANT: WANG, C.-G.
APPLICANT: HEPBURN, A. G.
TITLE OF INVENTION: TRIPLE-STRAND FORMATION.
NUMBER OF SEQUENCES: 365
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SSEE: PROFILE DIAGNOSTIC SCIENCES, INC.,
1: 510 EAST 73RD STREET,
NEW YORK
NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                   ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: DNA sequence, Fig. 7
US-08-259-148A-39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44Mb storage
COMPUTER: TBM FC/XT/AT
COMPUTER: TBM FC/XT/AT
COMPUTER: TBM FC/XT/AT
CORRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/173,489C
FILING DATE: 22 DEC 1993
CLASSIFICATION NUMBER: US/08/173,489C
FILING DATE: 29 DEC 1993
APPLICATION NUMBER: US/08,436
FILING DATE: 29 OCT 1992
APPLICATION NUMBER: US/08,436
FILING DATE: 29 OCT 1992
ATTORNEY/AGENT INFORMATION:
NAME: HANDELMAN, USGEPH H.
REGISTRATION NUMBER: 26,179
REPERBENCE/DOCKET NUMBER: US518-6
TELEPHONE: (ALLOHANTION:
TELEPHONE: (A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
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TELEFAX: (attorney) (212) 246-8959
INFORMATION FOR SEQ ID NO: 307:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 base pairs
TYPE: mucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        double stranded
                                                   TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 39
SEQUENCE CHARACTERISTICS:
LENGTH: 11 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
                               (415) 324-0880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 12.9
Best Local Similarity 90.5
Matches 10; Conservative
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                                                                                                                                                                                                                                                                                            unknown
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MOLECULE TYPE: DN
HYPOTHETICAL: NO
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US-08-173-489C-307
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STREET: 51
                           TELEPHONE:
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FEATURE:
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GENERAL INFORMATION:
APPLICANT: Morgan, Antony R.
APPLICANT: Severini, Alberto
ITILE OF INVENTION: Compositions and Methods for Determining the Activity
ITILE OF INVENTION: of DNA-Binding Proteins and of Initiation of
ITILE OF INVENTION: Transcription
ITILE OF INVENTION: Transcription
ITILE OF INVENTION: 0f DNA-Binding Proteins and of Initiation of
ITILE OF INVENTION: 0f DNA-Binding Proteins and of Initiation of
ITILE OF INVENTION: 0f DNA-Binding Proteins and of Initiation of
ITILE OF INVENTION: 09/344,300

FILE REPERENCE: 09/344,300

PRIOR FILING DATE: 1999-06-24

NUMBER OF SEQ ID NOS: 72

SEQ ID NO 2.

LENGTH: 11
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US-09-593-37-3/c
US-09-593-37-3/c
Sequence 3, Application US/09593323
Sequence 3, Application US/0959323
Sequence 3, Application US/0959323
Settle No. 6265213
TITLE OF INVENTION: Compositions and Methods for Determining the Activity TITLE OF INVENTION: OF DNA-Binding Proteins and of Initiation of TITLE OF INVENTION: Transcription
TITLE OF INVENTION: Transcription
FILE REFERENCE: DNAB-02921
CURRENT APPLICATION NUMBER: US/09/593,323
CURRENT SETTING DATE: 2000-06-13
PRIOR FILING DATE: 1999-06-24
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, OTHER INFORMATION: Description of Artificial Sequence: Synthetic US-09-593-323-2
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                                                                                                                                                                                                                                                                                                                                                               Score 9.4; DB 1; Length 11
Pred. No. 1.4e+02;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                             ORIGINAL SOURCE: INDIVIDUAL ISOLATE: DNA sequence, Fig. 7
(415) 324-0880
                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 90.9%;
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
ORGANISM: Artificial Sequence
                    TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 55
SEQUENCE CHARACTERISTICS:
LENGTH: 11 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                              915 TGGTCTTTGCC 925
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                                                                                                                                                                 TOPOLOGY: unknown
MOLECULE TYPE: DNA
HYPOTHETICAL: NO
                                                                                                                                                                                                                                         ANTI-SENSE: NO
TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 202
US-09-593-323-2/c
                                                                                                                                                                                                                                                                                                                 US-07-876-941A-55
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US-09-594-108-2/c

1 Sequence 2, Application US/09594108

2 Sequence 2, Application US/09594108

3 Factent No. 6284468

3 FATCH NO. 6284468

3 APPLICANT: Morgan, Antony R.

3 APPLICANT: Severini, Alberto

3 TITLE OF INVENTION: Compositions and Methods for Determining the Activity

3 TITLE OF INVENTION: Transcription

4 TITLE OF INVENTION: Transcription

5 TITLE OF INVENTION: Transcription

5 TITLE OF INVENTION: OF DNA-Binding Proteins and of Initiation of

6 TITLE OF INVENTION: Transcription

7 TITLE OF INVENTION

7 TIT
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; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-593-323-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Indels
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NUMBER OF SEQ ID NOS: 72
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 3
LENGTH: 11
TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      924 CCTTTTATCCC 934
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | Sequence 279, Application US/09249155A |
| Sequence 279, Application US/09249155A |
| Patent No. 6538173 |
| GENERAL INFORMATION: |
| APPLICANT: Hober-Katz, Ellen |
| TITLE OF INVENTION: Compositions and Methods for Wound |
| TITLE OF INVENTION: Healing |
| FILE REFERENCE: 00486, 78503 |
| CURRENT APPLICATION NUMBER: US/09/249,155A |
| CURRENT APPLICATION NUMBER: US 60/074,737 |
| PRIOR PLILING DATE: 1998-02-13 |
| PRIOR PLILING DATE: 1998-02-13 |
| PRIOR FILING DATE: 1998-08-16 |
| PRIOR FILING DATE: 1998-09-28 |
| NUMBER OF SEQ ID NOS: 346 |
| SOFTWARE: FastSEQ for Windows Version 4.0 |
| SEMINA 111
                                                                                                                                                                                                                       GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Heber-Katz, Ellen
TITLE OF INVENTION: Compositions and Methods for Wound
TITLE OF INVENTION: Healing
TITLE OF INVENTION: Healing
FILE REPERENCE: 00486.78503
CURRENT PELLORION NUMBER: US/09/249,155A
CURRENT PELLING DATE: 1999-02-13
PRIOR APPLICATION NUMBER: US 60/074,737
PRIOR APPLICATION NUMBER: US 60/097,937
PRIOR FILING DATE: 1998-08-26
PRIOR FILING DATE: 1998-09-28
NUMBER: OF SEQ ID NOS: 346
SOUTHWARE: FRASESQ for Windows Version 4.0
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Pred. No. 1.4e+02;
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Sequence 59, Application US/09249155A
Patent No. 6538173
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90.9%;
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Best Local Similarity 90.5
Best Local Similarity 90.5
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Matches 10, Conservative
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924 CCTTTTATCCC 934
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                                                     11 ccrrrrrrrcc 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Mus musculus
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Sequence 2, Application US/09344300B

Patent No. 6297013

GENERAL INFORMATION:

APPLICANT: Morgan, Antony R.

APPLICANT: Morgan, Antony R.

APPLICANT: Morgan, Antony R.

APPLICANT: Morgan, Antony R.

TITLE OF INVENTION: Compositions and Methods for Determining the Activity

TITLE OF INVENTION: Tenascription

FILE REFERENCE: DNAB-02921

CURRENT APPLICATION UNMERR: US/09/344,300B

CURRENT APPLICATION UNMERR: US/09/344,300B

CURRENT PILING DATE: 1999-06-24

NUMBER OF SEQ ID NOS: 72

SOFTWARE: PatentIN Ver. 2.0

SEQ ID NO 2

LENGTH: 11
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Patent No. 6297013

GENERAL INFORMATION:

APPLICANT: Worgan, Antony R.

APPLICANT: Worgan, Antony R.

APPLICANT: Severini, Alberto

TITLE OF INVENTION: Compositions and Methods for Determining the Activity

TITLE OF INVENTION: Transcription

SOFTWARKE: PATENT OF INVENTION: TRANSCRIPTION

SEQ ID NO 3.

LENGTH: 11
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                                 FEATURE:
, OTHER INFORMATION: Description of Artificial Sequence: Synthetic US-09-594-108-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic US-09-344-300-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12.9%; Score 9.4; DB 1; Length 11; 90.9%; Pred. No. 1.4e+02;
                                                                                                                                      12.9%; Score 9.4; DB 1; Length 11; 90.9%; Pred. No. 1.4e+02; tive 0; Mismatches 1; Indels
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        ORGANISM: Artificial Sequence
                                                                                                                                         Query Match
Best Local Similarity 90.9
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 12.9
Best Local Similarity 90.9
Matches 10; Conservative
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US-09-344-300-3/c
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US-09-344-300-2/c
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Sequence 3. Application US/08173489C

Sequence 3. Application US/08173489C

PREMIN No. 58527NT. WAG.

APPLICANT: HERMAL AND C. G.

STILLE OF INVARION: TRIDE-STRAND FORMATION:

COMPERSON SEQUENCES: 3.5

COMPENSON SEQUENCES: 3.5
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TITLE: by translocation; a model for translational JOHEMA: OPERCOALINGS of the National Academy of JOHEMA: CHEMICAL STATE 1948

**NATIONAL GLEGGES, USA
**NATIONAL SERVICE SERVICES IN SEQ ID NO: 9:FROM 1 TO 12
**NATIONAL SEGUES IN SEQ ID NO: 9:FROM 1 TO 12
**NATIONAL SEGUES IN SEQ ID NO: 9:FROM 1 TO 12
**NATIONAL SEGUES IN SEQ ID NO: 9:FROM 1 TO 12
**NATIONAL SEGUES IN SEQ ID NO: 9:FROM 1 TO 12
**NATIONAL SEGUES IN SEQ ID NO: 9:FROM 1 TO 12
**NATIONAL SEGUES IN SEQ ID NO: 9:FROM 1 TO 12
**NATIONAL SEGUES IN SEQ ID NO: 9:FROM 1 TO 12
**NATIONAL SEGUES IN SEQ ID NO: 9:FROM 1 TO 12
**NATIONAL SEGUES IN SEQ ID NO: 9:FROM 1 TO 12
**NATIONAL SEGUES IN SEGUES, INC., GLEAT AND PROMUTEN.
**NATIONAL SEGUES IN SEGUES, INC., GLEAT AND PROMUTEN.
**NATIONAL SEGUES IN SEGUES, INC., GLEAT AND STREET, SEGUES IN SEGUE
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .
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APPLICANT: Tyagi, Sanjay
APPLICANT: Tyagi, Sanjay
APPLICANT: Tizardi, Pered R.
APPLICANT: Lizardi, Pered R.
TITLE OF INVENTION: DETECTABLY LABELED DUAL CONFORMATION
TITLE OF INVENTION: OLIGONUCLEOTIDE PROBES, ASSAYS AND KITS
NUMBER OF SEQUENCES: 1
ADDRESSEE: Fish & Richardson, P.C.
STREET: 45 Rockefeller Pl., Suite 2800
CITY: New York
STATE: N.Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 9.4; DB 1; Length 14; Pred. No. 1.8e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ANTI-SENBE: no
PUBLICATION TON SEQ ID NO: 98 :FROM 1 TO 14
RELEVANT RESIDUES IN SEQ ID NO: 98 :FROM 1 TO 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
                                        SOFTWARE: Wordperfect Version 5.1
CURRENT APPLICATION DATA:
PRILIG DATE: 22 DEC 1993
FILING DATE: 22 DEC 1993
FILING DATE: 22 DEC 1993
RICHARD APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 07/968,436
FILING DATE: 29 OCT 1992
ATTORNEY/AGENT INFORMATION:
NAME: Handelman, Joseph H.
REGISTRATION NUMBER: 26,179
REFERENCE/DOCKET NUMBER: US 0.79
REPERENCE/DOCKET NUMBER: US 0.79
REPERENCE (attorney) (212) 708-1880
TELEPHONE: (attorney) (212) 246-8959
INFORMATION FOR SEQ ID NO: 98:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 bases
COMPUTER: IBM PC/XT/AT
OPERATING SYSTEM: MS-DOS version 6.2
SOFTWARE: Wordperfect Version 5.1
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COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ver
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/439,819
FILING DATE:
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APPLICATION DATA:
APPLICATION NUMBER: US 08/152,006
FILING DATE: 12-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: William J. Hone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 9, Application US/08439819
Patent No: 5925517
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid
STRANDEDNESS: single stranded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 90.9%;
Matches 10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 214
US-08-439-819-9
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US-09-874-601-88
i Sequence 88, Application US/09874601
j Patent No. 6632057
j GENERAL INFORMATION:
APPLICANT: LEWIN, ALPRED S.
J APPLICANT: GRANT, MARIA B.
TITLE OF INVENTION: THE TREATMENT OF RETINAL DISEASES
FILE REFERENCE: 4300.014100
CURRENT APPLICATION NUMBER: US/09/874,601
CURRENT PILING DATE: 2001-05-01
PRIOR FILING DATE: 1999-04-21
PRIOR FILING DATE: 1997-05-09
PRIOR FILING DATE: 1997-04-21
PRIOR FILING DATE: 1997-04-21
PRIOR FILING DATE: 1997-05-09
PRIOR FILING DATE: 1997-04-21
NUMBER OF SEQ ID NOS: 182
SOFFWARE: PatentIn Version 3.0
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                                                                                                                      Score 9.4; DB 1; Length 12;
Pred. No. 1.6e+02;
0; Mismatches 1; Indels
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US-08-173-489C-98
Sequence 98, Application US/08173489C
PREED NO. 28681244
GENERAL INFORMATION:
APPLICANT: WANG, C. -G.
TILLE OF INVENTION:
TILLE OF INVENTION: TRIPLE-STRAND FORMATION.
NUMBER OF SEQUENCES: 365
CORRESPONDENCE ADDRESS:
ADDRESSES: PROFILE DIAGNOSTIC SCIENCES, INC.,
STREET: 510 EAST 73RD STREET,
                                                  216 :FROM 1 TO 12
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OTHER INFORMATION: SYNTHETIC OLIGONUCLEOTIDE
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COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44Mb storage
; ANTI-SENSE: no
; PUBLICATION INFORMATION:
; RELEVANT RESIDUES IN SEQ ID NO:
US-08-173-489C-216
                                                                                                                           Query Match
Best Local Similarity 90.9%;
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: RNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4; Conservative
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2 UUCGUCUUUGC 12
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Matches 4; Conserv
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NEW YORK
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                                                  Score 9.4; DB 1; Length 14; Pred. No. 1.8e+02; 0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                          Sequence 147, Application US/08765340

Patent No. 6150092

GENERAL INFORMATION:

APPLICANT: UCHIDA, K.,

APPLICANT: UCHIDA, T.,

APPLICANT: TANAKA, Y.,

APPLICANT: KONDO, S.

TILLE OF INVENTION: COMPOUND

TITLE OF INVENTION: COMPOUND

TITLE OF INVENTION: APPLICANT: APPLICANT: SOURCES: 185

CORRESPONDENCE ADDRESS:

ADDRESSEE: ADDRESSE: ADDRESSE: ADDRESSEE: ADDRESSEE: MORGAN & FINNEGAN, L.L.P.

STREET: 345 PARK AVENUE

CITY: NEW YORK

STREET: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
SOFTWARE: #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/765,340
FILING DATE: 23-DEC-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: J11310/94
FILING DATE: 27-UN-1994
PRIOR APPLICATION NUMBER: J2-NOV-1994
FILING DATE: 21-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: SERUNIAN, LESLIE
REFERENCE/DOCKET NUMBER: 35,353
REFERENCE/TON INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
INPORMATION FOR SEQ ID NO: 147:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "synthetic DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                     12.9%;
90.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                     Query Match 12.9
Best Local Similarity 90.9
Matches 10; Conservative
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Best Local Similarity 90.9
Matches 10; Conservative
                                                                                                                                                     910 TTCTTTGGTCT 920
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TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 linear
                                                                                                                                                                                                                                                                                  RESULT 216
US-08-765-340-147
     US-08-838-545-50
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MOLECULE TYPE: other nucleic acid
MOLECULE TYPE: other nucleic acid (PNA),
DESCRIPTION: /desc = "peptide nucleic acid (PNA),
DESCRIPTION: where (decxy(ribose-phosphate linkages are replaced by
DESCRIPTION: where (decxy(ribose-phosphate linkages are replaced by
DESCRIPTION: where (decxy(ribose-phosphate linkages of the passes via bescription); glycine amino N through a methylenecarbonyl linker"
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                                                                                                                                                                                                                                                                                                                                                       Score 9.4; DB 1; Length 14;
Pred. No. 1.8e+02;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPREX: USA3

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM COMPATIBLE
CLASSIFICATION NUMBER: US 08/630,019
FILING DATE: 09-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Storella, John R.
REFERENCE/DOCKET NUMBER: 015389-001610US
TELEFONE: (415) 576-0200
TELEFONE: (415) 576-0300
INFORMATION FOR SEQ ID NO: 50:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
REGISTRATION NUMBER: 26,739
FREFERENCE/DOCKET NUMBER: 07763/027001
TELECOMMUNICATION INFORMATION:
TELEFHONE: 212-765-5070
TELEFAX: 212-259-2291
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 bases
                                                                                                                                                                                                                                                       TOPOLOGY: linear MOLECULE TYPE: DNA (oligonucleotide) US-08-439-819-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 215
US-08-838-545-50/c
; Sequence 50, Application US/08838545
; Parent No. 6046307
                                                                                                                                                                                                                                                                                                                                                          12.9%;
90.9%;
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Best Local Similarity 90.9
Matches 10, Conservative
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                                                                                                                                                                                                       TYPE: nucleic acid
STRANDEDNESS: single
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PROFILE DIAGNOSTIC SCIENCES, INC.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: Nucleic Acid
STRANDEDNESS: single stranded
TOPOLOGY: linear
                      : 510 EAST 73RD STREET,
NEW YORK
NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION TELEPHONE: (attorney) (212)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     908 TITICITIGGICIT 921
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (attorney) (21)
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11; Conservative
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PUBLICATION INFORMATION:
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                                                                                                                                       COMPUTER READABLE FORM:
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /desc = "peptide nucleic acid (PNA),
where (deoxy(ribose-phosphate linkages are replaced by
N-(2-aminoethyl)glycine units linked to nucleotide bases via
glycine amino N through a methylenecarbonyl linker"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
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              Sequence 50, Application US/09349532;
Patent No. 6294650;
GENERAL INFORMATION:
APPLICANT: Shay, Jerry W.
APPLICANT: Wright, Woodring E.
APPLICANT: Corey, David R.
APPLICANT: Corey, David R.
TITLE OF INVENTION: Modulation of Mammalian Telomerase by TITLE OF INVENTION: Peptide Nucleic Acids
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 9.4; DB 1; Length 14; Pred. No. 1.8e+02;
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Patent No. 5861244
GENERAL INFORMATION:
APPLICANT: WANG C. -G.
APPLICANT: HERBURN, A. G.
TITLE OF INVENTION: TRIPLE-STRAND FORMATION.
TITLE OF INVENTION: TRIPLE-STRAND FORMATION.
NUMBER OF SEQUENCES: 365
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRETT APPLICATION DATA:
APPLICATION NUMBER: US/09/349,532
                                                                                                                                                                                                                                                                                              ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, Eighth Floor CITY: San Francisco STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRICE APPLICATION DATA:
APPLICATION WUMBER: US 08/838,545
FILING DATE: 09-APR-1997
APPLICATION NUMBER: US 08/630,019
FILING DATE: 09-APR-1906
ATTORNEY/AGRAT INFORMATION:
NAME: Storella, John R.
REGISTATION NUMBER: 32,944
REFERENCE/DOCKET NUMBER: 015389-0016
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (415) 576-0200
TELEPAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 50: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 90.9
Matches 10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 14 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               nucleic acid
EDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy COMPUTER: IBM PC com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12 TTTTTGGTCT 2
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                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: USA
ZIP: 94111-3834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS:
    US-09-349-532-50/c
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US-08-173-489C-78
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MOLECULE TYPE: other nucleic acid
DESCRIPTION: third strand derived from
DESCRIPTION: retinoblastoma sequence region in Seq ID No. 586124477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12.6%; Score 9.2; DB 1; Length 14; 78.6%; Pred. No. 2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RELEVANT RESIDUES IN SEQ ID NO: 78 :FROM 1 TO US-08-173-489C-78
COMPUTER: 12.5 inch, 1.44Mb storage COMPUTER: 12M PC/XT/AT COMPUTER: 12M PC/XT/AT OPERATING SYSTEM: MS-DOS version 6.2 SOFTWARE: Wordperfect Version 5.1 CURRENT APPLICATION DATA: 40/08/173,489C FILING DATE: 22 DEC 1993 CLASSIFICATION: 435 PRIOR APPLICATION HOWBER: US 07/968,436 FILING DATE: 29 OCT 1992 ATPORNEY/AGENT INFORMATION: NAME: Handelman, JOSEPH H. REGISTRATION NUMBER: 26,179 REGISTRATION NUMBER: 26,179 REGISTRATION NUMBER: 26,179 REGISTRATION NUMBER: 26,179 REFERENCE DOCKET NUMBER: 26,179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                        y) (212) 708-1880
(212) 246-8959
O: 78:
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APPLICATION NUMBER: US/08/173,489C
FILING DATE: 22 DEC 1993
CLASSIFCATION: 435
PRIOR APPLICATION DATE:
APPLICATION NUMBER: US 07/968,436
FILING DATE: 29 OCT 1992
ATTORNEY/AGENT INFORMATION:
NAME: Handelman, Joseph H.
REGISTRATION NUMBER: 26,179
REFERENCE/DOCKET NUMBER: 05,179
REFERENCE/DOCKET NUMBER: 06,179
REFERENCE/DOCKET NUMBER: 10518-6
TELECHONE: (attorney) (212) 708-1880
TELECHONE: (attorney) (212) 708-1880
TELECHONE: (attorney) (212) 246-8959
INFORMATION FOR SEQ ID NO: 318:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 bases
TYPE: nucleic acid
STRANDEDNESS: single stranded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  931 TCCCTCCTCTTCAT 944
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-458-481B-2
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FILING DATE: 22 DEC 1993
CLASSIFICATION: 435
PRIOR ASPLICATION DAMBER: US 07/968,436
FILING DATE: 29 OCT 1992
ATDORNEY/AGENT INFORMATION:
NAME: Handelman, Useeph H.
REGISTRAATION NUMBER: 26,179
REFERENCE CHACKET NUMBER: 27,179
REFERENCE CHACKET NUMBER: 27,179
REFERENCE CHACKET NUMBER: 27,171
REFERENCE CHACKET NUMBER: 27,171
REFERENCE CHACKET NUMBER: CHACKET NUMBER: 27,171
RAPP POSITION IN GACCESSION # MITE, S, Shimada, AUTHORS: Macda, S, Mita, S, Araki, S, Shimada, AUTHORS: Macda, S, MITE, S, SHIMAGA, MITTER S, MITTER 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 318, Application US/08173489C
Patent No. 5861244
GENERAL INFORMATION:
THORMATION:
TITLE OF INVENTION: GENETIC SEQUENCE ASSAY USING DNA
TITLE OF INVENTION: TRIPLE-STRAND FORMATION:
NUMBER OF SEQUENCES: 365
CORRESPONDENCE ADDRESS:
ADDRESSEE: ADDRESSE: ADDRESSE:
ADDRESSEE: ADDRESSE: ADDRESSE:
ADDRESSEE: ADDRESSE:
ADDRESSEE: ADDRESSE:
ADDRESSEE: ADDRESSE:
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
COMPUTER READALE FORM:
MEDIUM TYPE: 3.5 inch, 1.44Mb storage
COMPUTER: IBM PC/XT/AT
COMPUTER: OPERATING SYSTEM: MS-DOS Version 6.2
SOFTWARE: ADDRESSEE: CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE: Structure and expression of TITLE: the mutant prealbumin gene associated with TITLE: Eautial amyloidotic polyneuropathy JOURNAL: Molecular Biological Medicine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VOLUME: 3

PAGES: 329-338

DATE: 1986

RELEVANT RESIDUES IN SEQ ID NO: 97 :FROM 1 TO 14

US-08-173-489C-97
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 78.6%
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14 rrrrrccrccrc
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Facent No. 6310048
GENERAL INFORMATION:
APPLICANT: KUMAR, Vijaya B.
FILLE OF INVENTION: ANTISENSE MODULATION OF AMYLOID BETA PROTEIN EXPRESSION
FILE REFERENCE: 16153-9250
CURRENT APPLICATION NUMBER: US/09/458,481B
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patentin Ver. 2.0
SOFTWARE: Patentin Ver. 2.0
LENGTH: 14
                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; OTHER INFORMATION: Description of Artificial Sequence: Antisense; OTHER INFORMATION: Oligonucleotide
US-09-458-481B-2
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0
MOLECULE TYPE: other nucleic acid
DESCRIPTION: third strand derived from H.
DESCRIPTION: influenzae 16s region in Seq 1D No. 5861244317
                                                                                                                                                                                                                                                       Query Match
12.6%; Score 9.2; DB 1; Length 14;
Best Local Similarity 78.6%; Pred. No. 2e+02;
Matches 11; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 12.6%; Score 9.2; DB 1; Length 14; Best Local Similarity 78.6%; Pred. No. 2e+02; Matches 11; Conservative 0; Mismatches 3; Indels
                                                                                     HYPOTHETICAL: yes

ANTI-SENSE: no

PUBLICATION INFORMATION:

RELEVANT RESIDUES IN SEQ ID NO: 318 :FROM 1 TO 14
US-08-173-489C-318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-535-249-118
; Sequence 118, Application US/08535249
; Patent No. 6455899
; GENERAL INFORMATION;
; APPLICANT: Schlingensiepen, Georg-Ferdinand
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                                            FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Target
OTHER INFORMATION: sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: Description of Artificial Sequence: Target OTHER INFORMATION: sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 9.2; DB 1; Length 14;
Pred. No. 2e+02;
0; Mismatches 3; Indels
                                                                                                                                                         Score 9.2; DB 1; Length 14; Pred. No. 2e+02;
                                                                                                                                                                                                        3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 182, Application US/08388353
; Patent No. 6010895
; GENERAL INFORMATION:
; APPLICANT: Deacon, Nicholas J.
APPLICANT: McPhee, Dale A.
; APPLICANT: Crowe, Suzanne
APPLICANT: Crowe, Suzanne
APPLICANT: Croper, David
ITILE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
NUMBER OF SEQUENCES: 800
CORRESPONDENCE ADDRESS:
ADDRESSEE: Scully, Scott, Murphy & Presser
STREET: 400 Garden City Plaza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: FRESCO, Jacques R.
APPLICANT: FRESCO, Jacques R.
TITLE OF INVENTION: TRIPLEX IN-SITU HYBRIDIZATION
FILE REPERENCE: 2448-103
CURRENT PILING DATE: 2000-09-08
PRIOR APPLICATION NUMBER: US/09/531,000
PRIOR APPLICATION NUMBER: 60/064,997
PRIOR PILING DATE: 1998-11-10
PRIOR FILING DATE: 1997-11-10
NUMBER OF SEQ ID NOS: 77
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO. 48
                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                             US-09-531-000-48/c
; Sequence 48, Application US/09531000
; Patent No. 6461810
; GENERAL INFORMATION:
    TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                              Query Match
Best Local Similarity 78.6%;
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 78.6%;
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 11530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                          921 TIGCCTITIDATCCC 934
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   920 TITGCCTTTTATCC 933
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United States
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-388-353-182/c
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                                                                                                                  US-09-531-000-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-531-000-48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ð
                                                                                                                                                                                                                                                            à
APPLICANT: Schlingensiepen, Karl-Hermann
APPLICANT: Schlingensiepen, Reimar
APPLICANT: Schlingensiepen, Reimar
APPLICANT: Schlingensiepen, Reimar
APPLICANT: Schlingensiepen, APPLICANT: Schlingensiepen, Reimar
TITLE OF INVENTION: Antisense-oligonuclectides for the treatment of
TITLE OF INVENTION: immuno-suppressive effect of transforming-growth-factor beta
TUMBER OF SEQUENCES: 137
CORRESPONDENCE ADDRESS:
ADDRESSEE: Jacobson, Price, Holman & Stern
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ô
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 223
US-09-531-000-14/C

Sequence 14, Application US/09531000
Patent No. 6461810
GENERAL INFORMATION:
APPLICANT: FRESCO, Jacques R.
TITLE OF INVENTION: FRIPLEX IN-SITU HYBRIDIZATION
FILE REPERENCE: 2448-103
CURRENT APPLICATION NUMBER: US/09/531,000
CURRENT FILING DATE: 1998-11-10
PRIOR PILING DATE: 1998-11-10
PRIOR FILING DATE: 1998-11-10
PRIOR FILING DATE: 1998-11-10
PRIOR PILING DATE: 1998-11-10
NUMBER OF SEQ ID NOS: 77
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
GURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/535,249
                                                                                                                                                              3: Jacobson, Price, Holman & Stern
400 Seventh St. N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 93 107 089.0
FILING DATE: 30-APR-1993
PRIOR APPLICATION UNMBER: EP 93 107 849.7
APPLICATION WUMBER: EP 93 107 849.7
FILING DATE: 13-MAY-1993
ATTORNEY, AGENT INFORMATION:
NAME: Player, William E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10577/P58418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Player, William E. REGISTRATION NUMBER: 31,409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 10
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)638-6666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (202) 393-5350
TELEX: RCA 248693 IDEA UR
INFORMATION FOR SEQ ID NO: 118:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              945 TGGTTTAATGTATC 958
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 TGGGTTCGTGTATC 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 78.69
Matches 11, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 nucleic acid
EDNESS: unknown
                                                                                                                                                                                STREET: 400 Seven...
CITY: Washington D.C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     unknown
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MOLECULE TYPE: D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS:
                                                                                                                                                                                                                                                               20004
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; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-388-353-183
                                                                                                                    Query Match
Best Local Similarity 100.0%;
Matches 9; Conservative 0
         single
                                                                                                                                                                                                              933 CCTCCTCTT 941
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TOPOLOGY: linear; MOLECULE TYPE: DNA US-08-488-5518-182
         STRANDEDNESS:
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US-08-388-35-183/C
Sequence 183, Application US/0838353
Sequence 184, Application US/0838353
SPECTANT: Crowe, Suzame
APPLICANT: Crowe, Suzame
APPLICANT: Crowe, David
TILLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
NUMBERS OF SEQUENCES: 800
CORRESCE: Scully, Scott, Murphy & Presser
STREET: 400 Garden City Plaza
CITY: Garden City Plaza
COUNTRY: United States
ZIP: 11530
COMPUTER: Elempth City
STATE: New York
COMPUTER: Elempth Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PROPER PROPER IN SCOTTAINS
SOFTWARE: PROPENTION: NAWBER: US/08/388,353
FILING DATE: 14-FEB-1995
CLASSIFICATION NUMBER: 31,346
STELEPAX: (516) 742-4343
TTELEPAX: (516) 742-4343
TTELEPAX: 230 901 SAMS UR
TTELEPAX: 230 901 SAMS UR
TTELEPAX: 230 901 SAMS UR
TTELEPAX: 10 base pairs
TTPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 12.3%; Score 9; DB 1; Length 10; Best Local Similarity 100.0%; Pred. No. 1.5e+02; Matches 9; Conservative 0; Mismatches 0; Indels
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
PPLICATION NUMBER: US/08/388,353
FILING DATE: 14-FEB-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Didigilo, Frank S.
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 9606
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
TELEPHONE: (516) 742-4366
TELECOMMUNICATION INFORMATION:
TELETEX: 239 901 SANS UR
TELEX: 239 901 SANS UR
SEQUENCE CHARACTERISTICS:
LENGTH: 10 base pairs
TYPE: MULDIC acid
STRANDEDNES: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-388-353-182
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Gaps
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KENLIN. 227
US-08-468-551B-182/C
US-08-468-551B-182/C
Sequence 182, Application US/08488551B
Patent No. 6015661
Patent No. 6015661
Patent No. 6015661
APPLICANT: David Cooper
APPLICANT: David Cooper
TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
NUMBER OF SEQUENCES: 841
CORRESPONDENCES: 841
CORRESPONDENCES: ADARDERSS:
ADDRESSE: SCULLY, SCOTT, MURPHY & PRESSER
STRATE: NEW YORK
COUNTRY: US-NA.
CITY: GARDEN CITY
COMPUTER: IS NO COMPATIBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IS NO COMPATIBLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: BATCATION DATA:
APPLICATION NUMBER: US/08/488,551B
FILING DATE: 07-UTN-1995
RELING DATE: 14-FEB-1994
APPLICATION NUMBER: PM024 (AU)
FILING DATE: 14-FEB-1995
APPLICATION NUMBER: PN028 (AU)
FILING DATE: 14-FEB-1995
APPLICATION NUMBER: PN028 (AU)
FILING DATE: 17-MAY-1995
ATTOR APPLICATION NUMBER: PN028 (AU)
FILING DATE: 17-MAY-1943
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 12.3%; Score 9; DB 1; Length 10; Best Local Similarity 100.0%; Pred. No. 1.5e+02; Matches 9; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (516) 742-4366
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 10 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        933 CCTCCTCTT 941
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MOII OCC TO T#:#0:T/ Z00;

Gabs

; 0

0; Indels

Score 9; DB 1; Length 10; Pred. No. 1.5e+02; 0; Mismatches 0; Indels

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Gaps
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i Sequence 80, Application US/09508753B

j Patent No. 6544736

i GENERAL INFORMATION:
APPLICANT: Akira SHIRAMOTO
APPLICANT: Yac SHIRAM
APPLICANT: Yac SHIRAM
APPLICANT: Hiroko FUNAKI
APPLICANT: Masanori WATAHIKI
TITLE OF INVENTION: Method for Synthesizing cDNA from mENA sample
FILE REPERENCE: 0016-62/HG
CURRENT APPLICATION NUMBER: US/09/508,753B
CURRENT FILING DATE: 2000-06-16
FRICH APPLICATION NUMBER: US/09/508,753B
CURRENT PILING DATE: 1997-09-18
NUMBER OF SEQ ID NOS: 472

SEQ ID NO 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 60, Application US/09508753B
Fatent No. 6544736
FARENCE INFORMATION
APPLICANT: Akira SHIMAMOTO
APPLICANT: Yasuhiro FURUICHI
APPLICANT: Yuko SHIBATA
APPLICANT: Hiroko FUNAKI
APPLICANT: HONGER: 00162/HG
CURRENT APPLICATION NUMBER: UP 9/270324
FRIOR FILING DATE: 1997-09-18
NUMBER: OF SEQ ID NOS: 472
SEQ ID NO 60
LENGTH: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; OTHER INFORMATION: Description of Artificial Sequence: Primer US-09-508-753B-60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12.3%; Score 9; DB 1; Length 10; 100.0%; Pred. No. 1.5e+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 10;
                                                                                                                                                                                      TYPE: DNA
ORGANISM: Artificial Sequence
FRATURE:
OTHER INFORMATION: Majority consequences sequence.
US-09-445-388A-5
                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
12.3%; Score 9; DB 1; Le
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 9; Conservative 0; Mismatches 0;
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PatentIn version 3.1
SEQ ID NO 5
LENGTH: 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 100.
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           939 CTTCATTGG 947
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       917 GTCTTTGCC 925
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US-09-445-388A-5/c
; Sequence S, Ap42ication US/09445388A
; Sequence S, Ap42ication US/09445388A
; Patent No. 6534259
; GENERAL INFORMATION:
; APPLICANT: Wakefield, Andrew J.
; FILE REFERENCE: ABLE-0012
; CURRENT APPLICATION NUMBER: US/09/445,388A
; CURRENT FILING DATE: 2000-03-23
; PRIOR APPLICATION NUMBER: PCT/GE98/01637
; PRIOR FILING DATE: 1998-06-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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                                                                                                                                Sequence 183, Application US/08488551B
Patent No. 6015661
GENERAL INFORMATION:
APPLICANT:
Dale A. McPhee
APPLICANT:
Dale A. McPhee
APPLICANT:
DAID GOODERS:
ADDRESSES:
ADDRESSES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1; Length 10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 11530-0299
COMPUTER: EADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: EBM FC Compatible
OPERAITIG SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAtentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
PPLICATION NUMBER: US/08/488,5518
FILING DATE: 07-JUN: 1995
FILING DATE: 14-FEB-1994
APPLICATION NUMBER: PM0284 (AU)
FILING DATE: 21-FEB-1994
APPLICATION NUMBER: PW0284 (AU)
FILING DATE: 21-FEB-1994
APPLICATION NUMBER: PW0284 (AU)
FILING DATE: 14-FEB-1995
APPLICATION NUMBER: PW0284 (AU)
FILING DATE: 14-FEB-1995
APPLICATION NUMBER: PW0284 (AU)
FILING DATE: 17-MAY-1995
APPLICATION NUMBER: PW0284 (AU)
FILING DATE: 17-MAY-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12.3%; Score 9; DB 1
100.0%; Pred. No. 1.5
tive 0; Mismatches
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Best Local Similarity 100.
Matches 9; Conservative
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                                                                                                             -08-488-551B-183/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-488-551B-183
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COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 MD
MEDIUM TYPE: 3.5" Diskette, 1.44 MD
MEDIUM TYPE: SCOMPAGE
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/373,124A
FILING DATE: January 13, 1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/245,466
FILING DATE: MAY 18, 1994
APPLICATION NUMBER: 08/245,466
FILING DATE: MAY 18, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               February 7, 1994
UMBER: 07/987,132
December 7, 1992
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             925 CTTTTATCC 933
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APPLICATION NUMBER:
FILING DATE: Decemb
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US-09-508-753B-143

// Sequence 143, Application US/0950B753B
// APPLICANT: Aria SHIMAMOTO
// APPLICANT: Yuko SHIBATA
// APPLICANT: Hiroko FUNAKI
// APPLICANT: Hiroko FUNAKI
// APPLICANT: Hiroko FUNAKI
// APPLICANT: Hiroko FUNAKI
// APPLICANT: Masnori WATAHIKI
// APPLICANT: Masnori WATAHIKI
// TITLE OF INVENTION: WARCHOOM for Synthesizing CDNA from mRNA sample
// CURRENT APPLICATION NUMBER: US/09/508,753B
// CURRENT APPLICATION NUMBER: US/09/508,753B
// PRIOR FILING DATE: 1997-09-18
// NUMBER OF SEQ ID NOS: 472
// SEQ ID NO 143
// LENTH: 10
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; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-508-7538-143
                                                            ; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-508-753B-80
                                                                                                                                          DB 1; Le.,
40. 1.5e+02;
0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12.3%; Score 9; DB 1; Length 10; 100.0%; Pred. No. 1.5e+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-01-844-596B-6

Sequence 6, Application US/07854596B

Sequence 6, Application US/07854596B

Patent No. 5434010

Patent No. 5434010

APPLICANT: Dawson, Keith M

APPLICANT: Cappleski, Dioyd

APPLICANT: Cappleski, Dioyd

TITLE OF INVENTION: Proteins and nucleic acids

NUMBER OF SEQUENCES: 73

CORRESPONDENCE ADDRESS:

ADDRESSEE: Dr. John J. McDonnell

STREET: Ten South Wacker Drive, Suite 3000

CITY: Chicago

STRATE: IL

COUNTRY: USA

ZIP: 60606

COMPITY: Floppy disk

MEDIUM TYPE: Floppy disk

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: DatentIn Release #1.0, Version #1.25
                                                                                                                                                   Query Match 12.3%; Score 9; DB 1
Best Local Similarity 100.0%; Pred. No. 1.5
Matches 9; Conservative 0; Mismatches
                TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 100.9
Matches 9, Conservative
                                                                                                                                                                                                                                             911 TCTTTGGTC 919
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LENGIH: 10
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APPLICATION UNMER: US/07/854,596B
FILING DATE: US/07/854,596B
FATORNEY/AGENT INFORMATION:
NAME: MCDORNELL, John J
FREETRACTON NUMBER: 26,949
FRETERENCE/DOCKET NUMBER: 26,949
FRETERENCE/DOCKET NUMBER: 312-715-1000
FELETAX: 312-715-1000
FELETAX: 312-715-1234
FELETAX: 312-715-1337
FELETAX: 312-715-1334
FELETAX: 312-715-1334
FELETAX: 312-715-1334
FELETAX: 312-715-1537
INPORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS:
LENGTH: 11 base pairs
FYPE: nucleic acid
STRANDEDNESS: single
FOLOCY: linear
FOLOCY: Lin ö ö Query Match 12.3%; Score 9; DB 1; Length 11; Best Local Similarity 100.0%; Pred. No. 1.7e+02; Matches 9; Conservative 0; Mismatches 0; Indels RESULT 234
US-08-373-124A-46/C

Sequence 46, Application US/08373124A

Patent No. 5646042

GENERAL INFORMATION:
APPLICANT: Stinchcomb, Dan T.
APPLICANT: Stinchcomb, Dan T.
APPLICANT: Draper, Kenneth
APPLICANT: Drayis, Thale
TITLE OF INVENTION: TREATMENT OF RESTENOSIS AND
TITLE OF INVENTION: CANCER USING RIBOZYMES
NUMBER OF SEQUENCES: 2627
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: STATE: STATE: CALIFORNIA
STREET: CALIFORNIA
COUNTRY: U.S.A.
COUNTRY: U.S.A.

Gaps

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3. 1.7e+02;
ches 0; Indels
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MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: BE PC compatible
COMPUTER: BE PC compatible
COMPUTER: BEACHILI BM PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
CUBRENT APPLICATION DATA:
APPLICATION NUMBER: 07/982,759
FRIOR APPLICATION DATA:
APPLICATION NUMBER: 08 9127319.3
FRING DATE: 18-0C-1991
FRING DATE: 14-0CT-1992
ATPLING DATE: 14-0CT-1993
ATPLING DATE: 14-0CT-1993
ATPLING DATE: 14-0CT-1993
ATPLING DATE: 17-0CT-1993
ATPLING PORE SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
TITLE OF NIVENTION: Stem Cell Inhibiting Proteins NUMBER OF SEQUENCES: 178
CORRESPONDENCE ADDRESS:
ADDRESSEE: HALE and DORR
STREET: 60 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: misc_feature
| NAME/KEY: misc_feature
| LOCATION: 1..11
| OTHER INFORMATION: /product= "BOTTOM STRAND OF OTHER INFORMATION: OLIGONUCLEOTIDE ADAPTOR"
| US-08-450-9058-33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 12.3%; Score 9; DB 1
Best Local Similarity 100.0%; Pred. No. 1.7
Matches 9; Conservative 0; Mismatches
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Sequence 33, Application US/08450905B
Patent No. 5856301
GENERAL INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEX: (7-3510
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  906 CATTITCIT 914
                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear MOLECULE TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-435-628-46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET:
CITY: BO
STATE: M
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12.3%; Score 9; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 9; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 46, Application US/08435628
Patent No. 5817796
GENERAL INFORMATION:
APPLICANT: Stinchcomb, Dan T.
APPLICANT: Draper, Kenneth
APPLICANT: Draper, Kenneth
APPLICANT: McSwiggen, James
APPLICANT: Jarvis, Thale
ITILE OF INVENTION: TREATMENT OF RESTENOSIS AND
ITILE OF INVENTION: TREATMENT OF RESTENOSIS AND
ITILE OF SEQUENCES: 2627
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITAL: SULCE TO CONTRY: LOS ADGGLES STATE: California COUNTRY: U.S.A.

ZIP: 90071

ZIP: 90071

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb MEDIUM TYPE: STORME COMPUTER: ENORAGE COMPUTER: IBM Compatible OPERATING SYSTEM: IBM P.C. DOS 5.0 SOFTWARE: WORD FREECT 5.1

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/435,628 FILING DATE: 05-MAY-1995

FILING DATE: Dannary 13, 1995
APPLICATION NUMBER: 08/373,124
FILING DATE: May 18, 1994
APPLICATION NUMBER: 08/192,943
FILING DATE: FEBRUARY 7, 1994
APPLICATION NUMBER: 07/931,132
FILING DATE: December 7, 1994
APPLICATION NUMBER: 07/931,132
FILING DATE: PROFUNER: 07/931,132
FILING DATE: PROFUNER: 07/931,132
FILING DATE: PROFUNER: 07/931,132
APPLICATION NUMBER: 07/931,132
FILING DATE: PROFUNER: 07/931,132
FILING DATE: PROFUNER: 07/931,132
APPLICATION NUMBER: 07/931,132
FILING DATE: PROFUNER: 07/931,132
APPLICATION NUMBER: 07/931,132
APPLICATION NUMBER: 07/931,132
APPLICATION NUMBER: 07/931,132
APPLICATION NUMBER: 07/936,422
                                                                                                                                  MAME: Warburg, Richard

REGISTRATION NUMBER: 32,327

REFERENCE/DOCKET NUMBER: 209/035

TELECOMMUNICATION INFORMATION:

TELEPHONE: (213) 489-1600

TELEPHONE: (213) 955-0440

TELEPHONE: (213) 955-0440

TELEPHONE: (213) 955-0440

INFORMATION FOR SEQ ID NO: 46: SEQUENCE CHARACTERISTICS: LENGTH: 11 base pairs

TYPE: nucleic acid

STAPE: Nucleic aci
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Warburg, Richard
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 209/035
                 APPLICATION NUMBER: 07/936,422
FILING DATE: August 26, 1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              906 CATTTTCTT 914
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US-08-435-628-46/c
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MOLECULE TYPE: other nucleic acid
DESCRIPTION: third strand derived from Hepatitis B
DESCRIPTION: isolate ayw sequence region in Seq ID No, 5861244159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
12.3%; Score 9; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 9; Conservative 0; Mismatches 0; Indels
                   APPLICANT: WANG, C. -G.
APPLICANT: WANG, C. -G.
APPLICANT: HEPBURN: GENERAL CROUENCE ASSAY USING DNA
TITLE OF INVENTION: TRIPLE-STRAND FORMATION.
NUMBER OF SEQUENCES: 365
CORRESPONDENCE ADDRESS:
ADDRESSEE: PROFILE DIAGNOSTIC SCIENCES, INC.,
STREET: SIO EAST 73RD STREET,
CITY: NEW YORK
STATE: NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; RELEVANT RESIDUES IN SEQ ID NO: 160 :FROM 1 TO 11
US-08-173-489C-160
                                                                                                                                                                                                              COUNTRY: USA
ZIF: 10021.
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44Mb storage
COMPUTER: 1BM FOXTYTA
OPERATING SYSTEM: MS-DOS version 6.2
SOFTWARE: Wordperfect Version 5.1
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/08/173,489C
FILING DATE: 22 DEC 1993
CLASSIFICATION DATA:
APPLICATION NUMBER: US/08/436
FILING DATE: 29 OCT 1992
ATTORNEY/AGENT INFORMATION:
NAME: Handelman, Joseph H.
REGISTRATION NUMBER: 26,179
REFERENCE/DOCKET NUMBER: 26,179
REFERENCE/DOCKET NUMBER: 26,179
REFERENCE/DOCKET NUMBER: 26,179
REFERENCE/CONCET NUMBER: 26,179
REFERENCE CHARACTERISTICS:
TELEPRATION NUMBER: 26,179
REFERENCE CHARACTERISTICS:
TELEPROME: (attorney) (212) 246-8959
INFORMATION POR SEQ ID NO: 160:
SEQUENCE CHARACTERISTICS:
LUBGTH: 11 bases
TYPE: nucleic acid
STRANDEDNESS: single stranded
TYPE: nucleic acid
STRANDEDNESS: single stranded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ANTI-SENSE: no PUBLICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    932 CCCTCCTCT 940
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                                         ö
                                         Gaps
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STRANDEDNESS: single stranded
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: third strand derived from Hepatitis B
DESCRIPTION: isolate adr sequence region in Seq ID No. 5861244133
                                         .
0
                                                                                                                                                                                          Query Match
12.3%; Score 9; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 9; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12.3%; Score 9; DB 1; Length 11; 100.0%; Pred. No. 1.7e+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ANTI-SENSE: no
PUBLICATION INFORMATION:
RELEVANT RESIDUES IN SEQ ID NO: 134 :FROM 1 TO 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 238
2.08-173-489C-160
3. Sequence 100, Application US/08173489C
5. Patent No. 5861244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 12.3
Best Local Similarity 100.
Matches 9; Conservative
                                                                       925 CTTTTATCC 933
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2 CTTTTATCC 10
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                                                                                                                                                                  RESULT 237
US-08-173-489C-134
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US-08-173-489C-196

| Sequence 196, Application US/08173489C|
| Patent No. 5861244|
| APPLICANT: HEPBURN, C. -G. APPLICANT: HEPBURN, A. G. +TITLE OF INVENTION: TRIPLE-STRAND FORMATION.
| TITLE OF INVENTION: TRIPLE-STRAND FORMATION.
| NUMBER OF SEQUENCES: 365 |
| CORRESPONDENCE ADDRESS: ADDRESSEE: PROFILE DIAGNOSTIC SCIENCES, INC., STREET; 510 EAST 73RD STREET,
| STREET: NEW YORK STATE: NEW YORK
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Gaps

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Patent No. 6622930
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: LU, CHANGDE
TITLE OF INVENTION: NEW TRIPLEX FORMING OLIGONUCLECTIDES AND THEIR USE IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
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| Sequence 222, Application US/09249155A
| Sequence 222, Application US/09249155A
| Patent No. 6538173
| GENERAL INFORMATION:
| APPLICANT: Heber-Katz, Ellen
| TITLE OF INVENTION: Compositions and Methods for Wound
| TITLE OF INVENTION: Healing
| TITLE OF INVENTION: Healing
| TITLE OF INVENTION: HOADER: US/09/249,155A
| CURRENT APPLICATION NUMBER: US 60/074,737
| PRIOR FILING DATE: 1998-02-12
| PRIOR FILING DATE: 1998-02-13
| PRIOR FILING DATE: 1998-02-6
| PRIOR FILING DATE: 1998-09-28
| PRIOR FILING DATE: 1998-09-28
| NUMBER OF SEQ ID NOS: 346
| SEQ ID NOS: 234
| SEQ ID NO 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12.3%; Score 9; DB 1; Length 11; 100.0%; Pred. No. 1.7e+02; cive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: misc_feature
LOCATION: 1..1
OTHER INFORMATION: /product= "BOTTOM STEAND OF
OTHER INFORMATION: OLIGONUCLEOTIDE ADAPTOR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1; Le
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 9; DB 1; red. No. 1.76 0; Mismatches
                                                                                                                                                           102378.120
GB 9221587.0
                       FILING DATE: 14-OCT-1992
ATTORNEY/AGENT INFORMATION:
NAME: BAKER, HOLLIE L.
REGISTRATION NUMBER: 31,321
REFERENCE/OCCET NUMBER: 1023
TELEPHONE: 617-526-600
INFORMATION FOR SEQ ID NO: 38: SEQUENCE CHARACTERISTICS: LENGTH: 11 Dase pairs
TYPE: nucleic acid
TYPE: nucleic acid
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match

Best Local Similarity 100.0%; Pr
Matches 9; Conservative 0;
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APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear MOLECULE TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-249-155A-222
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-07-982-759F-33
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear MOLECULE TYPE: other nucleic acid DESCRIPTION: third strand derived from Hepatitis B DESCRIPTION: third strand derived from Hepatitis B DESCRIPTION: isolate adw2 sequence region in Seq ID No. 5861244195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 9; DB 1; Length 11;
Pred. No. 1.7e+02;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: CRAIG, Stewart
APPLICANT: CRAIG, Michael
APPLICANT: CRAIG, Michael
APPLICANT: CZAPLEWSKI, Liloyd George
APPLICANT: CZAPLEWSKI, Liloyd George
TITLE OF INVENTION: Stem Cell Inhibiting Proteins
NUMBER OF SEQUENCES: 178
CORRESPONDENCE ADDRESS:
ADDRESSEE: HALE and DORR LLP
STREET: 60 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RELEVANT RESIDUES IN SEQ ID NO: 196 :FROM 1 TO 11 US-08-173-489C-196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION 12.505/16.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/982,759F
FILING DATE: 08-WAR-1993
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
FILING DATE: 23-25C-1991
FILING APPLICATION DATA:
                       COMPUTER: BADABLE FORM:
COMPUTER: IBM PC/XT/AT
COMPUTER: Wordperfect Version 6.2
SOFTWARE: Wordperfect Version 5.1
CURRENT APPLICATION NUMBER: US/08/173,489C
FILING DATE: 22 DEC 1993
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: US/05/8,436
FILING DATE: 29 OCT 1992
ATTOMEN'AGENT INFORMATION:
NAME: Handelman, Joseph H.
REGISTRATION NUMBER: 26,179
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFRAX: (attorney) (212) 246-8959
INFORMATION FOR SEQ ID No: 196:
ENDTH: IL DAGES
TENTH: IL DAGES
T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 33, Application US/07982759F
Patent No. 6057123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: nucleic acid
STRANDEDNESS: single stranded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 12.3%; Soc
Best Local Similarity 100.0%; P:
Matches 9; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ANTI-SENSE: no PUBLICATION:
   COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        932 CCCTCCTCT 940
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STREET: 6v -
CITY: Boston
STATE: MA
TP: 02109
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RESULT 244
US-06-663-824-88
is Squence 88, Application US/08663824
squence 88, Application US/08663824
state No. 6083693
is GRNERAL INFORMATION:
APPLICANT: Nandabalan, Krishnan
APPLICANT: ROTHBERGY, JOHANNAN
ITILE OF INVENTION: IDENTIFICATION AND COMPARISON OF PROTEIN-PROTEIN
ITILE OF INVENTION: IDENTIFICATION AND COMPARISON OF PROTEIN
ITILE OF INVENTION: 1108
ITILE REFERENCE: 7934-NO6
CURRENT FILING DATE: 1996-06-14
NUMBER OF SEQ ID NOS: 118
SOFTWARE: PATENTING OR 8
IENGTH: 12
SEQ ID NO 88
IENGTH: 12
SORTWARE: PATENTING SEQUENCE
SEQ ID NOS: 118
SORTWARE: REFERENCE: 2.0
SEQ ID NOS: 118
SORTWARE: REFERENCE: 3.0
SEQ ID NOS: 118
SORTWARE: DAS REFERENCE: 3.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; OTHER INFORMATION: Description of Artificial Sequence: linker US-09-231-303-88
                                                                                                                                                                                     Query Match 12.3%; Score 9; DB 1; Length 12; Best Local Similarity 100.0%; Pred. No. 1.9e+02; Matches 9; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12.3%; Score 9; DB 1; Length 12; 100.0%; Pred. No. 1.9e+02; tive 0; Mismatches 0; Indels
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ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 12.3
Best Local Similarity 100.
Matches 9; Conservative
            TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-874-825-88
                                                                                                                                                                                                                                                                                                       936 CCTCTTCAT 944
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Best Local Similarity
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US-OBE 174-825 BBB

US-OBE 174-825 BBB

ESERTAL NIVERNATION:

APPLICANT: Nariodalan, Krishnan

APPLICANT: Khight, James

APPLICANT: Khight, James

APPLICANT: Might, James

ADRESSES: Partice of the Americas

CONRESPONDENCE ADRESS: 122

CONRESPONDENCE ADRESS: 122

CONFESSIONERS DISACTE ORM:

MEDIUM TYPE: DisActe of the Americas

CONFINENT: UNA

CONFINENT: UNA

APPLICATION NOMER: US/08/874,825

FILING ARE PERSONDENCE ADRESS: Lesie

REDISTRATION NOMER: US/08/874,825

FILING ARE PERSONDENCE ADRESS: Lesie

REPERSONDENCE ALUNIADOR

APPLICATION NUMBER: US/08/874,825

FILING ARE NUMBER: US/08/874,825

FILING ARE NUMBER: US/08/874

ATTORNEY AGENT INFORMATION:

APPLICATION NUMBER: US/08/874

TELECHMUNICATION NUMBER: 139.72

REFERENCE DORGENTER STRUCTER STRU
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CTHER INFORMATION: Description of Artificial Sequence: Triplex

CTHER INFORMATION: forming oligomucleotide

CTHER INFORMATION: This oligo may or may not be 3'-monophosphorylated
US-09-5129-812A-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6
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FILE OF INVENTION: ANTI-HBV
CURRENT APPLICATION NUMBER: US/09/529,812A
CURRENT FILING DATE: 2000-07-24
FRIOR APPLICATION NUMBER: PCT/CN98/00248
FRIOR FILING DATE: 1998-10-19
FRIOR FILING DATE: 1997-10-21
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin Ver. 2.1
SOFTWARE: Patentin Ver. 2.1
SENGIT : 11
                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              932 CCCTCCTCT 940
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 670-9365
                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (510)670-9302
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                               NAME: Stephen C. Macevicz
REGISTRATION NUMBER: 30,28
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       nucleic acid
EDNESS: single
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TOPOLOGY: linear
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                                                                                                                                                                      Sequence 7, Application US/08280441
Sequence 7, Application US/08280441
Patent No. 5552278
GENERAL INFORMATION:
CENTAL INFORMATION:
TITLE OF INVENTION: DNA Sequencing by Stepwise Ligation and Cleavage NUMBER OF SEQUENCES:
ADDRESSEE: Stephen C. Macevicz
STREET: 21890 Rucker Drive
CITY: Cupertino
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 247
US-08-410-116B-24
Sequence 24, Application US/08410116B
Sequence 24, Application US/08410116B
Parent No. 5599675
GENERAL INFORMATION:
APPLICANT: Sydney Brenner, Glenn Albrecht, Andrew J. Blasband
TITLE OF INFORMATION: DNA Sequencing by Stepwise Ligation and Cleavage
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
    Gaps
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Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 13;
                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 95014
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch diskette
COMPUTER: IBM compatible
OPERATING SYSTEM: Windows 3.1/DOS 5.0
SOFTWARE: Microsoft Word for Windows, vers. 2.0
CURREMY APPLICATION DATA:
APPLICATION NUMBER: US/08/280,441
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12.3%; Score 9; DB 1
100.0%; Pred. No. 2e+
trive 0; Mismatches
  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/222,300
FILING DATE: 04-APR-94
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Stephen C. Macevicz
REGISTRATION NUMBER: 30.28
REFERENCE, DOCKET NUMBER: 61
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (415) 638-5552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (510)670-9302
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 13 nucleotides
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 12.3
Best Local Similarity 100.
Matches 9; Conservative
    Conservative
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                                         936 CCTCTTCAT 944
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                                                                              3 CCTCTTCAT 11
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: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: Cali
COUNTRY: US
ZIP: 94545
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                                                                                                                                                             US-08-280-441-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-280-441-7
    Matches
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US-00-667-689A-24

US-00-667-689A-24

Sequence 24, Application US/08667689A

TILLE OF INVENTION: DNA Sequencing by Stepwise Ligation and Cleavage NUMBER OF SEQUENCES: 41

CORRESPONDENCES: 41

CORRESPONDENCES: 42

CORRESPONDENCES: 432 Bay Center Place

TITLE OF INVENTION: USA

STREET: 3832 Bay Center Place

COUNTRY: USA

ZIP: 94545

COUNTRY: USA

ZIP: 94545

COUNTRY: USA

ZIP: 94545

COUNTRY: USA

ZIP: MACCOSOFT WINGOWS 3.1/DOS 5.0

SOFTWARE: MINIORORY 3.1/DOS 5.0

COUNTRY: APPLICATION DATA: 08/410/116

PRIOR APPLICATION DATA: 08/410/116

FILING DATE: 24-MAR-95

PRIOR APPLICATION DATA: 08/222,300

FILING DATE: 04-ARR-95

PRIOR APPLICATION DATA: 08/222,300

FILING DATE: 24-MAR-95

PRIOR APPLICATION DATA: APPLICAT
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12.3%; Score 9; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 9; Conservative 0; Mismatches 0; Indels
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch diskette
COMPUTER: 11m compatible
COMPUTER: 11m compatible
CORREATING SYGTEM: Windows 3.1/DOS 5.0
SOFTWARE: Microsoft Word for Windows, vers. 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/410,116B
FILING DATE: 24-MAR-95
CLASSIFICATION 1435
PRIOR APPLICATION NUMBER: 08/222,300
FILING DATE: 04-APR-94
PRIOR APPLICATION NUMBER: 08/220,411
FILING DATE: 25-JUL-94
ATPONEY/AGENT INFORMATION:
AMPRIOR APPLICATION NUMBER: 08/280,441
FILING DATE: 25-JUL-94
ATPONEY/AGENT INFORMATION:
AMPLICATION NUMBER: 08/280,441
FILING DATE: 25-JUL-94
ATPONEY/AGENT INFORMATION:
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US-09-516-667-87/c

Sequence 87, Application US/09516667

Sequence 87, Application US/09516667

Sequence 87, Application US/09516667

APPLICANT: Incuye, Masayori

APPLICANT: Mang, Nan

APPLICANT: Yamanaka, Kunitoshi

TITLE OF INVENTION: COLD-SHOCK REGULATORY ELEMENTS, CONSTRUCTS THEREOF, AND
                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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0
                         Indels
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                                                                                                                                                                                                                                                                                UNSOLIT 239A-24

Sequence 24, Application US/08478239A

Sequence 24, Application US/08478239A

Sequence 24, Application US/08478239A

Patent No. 58560A

GENERAL INFORMATION:

APPLICANT: Sydney Brenner

TITLE OF INVENTION:

MADRESSEE: Stephen C. Macevicz, Spectragen, Inc.
STREET: 3832 Bay Center Place
CITY: Hayward
STATE: California
COUNTRY: USA
ZIP: 94445
ZIP: 94445
ZIP: 94445
ZIP: 94445
ZIP: 04445
ZIP: 04445
ZIP: 04445
ZIP: 04445
ZIP: 04445
ZIP: 04441
ZILING DATE: US/08/478,239A
FILING DATE: US/08/478,239A
FILING DATE: US/08/478,239A
FILING DATE: 24-MAR-95
FILING DATE: 24-MAR-94
FILING DATE: 25-UL-94
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                         0; Mismatches
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0; Mismatches
                         Conservative
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; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-478-239A-24
                                                                                          935 TCCTCTTCA 943
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Best Local Similarity
Matches 9; Conserv
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                         Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Sydney Brenner
TITLE OF INVENTION: Kits for DNA Sequencing by Stepwise Ligation and Cleavage
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: Stephen C. Macevicz, Spectragen, Inc.
STREET: 3832 Bay Center Place
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12.3%; Score 9; DB 1; Length 13; 100.0%; Pred. No. 2e+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12.3%; Score 9; DB 1; Length 13; 100.0%; Pred. No. 2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: USA

ZIP: 94545

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch diskette
COMPUTER: IBM compatible
OFBRATING SYSTEM: Windows 3.1/DOS 5.0
SOFTWARE: MICTOSOft Word for Windows, vers. 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/712,011
FILING DATE: 11-SER-96
CLASSIFICATION 435
PRIOR APPLICATION WHER: 08/410,116
FILING DATE: 24-WAR-95
PRIOR APPLICATION NUMBER: 08/22,300
FILING DATE: 04-APR-94
PRIOR APPLICATION NUMBER: 08/280,441
FILING DATE: 25-UUL-94
ATTORNEY/AGENT INFORMATION:
NAME: Stephen C. Macevicz
REGISTRATION NUMBER: 30,285
REFERENCE/DOCKET NUMBER: 30,285
TELEFRAN: (510)670-9302
TELEFRAN: (510)670-9302
TELEFRAN: MICHORIA (510)670-9302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 24, Application US/08712011
Patent No. 5831065
NAME: Stephen C. Macevicz
REGISTRATION NUMBER: 30,285
REPRENCE/POCKET NUMBER: 801-0
TELECOMUNICATION INFORMATION:
TELEPHONE: (510) 670-9365
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 nucleotides
INFORMATION FOR SEQ ID NO: 27PE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 100.0
Matches 9, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             935 TCCTCTTCA 943
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STRANDEDNESS: sing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Hayward
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                    ;
US-08-667-689A-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 249
US-08-712-011-24
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US-08-412-913-2/c
195-08-412-913-2/c
195-08-412-913-2/c
195-08-412-913-2/c
195-08-412-913-2/c
195-08-412-913-2/c
195-08-412-913-2/c
195-08-412-913-2/c
195-08-412-913-2/c
195-08-412-913-3/c
195-08-412-913
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Pred. No. 2e+02;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2e+02;
----- 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 6.1 for Windows
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/412,913
FILING DATE: March 29, 1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: Greenfield, Michael S.
REGISTRATION NUMBER: 37,142
REFERENCE/DOCKET NUMBER: 92,620-R
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312)715-1000
TELEFAX: No. 5652103e
INFORMATION FOR SEQ ID No: 2:
SEQUIENCE CHARACTERISTICS:
LENGTH: 12 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NS-08-41-887A-30/c
Sequence 30 Application US/08441887A
Patent No. 5837832
APPLICANT: Chee, Mark
APPLICANT: Croin, Maureen T.
APPLICANT: Huang, Xiachua X.
APPLICANT: Huang, Xiachua X.
APPLICANT: Lipshuz, Robert J.
APPLICANT: Libshuz, Robert J.
APPLICANT: Libshuz, Robert J.
APPLICANT: Libshuz, Robert J.
APPLICANT: Loben, Peter E.
APPLICANT: Morris, Macdonald S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: YES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12.1%;
83.3%;
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Matches 10, Conservative
                                                        12 cerrererear 1
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STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-412-913-2
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Patent No. 5403709
GENERAL INFORMATION:
APPLICANT: Agrawal, Sudhir
APPLICANT: Tang, Jin-Yan
TITLE OF INVENTION: Method of Sequencing Synthetic
TITLE OF INVENTION: Oligonuclectides Containing No. 5403709-Phosphodiester
TITLE OF INVENTION: Internuclectide Linkages
NUMBER OF SEQUENCES: SCORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1; Length 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Ouery Match 12.3%; Score 9; DB 1; Length 13; Best Local Similarity 100.0%; Pred. No. 2e+02; Matches 9; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMpatible
OMPUTER: IBM PC COMPATIBLE
OMPUTER: BA PC COMPATIBLE
OMPUTER: DETAIL Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/958,133
FILING DATE: 19921006
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
12.1%; Score 8.8; DB 1;
Best Local Similarity 83.3%; Pred. No. 2e+02;
Matches 10; Conservative 0; Mismatches
                                                        CURRENT APPLICATION NUMBER: US/09/516,667
CURRENT FILING DATE: 2001-08-01
NUMBER OF SEQ ID NOS: 87
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 87
LENGTH: 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Allegretti & Witcoff, Ltd.
STREET: 75 State Street, Suite 2300
CITY: Boston
TITLE OF INVENTION: METHODS OF USE
FILE REFERENCE: 1053-00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Kecwn, Wayne A
REGISTRATION NUMBER: 33,923
REFREENCE/DOCKET NUMBER: 92,6
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/345-9101
TELEPHONE: 617/345-9111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 617/345-9111
TELEX: No. 5403709e
INFORMATION FOR SEQ ID NO. 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA (genomic)
                                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Massachusetts
: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13 TITGGICIT 5
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US-07-958-133-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: 1ir
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 252
US-07-958-133-2/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
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Gaps
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Pred. No. 2e+02;
0; Mismatches 2; Indels
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| Sequence 165, Application US/08173489C
| Patent No. 5861244
| GENERAL INFORMATION:
| APPLICANT: MANG, C. -G.
| APPLICANT: HEPBURN, A. G.
| TITLE OF INVENTION: GENERIC SEQUENCE ASSAY USING DNA-
| TITLE OF INVENTION: TRIPLE-STRAND FORMATION.
| NUMBER OF SEQUENCES: 365
| CORRESPONDENCE ADDRESS:
| ADDRESSEE: SLO EAST 73RD STREET,
| CITY: NEW YORK |
| STATE: NEW YORK |
| STATE |
| STATE
                                                                                  COMPUTER READABLE FORM:

REDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
CONFUTER: IBM PC COMPATIBLE
CONFUTER: IBM PC COMPATIBLE
CONFUTER: IBM PC COMPATIBLE
CONFORTS: DEATHIN RELEASE #1.0, Version #1.25
SOFTWARE: PETENTION DATA:
APPLICATION NUMBER: US/08/441,887A
FILING DATE: 16-MAY-1995
CLASSIFICATION NUMBER: US 08/143,312
FILING DATE: 26-CCT-1993
CLASSIFICATION NUMBER: US 08/082,937
FILING DATE: 26-CCT-1993
APPLICATION NUMBER: US 08/082,937
FILING DATE: 25-JUN-1993
ATTORNEY/AGENT INFORMATION:
APPLICATION NUMBER: US 08/082,937
FILING DATE: 25-JUN-1993
ATTORNEY/AGENT INFORMATION:
APPLICATION NUMBER: 37,505
REGISTRATION NUMBER: 37,505
REGISTRATION NUMBER: 37,505
REGISTRATION NUMBER: 37,505
REGISTRATION NUMBER: 37,505
TELEPHONE: 650-326-2400
TELEPHONE: 650-326-2400
TELEPHONE: 650-326-2400
TELEPHONE: CHARACTERISTICS:
LENGTH: 12 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CONTINUE TO STATE TO 
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Best Local Similarity 83.3%;
Matches 10; Conservative
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MOLECULE TYPE: DNA (probe)

US-08-441-887A-197
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                 California
: USA
                       STATE: C
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Pred. No. 2e+02;
0; Mismatches 2; Indels
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US-08-441-887A-197/C
; Sequence 197, Application US/08441887A
; Sequence 197, Application US/08441887A
; Setent No. 5837832
; GENERAL INFORMATION:
; APPLICANT: Chee, Mark
; APPLICANT: Huang, Xiachua X.
; APPLICANT: Hubbell, Earl A.
; APPLICANT: Lipshutz, Robert J.
; APPLICANT: Lipshutz, Robert J.
; APPLICANT: Lobban, Peter E.
; APPLICANT: Macdonald S.
; APPLICANT: Morris, Macdonald S.
; APPLICANT: Morris, Macdonald S.
; APPLICANT: Beldon, Edward L.
; TITLE OF INVENTION: Arrays of Nucleic Acid Probes on TITLE OF INVENTION: Biological Chips
; NUMBER OF SEQUENCES: 360
; CORRESPONDENCE ADDRESS:
; ADDRESSE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: USA

ZIP: 94111

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC COMPA:
COMPUTER: IBM PC COMPA:
OPERATION SYSTEM: PACHOLN BATA:
SOFTWARE: PatentIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/441,887A
FILING DATE: 16-MAY-1995
CLASSIPICATION NUMBER: US 08/143,312
FILING DATE: 26-OCT-1993
CLASSIPICATION NUMBER: US 08/082,937
FILING DATE: 25-UN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Liches-Chuetz, Joseph O.
REGISTRATION NUMBER: 37,505
REGISTRA
APPLICANT: Sheldon, Edward L.
TITLE OF INVENTION: Arrays of Nucleic Acid Probes on
TITLE OF INVENTION: Biological Chips
NUMBER OF SEQUENCES: 360
CORRESPONDENCES: 360
CORRESPONDENCES: Townsend and Cownier ADDRESSEE: Townsend and Townsend and Crew LIP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 83.3%;
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear MOLECULE TYPE: DNA (probe)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           915 TGGTCTTTGCCT 926
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Score 8.8; DB 1; Length 12;
Pred. No. 2e+02;
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US-08-173-489C-227/C
Sequence 227, Application US/08173489C
Fatent No. 5861244
Fatent No. 5861244
FAPLICANT: WANG, C. -G.
APPLICANT: HEPBURN, A. G.
TITLE OF INVENTION: TENTELE-STRAND FORMATION.
FITLE OF INVENTION: TRIPLE-STRAND FORMATION.
NUMBER OF SEQUENCES: 365
CORRESPONDENCE ADDRESS:
ADDRESSEE: REOFILE DIAGNOSTIC SCIENCES, INC.,
STREET: 510 EAST 73RD STREET,
                                                                                                                                                                                                                                                                                                                                                                   ANTI-SENSE: no
ORIGINAL SOURCE:
ORGANISM: Hepatitis B virus
INDIVIDUAL ISOLATE: adw2
PUBLICATION INFORMATION:
AUTHORS: Valenzuela, P. Quiroga, M, Zaldivar, J,
AUTHORS: Gray, P. Ruter, W J.
TITLE: the Hepatitis B viral genome and the
TITLE: identification of the major viral genes
JOURNAL: Jaenisch, R, Fox C F eds
VOLUME:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DATE: 1980
RELEVANT RESIDUES IN SEQ ID NO: 187 :FROM 1 TO 12
US-08-173-489C-187
NAME: Handelman, Joseph H.

REGISTRATION NUMBER: 26,179
REPRENCE/DOCKET NUMBER: 10518-6
TELECOMUNICATION INFORMATION:
TELEPHONE: (attorney) (212) 708-1880
TELEFRAX: (attorney) (212) 708-1880
TELEFAX: (attorney) (212) 246-8959
INFORMATION FOR SEQ ID NO: 187:
SEQUENCE CHARACTERISTICS:
LENOTH: 12 base pairs
TYBRIDEDNESS: double stranded
STRANDEDNESS: double stranded
TOPOLOGY: linear
MOLECULE TYPE: genomic DNA
DESCRIPTION: hepatitis B virus adw2 isolate,
HYPOTHERICAL: no
ANTT. CONVENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:

MEDIUM TYPES: 3.5 inch, 1.44Mb storage
COMPUTER: 1BM PC/XT/AT
COMPUTER: 1BM PC/XT/AT
OPERATING SYSTEM: MS-DOS version 6.2
SOFTWARE: Wordperfact Version 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/173,489C
FILING DATE: 22 DEC 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 22 DEC 1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/968,436
FILING DATE: 29 OCT 1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROFILE DIAGNOSTIC STOPELE DIAGNOSTIC CITY: NEW YORK STATE: NEW YORK COUNTRY: 112"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      933 CCTCCTCTTCAT 944
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10, Conservative
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Pred. No. 2e+02;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Hepatitis B virus
INDIVIDUAL ISOLATE: ayw
INDIVIDUAL ISOLATE: ayw
PUBLICATION INFORMATION:
AUTHORS: Galibert, F, Mandart, E, Fitoussi, F,
AUTHORS: Tiollais, P, Charnay, P.
TITLE: Hepatitis B virus genome (subtype ayw) cloned
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: WANG, C. -G.
APPLICANT: WANG, C. -G.
APPLICANT: HEBDRN, A. G.
TITLE OF INVENTION: TRIPLE-STRAND FORMATION.
NUMBER OF SEQUENCES: 365
CORRESPONDENCE ADDRESS:
ADDRESSEE: PROFILE DIAGNOSTIC SCIENCES, INC.,
STREET: 510 EAST 73RD STREET,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; RELEVANT RESIDUES IN SEQ ID NO: 165 :FROM 1 TO 12 US-08-173-489C-165
                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: genomic DNA
DESCRIPTION: hepatitis B virus ayw isolate,
DESCRIPTION: nucleotides 2750 to 2761
HYPOTHERICAL: no
ANTI-SENSE: no
ORIGINAL SOURCE::::: D virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44Mb storage
COMPUTER: 18M PC/XT/AT
OPERATING SYSTEM: MS-DOS version 6.2
SOFTWARE: Wordperfect Version 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/173,489C
FILING DATE: 2 DEC 1993
CLASSIFICATION DATA:
APPLICATION NUMBER: US 07/968,436
FILING DATE: 29 OCT 1992
ATTORNEY/AGENT INFORMATION:
                                                           REGISTRATION NUMBER: 26,179
REGISTRATION NUMBER: 26,179
REFERENCE/DOCKET NUMBER: 09518-6
TELECOMUNICATION INFORMATION:
TELEPAX: (attorney) (212) 246-8959
INFORMATION FOR SEQ ID NO: 165:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 base pairs
TYPE: nucleic acid
STRANBEDNESS: double stranded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 257
20.08-17-490C-187
; Sequence 187, Application US/08173489C
; Patent No. 5861244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 83.3%;
Matches 10; Conservative
                                            ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           933 CCTCCTCTTCAT 944
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STATE: NEW YORK
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : 646-650
1979
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VOLUME: 2
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TOPOLOGY: linear
MOLECULE TYPE: genomic DNA
DESCRIPTION: 23s rRNA gene from Leptospira
DESCRIPTION: interrogans (Accession # X14249) nucleotides
DESCRIPTION: mterrogans (Accession # X14249) nucleotides
DESCRIPTION: 842 to 853
HYPOTHERICAL: no
ANTI-SENSE: no
ORIGINAL SOURCE:
ORIGINAL Multon:
TITLE: Nucleotide sequence of a 23s
TITLE: ribosomal RNA gene for Leptospira interrogans
TITLE: serovar canicola strain moulton
JOUGNAL: Nucleic Acids Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 12.1%; Score 8.8; DB 1; Length 12; Best Local Similarity 83.3%; Pred. No. 2e+02; Matches 10; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PAGES: 2123-2123

DATE: 1989

PRELEVANT RESIDUES IN SEQ ID NO: 237 :FROM 1 TO 12

US-08-173-489C-237
NAME: Handelman, Joseph H.
REGISTRATION NUMBER: 26,179
REFERENCE/DOCKET NUMBER: U9518-6
TELECOMUNICATION INFORMATION:
TELEPANE: (attorney) (212) 708-1880
TELEPANE: (attorney) (212) 246-8959
INFORMATION FOR SEQ ID NO: 237:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 base pairs
TYPE: nucleic acid
STRANDEDNESS: double stranded
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          924 CCTTTTATCCCT 935
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MOLECULE TYPE: genomic DNA
DESCRIPTION: 23s rRNA gene from Halococcus morrhuae
DESCRIPTION: (Accession # X05481) nucleotides 880 to 891
HYPOTHETICAL: no
ANTI-SENSE: no
ORIGINAL SOURCE:
ORGANISM: Halococcus morrhuae
PUBLICATION INFORMATION:
AUTHORS: Leffers, H. Kjems, J, Ostergaard, L,
AUTHORS: Larsen, N, Garrett, R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE: Evolutionary Relationship
TITLE: Amongst Archaebacteria: A Comparative Study of
TITLE: 23 & Ribosomal RNAs of a Sulphur-dependent
TITLE: Extreme Thermophile, an Extreme Halophile and a
TITLE: Thermophilic Methanosen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
12.1%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 2e+02;
Matches 10; Conservative 0; Mismatches 2; Indels
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US-08-173-489C-237/C
Sequence 237, Application US/08173489C
SEQUENCE INFORMATION:
TITLE OF INVENTION:
TITLE OF INVENTIO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PAGES: 43-61
DATE: 1987
FELEVANT RESIDUES IN SEQ ID NO: 227 :FROM 1 TO 12
US-08-173-4895-227
NAME: Handelman, Joseph H.

REGISTRATION NUMBER: 26,179

REFERENCE/DOCKET NUMBER: 10518-6

TELECOMUNICATION INFORMATION:

TELEPAX: (attorney) (212) 708-1880

INFORMATION FOR SEQ ID NO: 227:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 base pairs

TYPE: nucleic acid
STRANDEDNESS: double stranded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: WORDETECT VEISION 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/173,489C
FILING DATE: 22 DEC 1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/968,436
PILING DATE: 29 OCT 1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      924 CCTTTTATCCCT 935
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US-08-173-489C-249/C
iSequence 249 Application US/08173489C
iSequence 249 Application US/08173489C
iSequence 249 Application US/08173489C
iSequence 249 Application
iSequence 249 Application
iSequence 249 Application
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(attorney) (212) 708-1880
attorney) (212) 246-8959
SEQ ID NO: 263:
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; RELEVANT RESIDUES IN SEQ ID NO:
US-08-173-489C-259
                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Frankia sp.
PUBLICATION INFORMATION:
AUTHORS: No. 5861244mand, P.
TITLE: unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 83.3%;
Matches 10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12 CCTTTCACCCCT 1
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CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
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                                                                                                                                                                                                                                                                                                  HYPOTHETICAL: no
ANTI-SENSE: no
ORIGINAL SOURCE:
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0
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DESCRIPTION: 23s rRNA gene from Micrococcus luteus
DESCRIPTION: (Accession # X06484) nucleotides 859 to 870
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 261
US-08-173-489C-259/C
US-08-173-489C-259/C
Sequence 259, Application US/08173489C
Patent No. 5861244
GENERAL INFORMATION:
APPLICANT: WANG, C. -G.
APPLICANT: HEBBURN, A. G.
TITLE OF INVENTION: TRIPLE-STRAND FORMATION.
TITLE OF INVENTION: TRIPLE-STRAND FORMATION.
CORRESPONDENCE ADDRESS:
ADDRESSEE: PROFILE DIAGNOSTIC SCIENCES, INC.,
STREET: 510 EAST 73RD STREET,
CITY: NEW YORK
STATE: NEW YORK
STATE: NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
12.1%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 2e+02;
Matches 10; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                              AVII-SENSE: no
ORIGINAL SOURCE:
ORGANISM: Micrococcus luteus
STRAIN: dam 20030
PUBLICATION INFORMATION:
AUTHORS: Regensburger, A, Ludwig, W, Frank, R,
AUTHORS: Boloecker, H, Schleifer, K H.
TITLE: Complete nuclectide sequence
TITLE: of a 23S ribosomal RNA gene from Micrococcus
TITLE: luteus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; RELEVANT FEIDUES IN SEQ ID NO: 249 :FROM 1 TO 12 US-08-173-489C-249
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ZIP: 10021.

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44Mb storage
COMPUTER: 1BW PC/XT/AT
OPERATING SYSTEM: MS-DOS version 6.2
SOFTWARE: Wordberfect Version 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/173,489C
FILING DATE: 22 DEC 1993
CLASSIFICATION: 435
REGISTRATION NUMBER: 26,179
REFERNEC/DOCKET NUMBER: U9518-6
TELECOMMUNICATION INFORMATION:
TELEPHONE: (attorney) (212) 708-1880
TELEFAX: (attorney) (212) 246-8959
INFORMATION FOR SEQ ID NO: 249:
SEQUENCE CHARACTER.57ICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/968,436
FILING DATE: 29 OCT 1992
ATTORNEY/AGENT INFORMATION:
NAME: HANGELMAN, JOSEPH H.
REGISTRATION NUMBER: 26,179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      JOURNAL: Nucleic Acids Research
                                                                                                                                                                                       TYPE: nucleic acid
STRANDEDNESS: double stranded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          924 CCTTTTATCCCT 935
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                                                                                                                                                                                                                                     TOPOLOGY: linear
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REPERENCE/DOCKET NUMBER: U9518-6
TELECOMMUNICATION INFORMATION:
TELEFAX: (attorney) (212) 246-8959
TELEFAX: (attorney) (212) 246-8959
INFORMATION FOR SEQ ID NO: 259:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 base pairs
TYPE: nucleic acid
STRANDEDNESS: double stranded
TOPOLOGY: linear
MOLECULE TYPE: genomic DNA
DESCRIPTION: 23s TRRA gene from Frankia sp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 262
US-08-173-489C-263/C
Sequence 263, Application US/08173489C
Patent No. 5861244
GENERAL INFORMATION:
APPLICANT: WANG, C. -G.
APPLICANT: HEPBURN, A. G.
TITLE OF INVENTION: TRIPLE-STRAND FORMATION.
NUMBER OF SEQUENCES: 365
CORRESPONDENCE ADDRESSE:
ADDRESSEE: PROFILED DIAGNOSTIC SCIENCES, INC.,
STREET: 510 EAST 73RD STREET,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 8.8; DB 1; Length 12;
Pred. No. 2e+02;
0; Mismatches 2; Indels
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MEDIUM TYPE: 3.5 inch, 1.44Mb storage COMPUTER: 18M PC/XY/AT COMPUTER: 18M PC/XY/AT OPERATING SYSTEM: MS-DOS version 6.2 SOFTWARE: MOTOPERFECT VERSION 6.2 SOFTWARE: WOTOPERFECT VERSION 6.2 SOFTWARE: WOTOPERFECT 1993 CLASSIFICATION NUMBER: US/08/173,489C FILING DATE: 2.9 ECT 1993 APPLICATION NUMBER: US 07/968,436 FILING DATE: 2.9 OCT 1992 ATTORNEY/AGENT INFORMATION: NAME: Handelman, Joseph H. REGISTRATION NUMBER: 26,179 REFERENCE/DOCKET NUMBER: 26,17
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926 TITTATCCTCC 937
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                     TELEFAX: 215-504-4545 TELEX:
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US-07-715-183C-9
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SEQUENCE CHARACTERISTICS:
LENGTH:
LESCRIPTION:
LOSS
HYPOTHETICAL:
LOSS
HYPOTH
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VOLUME: 16
PAGES: 2343-2343
DATE: 1988
; RELEVANT RESIDUES IN SEQ ID NO: 263 :FROM 1 TO 12
US-08-173-489C-263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-927-165A-17/c

Sequence 17, Application US/08927165A

Patent No. 6410226

GENERAL INFORMATION:
APPLICANT: Kmiec, Eric B.
APPLICANT: Holloman, William K.
APPLICANT: Rice, Michael C.
APPLICANT: Smith, Sheryl T.
APPLICANT: Smith, Sheryl T.
APPLICANT: Shu, Zhigang
ITILE OF INVENTION: Mammalian and Human Rec2
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: PA
COMPUTER: TABORA
COMPUTER: TABORALE FORM:
MEDLUM TYPE: Diskette
COMPUTER: TEM Compatible
OMERATING SYSTEM: DOS
SOFTWARE: FastSED for Windows Version 2.0
SOFTRATION DATA:
APPLICATION NUMBER: US/08/927,165A
FILING DATE:
APPLICATION NUMBER: US/08/927,165A
FILING DATE:
APPLICATION NUMBER: US/08/927,165A
FILING DATE:
APPLICATION NUMBER: 36156
REGISTRATION NUMBER: 36156
REGISTRATION NUMBER: 36156
REGISTRATION NUMBER: 36156
REGISTRATION NUMBER: 36156
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-504-4444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Kimeragen, Inc. STREET: 300 Pheasant Run CITY: Newtown STAIE: PA. COUNTRY: USA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             924 CCTTTTATCCCT 935
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RESULT 267
20.08-173-489C-334
; Sequence 334, Application US/08173489C
; Patent No. 5861244
                   PC-DOS/MS-DOS
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REFERENCE/DOCKET NUMBER: 100 TELECOMMUNICATION INPORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 83.3%;
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 13 base pairs TYPE: mucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               inear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-651-835A-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
Sequence 9, Application US/07715183C
Patent No. 5304473
GENERAL INFORMATION
APPLICANT: Belagaje, Rama M
APPLICANT: Belagaje, Rama M
APPLICANT: Heath, William F
APPLICANT: Heath, William F
APPLICANT: Heath, William F
APPLICANT: Long, Harlan B
TITLE OF INVENTION: A-C-B PROINSULIN, METHOD OF
TITLE OF INVENTION: MANUFACTURING AND USING SAME, AND INTERMEDIATES IN
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS: ADDRESSE: Bli Lilly and Company
STREET: Lilly Corporate Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NESULT 266
US-08-651-835A-9
Squence 9, Application US/08651835A
Squence 7. TOO 100 Squence 1 Squence 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3: KLAUBER & JACKSON
Continental Plaza, 411 Hackensack Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIE: 46285
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/715,183C
FILING DATE: 19910611
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSE: Eli Lilly and Company
STREET: Lilly Corporate Center
CITY: Indianapolis
STATE: Indiana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:

CLASSIFTCATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Conrad, William A

RECISTRATION WINBER: 32,089

REFERENCE/DOCKET NUMBER: x-786

TELECOMMUNICATION INFORMATION:

TELEPHONE: 31-276-6013

INFORMATION FOR SEQ IN 00: 9:

SEQUENCE CHARACTERISTICS:

LENGTH: 13 base pairs

TYPE: NUCLEIC ACID
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: DNA (genomic)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               linear
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Matches 10; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-07-715-183C-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET:
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APPLICANT: WANG, C. -G.
APPLICANT: HEBBURN, A. G.
TITLE OF INVENTION: TRIPLE-STRAND FORMATION.
TITLE OF INVENTION: TRIPLE-STRAND FORMATION.
NUMBER OF SEQUENCES: 365
CORRESPONDENCE ADDRESS:
ADDRESSEE: PROFILE DIAGNOSTIC SCIENCES, INC.,
STREET: 510 EAST 73RD STREET,
CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER:
FILNG DATE: 1.2.MAY 1996
CLASSIFICATION DATE:
FILNG APPLICATION DATE:
APPLICATION NUMBER: 08/409,852
FILNG APPLICATION DATE: 13-MAR-1995
FILNG APPLICATION DATE: 03-MAR-1995
FILNG APPLICATION DATE: 03-MAR-1995
FILNG APPLICATION DATE: 03-MAR-1994
ATORNEY/AGENT INPORMATION:
REGISTRATION NUMBER: 26,742
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFRAX: (201) 343-1684
TELEFRAX: (201) 343-1684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 8.8; DB 1;
Pred. No. 2.2e+02;
0; Mismatches 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP:: 10021.
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44Mb storage
COMPUTER: 1BM PC/XT/AT
SOFTWARE: Wordperfect Version 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/173,489C
FILING DATE: 22 DEC 1993
CLASSIFICATION DATA:
APPLICATION NUMBER: US 07/968,436
FILING DATE: 29 OCT 1992
ATTOMBY AGENT INPORMATION:
AND ATTAMBER: 1992
ATTOMBY AGENT INPORMATION:
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of Pyrrole

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schultz1-899.rni
                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear MOLECULE TYPE: other nucleic acid DESCRIPTION: third strand derived from N. DESCRIPTION: genorrhoeae 16s region in Seq ID No. 5861244333 HYPOTHETICAL: yes
                                                                                                                                                                                                                                                                                                                                                                                                                                    HYPOTHETICAL: Yes

ANTI-SENSE: no

PUBLICATION INFORMATION:

RELEVANT RESIDUES IN SEQ ID NO: 334 :FROM 1 TO 13

US-08-173-489C-334
                                                                                                                                    TELEPHONE: (attorney) (212) 708-1880
TELEPAX: (attorney) (212) 246-8959
INFORMATION FOR SEQ ID NO: 334:
SEQUENCE CHARACTERISTICS:
LENGHH: 13 bases
TYPE: nucleic acid
STRANDEDNESS: single stranded
Mon Oct 18 14:40:17 2004
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923 GCCTTTTATCCC 934

12 GCTTTTTAACCC

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0.501.243C-18/c

Sequence 18, Application US/08761243C

Sequence 18, Application US/08761243C

Patent No. 5879819

Patent No. 5879819

APPLICANT: Kamal D. Mehta

TITLE OF INVENTION: No. 5879879el Cis-Acting Blement In The Human LDL Receptor Pro

NUMBER OF SEQUENCES: 28

CORRESPONDENCE ADDRESS: ö ö Length 13; Query Match
12.1%; Score 8.8; DB 1; Length 13
Best Local Similarity 83.3%; Pred. No. 2.2e+02;
Matches 10; Conservative 0; Mismatches 2; Indels CORRESPONDENCE ADDRESS:
ADDRESSE:
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CITY:
ADDICATION
STATE:
TEXAS
COUNTRY:
USA
ZIP:
TOTO!
COMPUTER:
MEDIUM TYPE:
POPPY disk
COMPUTER:
MEDIUM TYPE:
M 931 TCCCTCCTCT 942 1 TCCCTTCTTTC 12

g

DESCRIPTION: other nucleic acid LENGTH: 13 bp TYPE: nucleic acid STRANDEDNES: single-stranded TOPOLOGY: linear TOPOLOGY: 11 MOLECULE TYPE:

ANTI-SENSE: NO CRIGINAL SOURCE: US-08-761-243C-18

. Query Match 12.1%; Score 8.8; DB 1; Length 13; Best Local Similarity 83.3%; Pred. No. 2.2e+02; Matches 10; Conservative 0; Mismatches 2; Indels

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RESULT 269
US-08-607-078-2/c
; Sequence 2, Application US/08607078
; Patent No. 6090847
; GENERAL INFORMATION:
APPLICANT: California Institute of Technology
TITLE OF INVENTION: Method for the Synthesis of Pyrrole
TITLE OF INVENTION: and Inidazole Carboxamides on a
TITLE OF INVENTION: Solid Support
NUMBER OF SEQUENCES: 23
; CORRESPED Swanson & Bratschun, L.L.C.
STREET: 8400 E. Prentice Avenue, Suite 200
; CITY: Englewood
; STATE: Colorado
; COUNTRY: USA COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3 1/2 diskette, 1.44 MG

COMPUTER EBAPELE FORM:

MEDIUM TYPE: Diskette, 3 1/2 diskette, 1.44 MG

COMPUTER EBAPE COMPACE: WordPerfect

SOFTWARE: WordPerfect

COMPUTER FEDERATION DATA:

APPLICATION NUMBER: US/08/607,078

FILING DATE: FeDERATY 26, 1996

CLASSIFCATION DATA:

APPLICATION NUMBER: 1996

CLASSIFCATION NUMBER: 1997

FILING DATE:

ATIONNEY/AGENT INFORMATION:

NAME: ROSEMATY NUMBER: 21 2347

FELERRALION NUMBER: 39,726

REFERENCE/DOCKET NUMBER: 21 2347

TELERRALION NUMBER: 39,726

REFERENCE/DOCKET NUMBER: 21 2347

TELERRALION NUMBER: 39,726

REFERENCE/DOCKET NUMBER: 21 2347

TELERRALION NUMBER: 39,726

REFERENCE/DOCKET NUMBER: 31,726

REFERENCE/DOCKET NUMBER: 31,726

REFERENCE (303) 793-333

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CRARACTERISTICS:

LENGTH: 13 INCLOCITES LENGTH: 13 nucleotide TYPE: nucleic acid STRANDEDNESS: single TOPOLOGY: linear US-08-607-078-2

.. O 12.1%; Score 8.8; DB 1; Length 13; 83.3%; Pred. No. 2.2e+02; rive 0; Mismatches 2; Indels Query Match 12.1 Best Local Similarity 83.3 Matches 10; Conservative

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918 TCTTTGCCTTTT 929 TTTTTGTCTTTT 2 qq

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RESULT 270 US-08-930-798-4

Sequence 4, Application US/08930798
Patent No. 6150095
GENERAL INFORMATION:
TITLE OF INVENTION: A METHOD FOR ANALYSING A POLYNUCLECTIDE CONTAINING A TITLE OF INVENTION: VARIABLE SEQUENCE AND A SET OR ARRAY OF TITLE OF INVENTION: OLIGONOCLECTIDES THEREFOR (AS AMENDED)
FILE REFERENCE: 97-1173*/wmc/2.63
CURRENT APPLICATION NUMBER: US/08/930, 798
CURRENT FILING DATE: 1997-10-06
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patentin Ver. 2.0

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CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/862,795
FILING DATE: April 3, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Paul T. Clark
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 05140/002002
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
                                                                                                                                                                                                                           Sequence 2, Application US/09360344
Patent No. 6683189
GENERAL INFORMATION:
12.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA ORGANISM: Artificial Sequence
                                                                                  918 TCTTTGCCTTTT 929
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            918 TCTTTGCCTTTT 929
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 12.1
Best Local Similarity 83.3
Matches 10; Conservative
Query Match 12.1
Best Local Similarity 83.3
Matches 10; Conservative
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STATE: Massachusetts
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13 rrrrrcrcrrr 2
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| Patent No. 6545162
| GENERAL INFORMATION:
| APPLICANT: DERVAN, PETER B.
| APPLICANT: DERVAN, PETER B.
| TITLE OF INVENTION: METHOD FOR THE SYNTHESIS OF PYRROLE AND IMIDAZOLE
| TITLE OF INVENTION: CARBOXAMIDES ON A SOLID SUPPORT
| TITLE OF INVENTION: CARBOXAMIDES ON A SOLID SUPPORT
| FILE REFERENCE: 025099-1602
| CURRENT APPLICATION NUMBER: US/09/359,921
| CURRENT FILING DATE: 1999-07-22
| NUMBER OF SEQ ID NOS: 31
| SOFTWARE: Patentin Ver. 2.1
| SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: SOUTHERN, EDWIN

TITLE OF INVENTION: A METHOD FOR ANALYSING A POLYNUCLEOTIDE CONTAINING A TITLE OF INVENTION: OMALABLE SEQUENCE AND A SET OR ARRAY OF TITLE OF INVENTION: OLIGONUCLEOTIDES THEREFOR (AS AMENDED)

FILE REFERENCE: 97-1173*/wmc/263

CURRENT PEPLICATION NUMBER: US/09/502,778A

CURRENT FILING DATE: 2000-02-11

NUMBER OF SEQ ID NOS: 12

SOFTWARE: PATENTIN Ver. 2.0

SEQ ID NO 4

LENGTH: 13
                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; OTHER INFORMATION: Description of Unknown Organism:synthetic - other; OTHER INFORMATION: dna
US-09-502-778A-4
                                                                                        Description of Unknown Organism:synthetic - other
dna
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COTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-359-921-2
                                                                                                                                                                                                                                  ö
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                                                                                                                                                                                        Score 8.8; DB 1; Length 13; Pred. No. 2.2e+02; 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 8.8; DB 1; Length 13; Pred. No. 2.2e+02; 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 4, Application US/09502778A; Patent No. 6307039; GENERAL INFORMATION: APPLICANT: SOUTHERN, EDWIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12.1%;
83.3%;
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                                                                                                                                                                                          Query Match
Best Local Similarity 83.3%;
Matches 10; Conservative
                                                                                                                                                                                                                                                                            925 CTTTTATCCCTC 936
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Best Local Similarity 83.3
Matches 10; Conservative
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                                                                                    FEATURE:
COTHER INFORMATION:
COTHER INFORMATION:
US-08-930-798-4
                                            TYPE: DNA
ORGANISM: Unknown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 272
US-09-359-921-2/c
                                                                                                                                                                                                                                                                                                                                                                                  RESULT 271
US-09-502-778A-4
SEQ ID NO 4
LENGTH: 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
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                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: DERVAN, PETER B.
APPLICANT: BAIRO, EDDON E.
TITLE OF INVENTION: METHOD FOR THE SYNTHESIS OF PYRROLE AND IMIDAZOLE
TITLE OF INVENTION: CARBOXAMIDES ON A SOLID SUPPORT
TITLE OF INVENTION: CARBOXAMIDES ON A SOLID SUPPORT
FILE REPRENEUE: 02508-1604
CURRENT APPLICATION NUMBER: US/09/360,344
CURRENT FILING DATE: 1999-07-22
NUMBER OF SEQ ID NOS: 31
SOFTWARE: PATCHLIN VET. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ), OTHER INFORMATION: Description of Artificial Sequence: Synthetic; OTHER INFORMATION: Oligonucleotide
US-09-360-344-2
                                                                                 .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12.1%; Score 8.8; DB 1; Length 13; 83.3%; Pred. No. 2.2e+02;
Score 8.8; DB 1; Length 13
Pred. No. 2.2e+02;
Pred. No. 2.2e+02; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Alexander T. Young
TITLE OF INVENTION:
TITLE OF INVENTION: GENE THERAPY USING TARGETED
TITLE OF INVENTION: VIRAL VECTORS
NUMBER: OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rish & Richardson
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PS/2 Model 502 or 555X
COMPUTER: IBM PS/2 Model 502 or 555X
OPERATING SYSTEM: IBM P.C. DOS (Version 5.00)
SOFTWARE: WordDerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/02957
FILING DATE: 19930331
                                                                                 0; Mismatches
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Fatent No. 627571
GENERAL INFORMATION:
APPLICANT: FILLMONE, HELEN
APPLICANT: GILLIES, GEORGE
TITLE OF INVENTION: SEQUENTIAL CONSENSUS REGION-DIRECTED AMPLIFICATION OF
TITLE OF INVENTION: SEQUENTIAL CONSENSUS REGION-DIRECTED AMPLIFICATION OF
TITLE OF INVENTION: KNOWN AND NOVEL MEMBERS OF GENE FAMILIES
CURRENT APPLICATION NUMBER: US/09/163,485
CURRENT APPLICATION NUMBER: US/09/163,485
CURRENT APPLICATION NUMBER: US/09/163,485
SOFTWARE: PATENTH OF 132
SOFTWARE: PATENTH OF 132
SOFTWARE: PATENTH OF 1.2.0
SOFTWARE: PATENTH OF 1.2.0
SOFTWARE: PATENTH OF 1.2.0
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                                                                                                                                                      Gaps
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OGGANIGN: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
OTHER INFORMATION: oligonucleotide, consensus sequence from human
OTHER INFORMATION: matrix metalloproteinases
FEATURE:
NAME/KEY: MOD_RES
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                                                                                                  Length 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-07-61-710A-5/C

| Sequence 5, Application US/07651710A
| Sequence 5, Application US/07651710A
| Patent No. 5362864
| GENERAL INFORMATION:
| APPLICANT: Chua, Nam-Hai
| TITLE OF INVENTION: Trans-Activating Factor-1
| NUMBER OF SEQUENCES:
| ADDRESSEE: Pennie & Edmonds
| STREET: 1155 Avenue of the Americas
| CITY: New York
| COUNTRY: New York
| COUNTRY: US-A.
| 10036-2711
| COMPUTER READABLE FORM:
| MEDIUM TYEE: Floppy disk
| COMPUTER: IBM PC Compatible
| OPERATING SYSTEM: PC-DOS/MS-DOS
| COMPUTER: PATENTING SYSTEM: PC-DOS/MS-DOS
                                                                                                  Score 8.8; DB 1; L. Pred. No. 2.2e+02; 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; LOCATION: (9) TO CHER INFORMATION: A, T, C, G, other or unknown US-09-163-485-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/651,710A
                                                                                                  Query Match
Best Local Similarity 83.3%;
Matches 10; Conservative
                                                                                                                                                                                                  919 CTTTGCCTTTTA 930
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US-09-163-485-25/c
                            ; LENGTH: 13
5514646-34
     SEQ ID NO:34:
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; Patent No. 5514646
; Patent No. 5514646
; Patent No. 5514646
; RRUGH F. SHIELDS, JAMES E.
; TILE OF INVENTION: INSULIN ANALOGS MODIFIED AT POSITION
; 29 OF THE B CHAIN
; NUMBER OF SEQUENCES: 52
; CURRENT APPLICATION DATA:
; PRIOR APPLICATION NUMBER: US/08/57,201
; FILING DATE: OS-MAY-1993
; APPLICATION NUMBER: 886,632
; APPLICATION NUMBER: 388,201
; FILING DATE: O4-604-1989
; FILING DATE: 09-FEB-1989
; FILING DATE: 09-FEB-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MARIACATION THREATHAN, JACOB R., OPPENHEIM, AMOS B., GORECKI, MARIACATION THANGORN, RACHEL TITLE OF INVENTION: THERAPEUTIC COMPOSITIONS COMPRISING MIXTURE OF HUMAN CUZN SUPEROXIDE DISMUTASE ANALOGS NUMBER OF SEQUENCES: 30

CURRENT APPLICATION DATA: CAPPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION NUMBER: 449,125

FILING DATE: 08-DG-1989

FILING DATE: 09-DG-1989

FILING DATE: 09-DG-1986

FILING DATE: 19-AG-1986

FILING DATE: 19-AG-1985

APPLICATION NUMBER: 767,143

FILING DATE: 19-AG-1985

FILING DATE: 19-AG-1985

FILING DATE: 19-AG-1985

FILING DATE: 19-AG-1985

FILING DATE: 19-AG-1985
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Pred. No. 2.2e+02;
0; Mismatches 2;
                                                                                                                                                                                                                                                                        Score 8.8; DB 1;
Pred. No. 2.2e+02;
0; Mismatches 2
TELEPHONE: (617) 542-5070
TELERAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 83.3%;
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 83.3%;
Matches 10; Conservative
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                                                                                                                    TYPE: NUCLEIC ACID
STABLE: NUCLEIC ACID
STABLE: NUCLEIC ACID
STABLE: SINGle
TOPOLOGY: linear
PCT-US93-02957-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;Patent No. 5455029
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5455029-9
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                                                                                                                                                         11.5%; Score 8.4; DB 1; Length 10; 90.0%; Pred. No. 2e+02; tive 0; Mismatches 1; Indels
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11.5%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 2e+02;
Matches 9; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: other nucleic acid
DESCRIPTION: third strand derived from esterase D
DESCRIPTION: sequence region in Seq ID No. 586124467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: WANG, C. -G.
APPLICANT: HERBURN, A. G.
TITLE OF INVENTION: GENETIC SEQUENCE ASSAY USING DNA
TITLE OF INVENTION: TRIPLE-STRAND FORMATION.
NUMBER: OF SEQUENCES: 365
CORRESPONDENCE ADDRESSE:
ADDRESSEE: PROFILE DIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ANTI-SENSE: NO
PUBLICATION INFORMATION:
RELEVANT RESIDUES IN SEQ ID NO: 68 :FROM 1 TO 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTE: USAS

ZIP: 10021.

COMPUTER READABLE FORM:

REDIUM TYPE: 3.5 inch, 1.44Mb storage
COMPUTER: BM FO/XT/AT
OPERATING SYSTEM: MS-DOS version 6.2
SOSTWARE: Wordperfect Version 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/173,489C
FILING DATE: 22 DEC 1993
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/086,436
FILING DATE: 29 OCT 1992
ATTORNEY/AGENT INFORMATION:
NAME: Handelman, JOSEPH H.
REGISTRATION NUMBER: 26,179
REFERENCE/DOCKET NUMBER: 26,179
RELEPHONE (attorney) (212) 708-1880
TELECOMMUNICATION INFORMATION:
TELEPHONE (attorney) (212) 708-1880
TELEFRAX: (attorney) (212) 246-9959
INFORMATION FOR EQ. D. NO: 68:
                                                                                                                                                                                                                                                                                                                                                                      RESULT 280
US-08-173-489C-68
Sequence 68, Application US/08173489C
Patent No: 5861244
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: Nucleic Acid
STRANDEDNESS: single stranded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (attorney) (21 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
LENGTH: 10
                                                                                                                                                                                    Best Local Similarity 90.0
Matches 9, Conservative
                                            TYPE; nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-060-952C-11
                                                                                                                                                                                                                                                         941 TCATTGGTTT 950
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: NEW YORK
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US-08-060-952C-11
Sequence 11, Application US/08060952C
Patent No. 569532
GENERAL INFORMATION:
APPLICANT: Michael D. West
APPLICANT: Michael D. West
APPLICANT: JEIZADEH Blackburn
TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF CONDITIONS
TITLE OF INVENTION: TELATED TO TELOMERE LENGTH AND/OR
TITLE OF INVENTION: TELOMERASE ACTIVITY
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
ADDRESSES: Lyon & Lyon
STREET: Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 8.4; DB 1; Length 10;
Pred. No. 2e+02;
0; Mismatches 1; Indels
                 TILLASIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
RECISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 3288-014
TELEPHONE: 212 869864/9741
TELEFAX: 212 869864/9741
TELEFAX: 6141 PENNIE
TELEFAX: 6141 PENNIE
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGRATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
TYPE: NUCLEIC ACID
STRANDEDNESS: double
TOPOLOGY: unknown
MOLECULE TYPE: TAF-1 binding motif
US-07-651-710A-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/060,952C
FILLING DATE: May 13, 1993
CIASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/882,438
FILING DATE: May 13, 1992
APPLICATION NUMBER: 08/038,766
FILING DATE: March 24, 1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 20 TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 11:
                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 90.0%;
Matches 9; Conservative
    19910206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              958 CGCTACCAAC 967
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CITY: Los Angeles
STATE: California
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GENERAL INFORMATION:

APPLICANT: Walling, Linda L.
APPLICANT: Pautot, Veronique
APPLICANT: Chao, Wun Shaw
APPLICANT: Chao, Wun Shaw
TITLE OF INVENTION: Improved Promoters for Enhancing Plant
TITLE OF INVENTION: Productivity
NUMBER OF SEQUENCES::
ADDRESSE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTY: USA
ZIP: 9411-384
COMPUTER REDABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/892,770
FILING DATE: 15-JUL-1997
CLASSIFICATION NUMBER: US-41,261
REGISTATION NUMBER: P-41,261
REFERENCE/DOCKET NUMBER: P-41,261
REFERENCE/DOCKET NUMBER: 0.33070-072100US
TELEFORM TOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 Dase pairs
TUDENT: ALL Dase pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 11.5%; Score 8.4; DB 1; Length 10; Best Local Similarity 90.0%; Pred. No. 2e+02; Matches 9; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-388-353-49/c
; Sequence 49, Application US/08388353
; Patent No. 6010895
                                                                                                                                               Sequence 13, Application US/08892770
Patent No. 5962670
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              905 TCATTTTCTT 914
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10 TCTTTCCCTT 1
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                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: WANG, C. -G.
APPLICANT: HEPBURN, A. G.
TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
SCHEES-SCHEES:
ADDRESSE: PROFILE DIAGNOSTIC SCIENCES, INC.,
STREET: 510 EAST 73RD STREET,
CITY: NEW YORK
COUNTY: USA
ZIP: 10021.
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44Mb storage
COMPUTER: NEW YORK
STREET: SOFTWARE: WOORS version 6.2
COMPUTER: NEW PORK
STREET: SOFTWARE: WOORS version 5.1
COMPUTER: SOFTWARE: WOORS version 5.1
COMPUTER: SOFTWARE: WOORS version 5.1
CURRENT APPLICATION DATA: 489C
FILING DATE: 2. DEC 1993
CLASSIFICATION NUMBER: US 07/968,436
FILING DATE: 2. DCC 1992
CLASSIFICATION NUMBER: US 07/968,436
FILING DATE: 2. DCC 1992
ATTORNEY/AGENT INFORMATION:
APPLICATION NUMBER: US 07/968,436
FILING DATE: 2. DCC 1992
ATTORNEY/AGENT INFORMATION:
APPLICATION NUMBER: US 07/968,436
FILING DATE: 2. DCC 1992
ATTORNEY/AGENT INFORMATION:
APPLICATION NUMBER: US 07/968,436
FILING DATE: 2. DCC 1992
ATTORNEY/AGENT INFORMATION:
TELEFORMUNICATION NUMBER: 26,179
REFERENCE//DOCKET NUMBER: 26,179
REFERENCE//DOCKET NUMBER: 26,129
INFORMATION FOR SEQ ID NO: 71:
SEQUENCE CHARACTERISTICS:
LENGTH: 1.0 base pairs
TYPE: Nucleic Acid
STRANDEDESS: double stranded
TOPPOLINGY: 1 inpar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             POPULOGY: linear
MOLECULE TYPE: Genomic DNA
DESCRIPTION: esterase D gene (Accession # M13450)
DESCRIPTION: nucleotides 710 to 719
HYPOTHETICAL: No
ANTI-SENSE: No
ORIGINAL: SOURCE:
ORGANISM: Homo sapiens
POSITION IN GENOME:
CHROWOSOME/SEGRENT: chromosome 13
MAP POSITION: 13q14.1-q14.2
PUBLICATION INFORMATION:
AUTHORS: Lee, E Y H P, Lee, W H.
TITLE: Molecular cloning of the
TITLE: Molecular cloning of the
TITLE: Letinoblastoma
JOURNAL: Proceedings of the National Academy of
JOURNAL: Sciences, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    71 :FROM 1 TO 10
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US-08-173-489C-71
                                                                                                 US-08-173-489C-71/c; Sequence 71, Application US/08173489C; Patent No. 5861244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 90.0%
1 TCCTTTTCTT 10
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GENERAL INFORMATION:
APPLICANT: Deacon, Nicholas J.
APPLICANT: Learmont, Jennifer C.
APPLICANT: Crowe, Suzanne
APPLICANT: Crowe, Suzanne
APPLICANT: Cooper, David
TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
NUMBER OF SEGUENCES: 800
CORRESPONDENCE ADDRESS:
ADDRESSEE: Scully, Scott. Murch. ADDRESSEE: Scully, Scott, Murphy & Presser STREET: 400 Garden City Plaza CITY: Garden City

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Gaps

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Gaps ö

918 TCTTTGCCTT 927

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                                                                                                                                                                                                                                                                            Score 8.4; DB 1; Length 10;
Pred. No. 2e+02;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Learmont, Jennifer C.
APPLICANT: McPhee, Dale A.
APPLICANT: Crowe, Suzanne
APPLICANT: Croper, David
TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
NUMBER OF SEQUENCES: 800
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: TBM FC COMPATIBLE
OPPRATIG SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 14-FEB-1995
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSE: Scully, Scott, Murphy & Presser STREET: 400 Garden City Plaza CITY: Garden City STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 136, Application US/08388353
Patent No. 6010895
GENERAL INFORMATION:
APPLICANT: Deacon, Nicholas J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY AGENT INFORMATION:
NAME: DIGIGILO, Frank S.
REGIETRATION NUMBER: 31,346
REPRENCE/DOCKET NUMBER: 9606
TELEPHONE: (516) 742-434
TELEPHONE: (516) 742-436
TELERX: (516) 742-436
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 136:
                                135:
                                                                                LENGTH: 10 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                        11.5%;
90.0%;
TELEX: 230 901 SANS UR INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            United States
                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 90.0
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity 90.0
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LENGTH: 10 Dasc
TYPE: nucleic acid
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COUNTRY: Un
ZIP: 11530
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Best Local S
Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 135, Application US/08388353
Patent No. 6010895
GENERAL INFORMATION:
APPLICANT: Learmont, Jennifer C.
APPLICANT: Crowe, Suzame
APPLICANT: Crowe, Suzame
APPLICANT: Crowe, Suzame
TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
NUMBER OF SEQUENCES: 800
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                         CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/388,353
FILING DATE: 14-FEB-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:

NAME: Didiglio, Frank S.

REGISTRICATION NUMBER: 34,346
REFERENCE/DOCKET NUMBER: 9606
TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELEFAX: (516) 742-4343
TELEFEX: (516) 742-4366
TELEEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPIET READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/388,353
FILING DATE: 14-FEB-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAMME: Did3410, Frank S.
REGISTRATION NUMBER: 9606
TELEFRATION NUMBER: 9606
TELEFRATION NUMBER: 9606
TELEFRATION NUMBER: 9606
TELEFRATION INFORMATION:
TELEFRANCE/DOCKET NUMBER: 9606
TELEFRANCE/SOCKET NUMBER: 9606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     E: Scully, Scott, Murphy & Presser
400 Garden City Plaza
                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: DNA (genomic)
                          COUNTRY: United States ZIP: 11530 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy dis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      United States
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              918 TCTTTGCCTT 927
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 400 CTTTY: Garden City
        New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       linea
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 284
US-08-388-353-135/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-388-353-49
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11.5%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 2e+02;
Matches 9; Conservative 0; Mismatches 1; Indels
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Patent No. 6010895
GENERAL INFORMATION
APPLICANT: Deacon, Nicholas J.
APPLICANT: Learmont, Jennifer C.
APPLICANT: Crowe, Suzame
APPLICANT: Cooper, David
JITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
NUMBER OF SEQUENCES: 800
CORRESPONDENCE ADDRESS:
ADDRESSEE: Scully, Scott, Murphy & Presser
CONDENCE ADDRESS:
COMPUTER READABLE FORM:

MEDIUM TYEE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NN-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
SUSTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATE:
APPLICATION NUMBER: US/08/388,353
FILING DATE: 14-FEB-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Didiglio, Frank S.
REGISTRATION NUMBER: 9606
TELECOMMUNICATION INFORMATION:
TELERENCE/DOCKET NUMBER: 9606
TELECOMMUNICATION INFORMATION:
TELERENCE (516) 742-4336
TELERENCE (516) 742-4333
TELERENCE (516) 742-4333
TELERENCE (516) 742-4333
TELERENCE (516) 742-4336
TELERENCE (516) 742-4333
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TELERENCE (516) 742-4333
TELERENCE (516) 
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STREET: 400 Garden City Plaza
CITY: Garden City Plaza
CITY: Garden City
STATE: New York
COUNTRY: United States
ZIP: 11530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATE:
APPLICATION NUMBER: US/08/383,353
FLIANG DATE: 14-FEB-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Did3210, Frank S.
REGISTRATION NUMBER: 9606
TELERDOMONICATION INFORMATION:
TELEBRENCE/DOCKET NUMBER: 9606
TELECOMMUNICATION INFORMATION:
TELEBRAX: (516) 742-4343
TELEBRAX: (516) 742-4366
TELEEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 192:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-388-353-191
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US-08-388-353-192/c
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                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Deacon, Nicholas J.
APPLICANT: Deacon, Nicholas J.
APPLICANT: Deacon, Nicholas J.
APPLICANT: Crowe, Dale A.
APPLICANT: Crowe, Suzanne
APPLICANT: Crowe, Suzanne
APPLICANT: Crower, David
TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
NUMBER OF SEQUENCES: 800
CORRESOUDENES: 800
CORRESOUDENES: 800
CORRESOUDENE ADDRESS:
ADDRESSE: Scully, Scott, Murphy & Presser
CITY: Garden City Plaza
COUNTRY: United States
ZIP: 11530
COMPUTER READABLE FORM:
MEDIUM TYPE: Plopy disk
COMPUTER: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION: 424
ATTORNEY/AGENT INFORMATION:
APPLICATION: 424
ATTORNEY/AGENT INFORMATION:
REGISTRATION INFORMATION:
TELEPHONE: (516) 742-4343
TELEPHONE: (516) 742-4366
TELECPHONE: (516) 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             S-08-388-353-184/c
Sequence 184, Application US/08388353
Patent No. 6010895
GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)
US-08-388-353-184
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COUNTRY: United States
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6010895
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE:
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                                                                                                                                                            Query Match
11.5%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 2e+02;
Matches 9; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 252 Application US/0838353
Fatent No. 6010895
GENERAL INFORMATION:
APPLICANT: Deacon, Nicholas J.
APPLICANT: Carmont, Jennifer C.
APPLICANT: Crowe, Suzanne
APPLICANT: Crowe, Suzanne
APPLICANT: Crowe, Suzanne
APPLICANT: Crowe, Suzanne
APPLICANT: Cooper, David
ITILE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
NUMBER OF SEQUENCES: 800
CORRESPONDENCE ADDRESS:
ADDRESSEE: Scully, Scott, Murphy & Presser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER TAISON

MEDIUM TYPE: Floppy disk

COMPUTER: IF Ploppy disk

COMPUTER: IF PLOPPY disk

COMPUTER: Parentin Release #1.0, Version #1.25

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/388,353

FILING DATE: 14-FEB-1995

CLASSIFICATION: 44-FEB-1995

CLASSIFICATION: QFAART INFORMATION:

NAME: Didiglio, Frank S.

REGISTRATION NUMBER: 9606

REFERENCE/DOCKET NUMBER: 9606

TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Scully, Scott, Murphy & Presser
STREET: 400 Garden City Plaza
CITY: Garden City
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 290
US-08-388-353-230/c
; Sequence 230, Application US/0838353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 229:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 base pairs
                 TYPE: nucleic acid
STRANDENNESS: single
; TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-388-353-192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New York
: United States
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 90.0
Matches 9; Conservative
    10 base pairs
                                                                                                                                                                                                                                                           932 CCCTCCTCTT 941
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      912 CTTTGGTCTT 921
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10 CATTGGTCTT 1
                                                                                                                                                                                                                                                                                                          10 CCCACCTCTT 1
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                                                                                                                                                                                                                                                                                                                                                                            RESULT 289
US-08-388-353-229/c
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Gaps
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                                                                                                                                                                                                                                                                                                                    CAPTER 11330
CAPTER TEADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: TEM PC COMPATIBLE
OPERATING SYSTEM: PC-005/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/388,353
FILING DATE: 14-FFB-1995
CLASSIFICATION: 424
ATTONENTY/AGENT INFORMATION:
NAME: D16/301io, Frank S.
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 31,346
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Deacon, Nicholas J.
APPLICANT: Learmont, Jennifer C.
APPLICANT: Morphee, Dale A.
APPLICANT: Crowe, Suzanne
APPLICANT: Crowe, Suzanne
APPLICANT: Copper, David
TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
WINDBER OF SEQUENCES: 800
CORRESPONDENCE ADDRESS:
APPLICANT: Deacon, Nicholas J.
APPLICANT: Learmont, Jennifer C.
APPLICANT: McPhee, Dale A.
APPLICANT: Crowe, Suzanne
APPLICANT: Crower, David
TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    E: Scully, Scott, Murphy & Presser
400 Garden City Plaza
                                                                                                                                                                                     3: Scully, Scott, Murphy & Presser
400 Garden City Plaza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11.5%; Score 8.4; 90.0%; Pred. No. 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-388-353-275/c
; Sequence 275, Application US/08388353
Partent No. 6010895
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 230:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 base pairs
TYPE: nucleic acid
STRANDEDNES; single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                         New York
: United States
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             United States
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Matches 9, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                911 TCTTTGGTCT 920
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-10 Garden
STATE: New York
COUNTRY: Un'.
ZIP.
                                                                                                                                                                                                      STREET: 400 CITY
CITY: Garden City
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 49, Application US/08488551B
Sequence 49, Application US/08488551B
Sequence 49, Application US/08488551B
Sequence 49, Application US/08488551B
SERECANT: Nicholas J. Deacon
APPLICANT: DaleA. Morbee
APPLICANT: Now York
CORRESPONDENCE ADDRESS:
ADDRESSE: SCULLY, SCOTT, MURPHY & PRESSER
STREET: 400 GARDEN CITY PLAZA
CITY: GARDEN CITY PLAZA
CITY: GARDEN CITY PLAZA
CONPUTRY: U.S.A.
ZIP: 11530-0299
COMPUTRY: BM PC Compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOCTWARR: PREAFIL Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/488,551B
FILING DATE: 14-FEB-1994
APPLICATION NUMBER: PN4022 (AU)
FILING DATE: 12-FEB-1994
APPLICATION NUMBER: PN4024 (AU)
FILING DATE: 12-FEB-1994
APPLICATION NUMBER: PN3021/95
FILING DATE: 17-PRE-1994
APPLICATION NUMBER: PN3021/95
FILING DATE: 17-PRE-1994
APPLICATION NUMBER: PN3021/95
FILING DATE: 17-PRE-1995
ATTORNEY/AGENT INFORMATION:
NAME: FRANK: S. DIGIGIO
REFERENCE/DOCKET NUMBER: 9606Z
TELECOMMONICATION NUMBER: 17-PAX-1995
ATTORNEY/AGENT INFORMATION:
TELEPHONE: 17-PAX-1995
TELEPHONE: 17-PAX-1996
TELEPHONE: TELEPHONE: 17-PAX-1996
TELEPHONE: TELEPHONE: 15-194
TELEPHONE: TELEPHONE
                                                                                                                                                                    11.5%; Score 8.4; DB 1; Length 10; 90.0%; Pred. No. 2e+02; tive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 8.4; DB 1; Length 10; Pred. No. 2e+02; 0; Mismatches 1; Indels
                                                 ; MOLECULE TYPE: DNA (genomic) US-08-388-353-310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4366
INFORMATION FOR SEQ ID NO: 49: SEQUENCE CHARACTERISTICS: LENGTH: 10 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 90.0%;
Matches 9; Conservative (
                                                                                                                                                                         Query Match
Best Local Similarity 90.0
Matches , '9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                              908 TITICITIGG 917
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       918 TCTTTGCCTT 927
        TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                              ઠ
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11.5%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 2e+02;
Matches 9; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 310, Application US/08388353
Fatent No. 6010895
Fatent No. 6010895
FAPLICANT: Deacon, Nicholas J.
APPLICANT: Learmont, Jennifer C.
APPLICANT: Crowe, Suzane
APPLICANT: Crowe, Suzane
TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
NUMBER OF SEQUENCES: 800
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSE:
SCALLY, Scott, Murphy & Presser
STREET: 400 Garden City Plaza
CITY: Garden City
STREET: New York
CUNTRY: United States
ZIP: 11530
COMPUTER READABLE FORM:
MEDIUM TYPE: FIDPPY disk
COMPUTER READABLE FORM:
MEDIUM TYPE: FIDPPY disk
COMPUTER READABLE FORM:
MEDIUM TYPE: FIDPPY disk
COMPUTER READABLE FORM:
MEDIUM TYPE: LAFE1-1095
SOFTWARE: BATCATION DATA:
APPLICATION NUMBER: US/08/389,353
FILING DATE: 14-FEB-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Didsiglo, Frank S.
REGISTRATION NUMBER: 36.06
TELECOMMUNICATION NUMBER: 36.06
TELECOMMUNICATION NUMBER: 31.346
REFERENCE/DOCKET NUMBER: 96.06
TELECOMMUNICATION NUMBER: 31.346
TELEFAX: (516) 742-4343
TELEFAX: (516) 742-436
TELEFAX: (516) 742-436
TELEFAX: CHARACTERISTICS:
LENGTH: 10 base pairs
TTYPE: nucleic acid
                          SCHWALLE PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/388,353
FILNG DATE: 14-FEB.1995
CLASSIFICATION: 424
ATTONNEY/AGENT INFORMATION:
NAME: Didiglio, Frank S.
REGISTRATION NUMBER: 31,346
REGISTRATION NUMBER: 31,346
REGISTRATION NUMBER: 31,346
REGISTRATION NUMBER: 3606
TELEFRORCA/POCKET NUMBER: 9606
TELEFRAX: (516) 742-4343
TELEFRAX: (516) 742-436
TELEFRAX: (516) 742-4
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ) TOPOLOGY: linear
) MOLECULE TYPE: DNA (genomic)
US-08-388-353-275
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US-08-488-551B-184/C
US-08-488-551B-184/C
; Sequence 184, Application US/08488551B
; Patent No. 6015661
; GENERAL INFORMATION:
APPLICANT: Dale A. McPhee
APPLICANT: David Cooper
; TILLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
NUMBER OF SEQUENCES: 841
; CORRESPONDENCE ADDRESS:
ADDRESSEE: SCTLLY, SCOTT, MURPHY & PRESSER
STREET: 400 GARDEN CITY PLAZA
COUNTRY: USA.
COUNTRY: USA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 8.4; DB 1; Length 10;
Pred. No. 2e+02;
0; Mismatches 1; Indels
                                                                                                   CURPET READABLE FORM:
MEDIUM TYPE: READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin RC-Bese #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/488,551B
FILING DATE: 07-JUN 1995
PRIOR APPLICATION NUMBER: PM364 (AU)
FILING DATE: 14-FEB-1994
APPLICATION NUMBER: PM022 (AU)
FILING DATE: 21-FEB-1994
APPLICATION NUMBER: PM028 (AU)
FILING DATE: 21-BE-1994
APPLICATION NUMBER: PM3021/95
FILING DATE: 14-FEB-1995
APPLICATION NUMBER: PM3021/95
FILING BATE: 17-MAY-1995
ATORNEY AGENT INFORMATION:
NUMBER: S. MAY-1995
ATORNEY AGENT INFORMATION:
NUMBER: PRANK S. DIGIGIOLO
NUMBER: MAY-1995
ATORNEY AGENT INFORMATION:
NUMBER: MAY-1995
ATORNEY AGENT AMAY-1995
ATORNEY AGENT AMAY-1995
ATORNEY AMAY-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compactible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATE:
APPLICATION NUMBER: US/08/488,551B
FILING DATE: 07-UUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: (516) 742-4343
TELEPAX: (516) 742-4366
INFORMATION FOR SEQ ID NO: 136:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 96
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 10 base pairs
TYPE; nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 90.0
Matches 9; Conservative
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             953 TGTATCGCTA 962
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GARDEN CITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10 rerarrecra
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                                                                               XY: U.S.A.
11530-0299
                                   NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: li
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-488-551B-136
                                                                               COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 δ
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2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CUITY: GARLEN LLII
STATE: BEW YORK
COUNTRY: U.S.A.

ZITE: 11530-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER. IBM PC compatible
COMPUTER: IBM PC compatible
APPLICATION NUMBER: PM0284 (AU)
FILING DATE: 13-FEB-1994
APPLICATION NUMBER: PN0284 (AU)
FILING DATE: 13-FEB-1995
ATTORNEY/AGENT INFORMATION:
NAME: FRANK S. DIGIGIOIO
NAME: FRANK S. DI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Nicholas J. Deacon
APPLICANT: Nacholas J. McPhee
APPLICANT: David Cooper
TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
NUMBER OF SEQUENCES: 841
CORRESPONDENCE ADDRESS:
ADDRESSE: SCULLY, SCOTT, MURPHY & PRESSER
STREET: 400 GARDEN CITY PLAZA
                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Nicholas J. Deacon
APPLICANT: Dale A. McPhee
APPLICANT: David Cooper
TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
NUMBER OF SEQUENCES: 841
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
STREET: 400 GARDEN CITY PLAZA
CITY: GRADEN CITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 8.4; DB;
Pred. No. 2e+02
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 295
US-08-488-551B-136/c
; Sequence 136, Application US/08488551B
; Patent No. 6015661
           RESULT 294
2.08-08-88-551B-135/c
3.8equence 135, Application US/08488551B
3.Patent No. 6015661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11.5%;
90.0%;
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Best Local Similarity 90.0
Matches 9; Conservative
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              954 GTATCGCTAC 963
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-488-551B-135
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Query Match
Best Local Similarity 90.0%; Pred. No. 2e+02;
Matches 9; Conservative 0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-48E-551B-192/c
) Sequence 192, Application US/08488551B
) Patent No. 0155611
) Patent No. 0155611
) GENERAL INFORMATION:
APPLICANT: Dai-A. McPhee
APPLICANT: David Cooper
APPLICANT: ON SEQUENCES: 841
CORRESSED SCULLY, SCOTT, MURPHY & PRESSER
STREET: ADRESSE: SCULLY, SCOTT, MURPHY & PRESSER
CITY: GARDEN CITY
STATE: NEW YORK
COUNTRY: US-0299
COMPUTER READABLE FORM:
MENTIM TYPE: FLOURY SIGN:
MENTIM TYPE: FLOURY SIGN:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FURN:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
SOFTWARE: Batentin Release #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/488,551B
FILING DATE: 14-FBB-1994
APPLICATION NUMBER: PM0284 (AU)
FILING DATE: 21-FBB-1994
APPLICATION NUMBER: PM0284 (AU)
FILING DATE: 23-DEC-1994
APPLICATION NUMBER: PM0384,353
FILING DATE: 17-MAY-1995
APPLICATION NUMBER: PM3021/95
FILING DATE: 17-MAY-1995
APPLICATION NUMBER: PM3021/95
FILING DATE: 17-MAY-1995
APPLICATION NUMBER: PM03021/95
APPLICATION NUMBER: PM03021/9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11.5%; Score 8.4;
        TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
TELEPAX: (516) 742-4366
TELEPAX: (516) 742-4366
TELEPAX: (516) 742-4366
TENGRATION FOR SEQ ID NO: 191:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
TOPOLOGY: linear
US-08-488-551B-191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           933 CCTCCTCTTC 942
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11.5%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 2e+02;
Matches 9; Conservative 0; Mismatches 1; Indels
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US-08-488-551B-191/C

Sequence 191, Application US/08488551B

Sequence 191, Application US/08488551B

Sequence 191, Micholas J. Deacon

APPLICANT: Naicholas J. Deacon

APPLICANT: Dale A. McPhee

APPLICANT: Carkes County, SCOTT, MURPHY & PRESSER

COUNTRY: U. S. A.

ZIPHE A. A. A. A.

SOTTWARE: The Compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOTTWARE: PLORY DATA:

APPLICATION NUMBER: US/08/488,551B

FILING DATE: 07-JUN 1995

APPLICATION NUMBER: PH002 (AU)

FILING DATE: 21-FEB-1994

APPLICATION NUMBER: PN002 (AU)

FILING DATE: 21-FEB-1995

APPLICATION NUMBER: PN002 (AU)

FILING DATE: 11-FEB-1995

APPLICATION NUMBER: PN002 (AU)

FILING DATE: 21-FEB-1995

APPLICATION
APPLICATION ...

RILING DATE: 14-FEB-1994
APPLICATION NUMBER: PM4002 (AU)
FILING DATE: 21-FEB-1994
APPLICATION NUMBER: PN0284 (AU)
FILING DATE: 23-DEC-1994
APPLICATION NUMBER: US 08/388,353
FILING DATE: 14-FEB-1995
APPLICATION NUMBER: PN3021/95
FILING DATE: 17-MAY-1995
ATTORNEY AGENT INFORMATION:
NAME: FRANK S. DIGIGLIO
REFERENCE/DOCKET NUMBER: 9606Z
TELEPHONE: (516) 742-4343
TELEPHONE: (516) 742-4343
TELEPHONE: (516) 742-4366
INFORMATION FOR EQG ID NO: 184:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-488-551B-184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        931 TCCCTCCTCT 940
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COMPUTER READABLE FORM:
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                   1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER TABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: Floppy disk
COMPUTER: THE FC COMPATION
COPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTING DATA:
APPLICATION NUMBER: US/08/488,551B
FILING DATE: 14-FEB-1994
APPLICATION NUMBER: PM4002 (AU)
FILING DATE: 12-FEB-1994
APPLICATION NUMBER: PM0284 (AU)
FILING DATE: 12-FEB-1995
APPLICATION NUMBER: PN0284 (AU)
FILING DATE: 13-FEB-1995
APPLICATION NUMBER: PN0284 (AU)
FILING DATE: 17-MAY-1995
ATTORNEY/AGENT INFORMATION:
NAME: FRANK S. DIGIGILO
REFERENCE/ACENT NUMBER: 9606Z
TELEREPONE: (S16) 742-4343
                                                                                                                                                                                                                             APPLICANT: Nicholas J. Deacon
APPLICANT: Dale A. McPhee
APPLICANT: David Cooper
TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
WUMBER OP SEQUENCES: 841
CORRESPONDENCE ADDRESS:
Pred. No. 2e+02;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                               MURPHY & PRESSER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 8.4; DB
Pred. No. 2e+0
0; Mismatches
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US-08-488-551B-230/c
; Sequence 230, Application US/08488551B
; Patent No. 6015661
; GENERAL INFORMATION:
                                                                                                                                                               US-08-488-551B-229/c
; Sequence 229, Application US/08488551B
; Patent No. 6015661
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                   SSEE: SCULLY, SCOTT, MUR
T: 400 GARDEN CITY PLAZA
GARDEN CITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11.5%;
Best Local Similarity 90.0%;
Matches 9; Conservative
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INFORMATION FOR SEQ ID NO: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 10 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 90.0
Matches 9; Conservative
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                                                     932 CCCTCCTCT 941
                                                                                        10 CCCACCTCT 1
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                                                                                                                                                                                                                                                                                                                                                                                                    NEW YORK
: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 11530-0299
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                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE:
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APPLICANT: Dale A. McRee

APPLICANT: Dale A. McRee

MITTER OF INVESTICES NOW-INCORNIC STRAINS OF HIV-1

NUTLES OF INVESTICES NOW-INCORNIC STRAINS OF HIV-1

NUTLES OF INVESTICES NOW-INCORNIC STRAINS OF HIV-1

COMPRESSED SCULLY, SCOTT, MURRIY & PRESSER

STREET: AND NOW-INCORNIC STRAINS OF HIV-1

COMPLYER HEADABLE FORM GAREE

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COMPLYER THE PROPERTY NOW-INCORNIC STRAINS OF HILDS

COMPLYER THE PROPERTY NOW-INCORNIC STRAINS OF HILDS

PRILITING DATE: 12 PECTATION NOW-INCORNIC STRAINS OF STRAIN
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APPLICANT: HAN, YE SUN
APPLICANT: TY, GYU YU
APPLICANT: YY, GYU YU
APPLICANT: KIM, SUNG HOU
APPLICANT: LIM, JAE HWAN
APPLICANT: LIM, JAE RYBO
APPLICANT: CHOI, IN GENE SEQUENCE OF AQUIFEX PYROPHILUS
TITLE OF INVENTION: SUPERCXIDE DISMUTASE AND PROTEIN EXPRESSED IN ESCHERICHIA
TITLE OF INVENTION: COLI
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESSE: 06LON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESSEE: P.C.
STRET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR
CITY: ARLINGTON
STATE: VA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 8.4; DB 1; Length 10;
Pred. No. 2e+02;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/008,303
FILING DATE: 16-JAN-1998
CLASSIFICATION: 536
FRICK APPLICATION DATA:
APPLICATION NUMBER: US/09/008,303
FILING DATE: 16-JAN-1997
FILING DATE: 16-JAN-1997
ATTORNEY/AGRYT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 29.01-0109-0
TELEPHONE: 703-413-2000
FILING DATE: 23-DEC-1994

APPLICATION NUMBER: US 08/388,353
FILING DATE: 14-FEB-1995
APPLICATION NUMBER: PN3021/95
FILING DATE: 17-MAY-1995
ATTORNEY/AGENT INFORMATION:
NAME: FRANK S. DIGIGIL:
REFERENCE/DOCKET NUMBER: 9606Z
TELECHMONICATION INFORMATION:
TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4343
TELEFAX: (516) 742-4366
INFORMATION FOR SEQ ID NO: 310:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 base pairs
TYPE: MUCLeic acid
STRANDEDNES: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 3, Application US/09008303; Patent No. 6033889; GENERAL INFORMATION: APPLICANT: HAN, YE SUN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11.5%;
90.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 90.0
Matches 9; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear;
MOLECULE TYPE: DNA
US-08-488-5518-310
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Pred. No. 2e+02;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Indels
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APPLICANT: Nicholas J. Deacon
APPLICANT: Dale A. Worbee
APPLICANT: David Cooper
TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
NUMBER OF SEQUENCES: 841
CORRESPONDENCES: 841
CORRESPONDENCES: SCULLY, SCOTT, MURPHY & PRESSER
STREET: 400 GARDEN CITY PLAZA
CITY: GARDEN CITY
STATE: NEW YORK
COUNTYS: 0.5.A.
ZIP: 1120-0.299
COMPUTER READABLE FORM:
MEDIUM TYPE: Flopy disk
COMPUTER READABLE FORM:
MEDIUM TYPE: Plopy disk
COMPUTER: DAPPO: 0.209
COMPUTER: PREDABLE FORM:
MEDIUM TYPE: PLOPSY disk
COMPUTER: DAPPO: 0.209
COMPUTER: DAPPO: 0.209
SOFFWARE: PRECATION DATA:
APPLICATION NUMBER: W33864 (AU)
FILING DATE: 0.7-UM-1995
PRILING DATE: 14-FEB-1994
APPLICATION NUMBER: PM4002 (AU)
FILING DATE: 21-FEB-1994
APPLICATION NUMBER: PN0284 (AU)
                                COMPUTER: A.D. A.C. COMPUTER: A.D. A.C. COMPUTER: A.D. A.C. COMPUTER: A.D. A.C. CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/488,551B
FILING DATE: 07-UN-1995
PRIOR APPLICATION NUMBER: PM364 (AU)
FILING DATE: 14-FEB-1994
APPLICATION NUMBER: PM028 (AU)
FILING DATE: 12-FEB-1994
APPLICATION NUMBER: PM384 (AU)
FILING DATE: 12-FEB-1994
APPLICATION NUMBER: PM384 (AU)
FILING DATE: 13-FEB-1995
APPLICATION NUMBER: PM3021/95
FILING DATE: 17-MAY-1995
APPLICATION NUMBER: PM3021/95
FILING DATE: 17-MAY-1995
ATTORNEY/AGNT INFORMATION:
NAME: FRANK S. DIGIGIO
REFERENCE/DOCKET UNBER: 9666Z
TELEPHONE: (516) 742-4366
INFORMATION FOR SEQ ID NO: 275:
SEQUENCE CHARACTERISTICS:
LEMGTH: 10 base pairs
LEMGTH: 10 base pairs
TTELEPHONES: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 302
20-08-488-551B-310/c
; Sequence 310, Application US/08488551B
; Patent No. 6015661
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11.5%;
90.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 90.0
Matches 9; Conservative
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US-08-488-5518-275
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Sequence 15, Application US/08675816
Patent No. 6171864
GENERAL INFORMATION:
APPLICANT: Couplian, Sean J.
TITLE OF INVENTION: CALRETICULIN AND CALNEXIN GENES AND PROMOTER REGIONS AND USES NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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O
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Pred. No. 2e+02;
0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/675,816
FILING DATE: 05-UTL-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 8.4; DB 1;
Pred. No. 2e+02;
0; Mismatches
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750027.401
NAME: No. 6171864tenburg, Carol
REGISTRATION NUMBER: 39,317
REFERENCE/DOCKET NUMBER: 750027.401
TELECOMMUNICATION:
TELECHONE: (206-622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEE: Seed and Berry
: 701 Fifth Ave. Suite 6300
Seattle
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TELEPHONE: (206-622-4900
                                                                                                            TELEPHANE: (206-622-4900
TELEFAX: (206)-682-6031
INFORMATION FOR SEQ ID NO: 10:
SEGUIENCE CHARACTERISTICS:
LENGTH: 10 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (206)-682-6031
INFORMATION FOR SEQ ID NO: 15:
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ATTORNEY/AGENT INFORMATION:
NAME: No. 6171864tenburg,
REGISTRATION NUMBER: 39,31,
REFERENCE/DOCKET NUMBER: 7
                                                                                                                                                                                                                                                                                                                                                                                                                        11.5%;
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LENGTH: 10 base pairs
                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 90.0.
Thes 9; Conservative
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Best Local Similarity 90.0
Matches 9; Conservative
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STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                     TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               90S TCATTTTCTT 914
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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                                                                                                                                                                                                                                                                                                                                  linear
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ZIP: 98104-7092
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STREET: 70
CITY: Seat
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                                                                                                                                                                                                                                                                                                                                                            US-08-675-816-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-675-816-15
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US-08-675-816-10
Sequence 10. Application US/08675816
Patent No. 6171864
Facultan No. 617186
Facultan No. 61718
Facultan 
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APPLICANT: LOPEZ-NIETO, CARLOS E
APPLICANT: LOPEZ-NIETO, CARLOS E
APPLICANT: MIGAM, SANJAY KUMAR
TITLE OF INVENTION: PROCESSES, APPARATUS AND COMPOSITIONS FOR
TITLE OF INVENTION: CHARACTERIZING NUCLEOTIDE SEQUENCES
FILE REFERENCE: 2458-4029
CURRENT APPLICATION NUMBER: US/08/522,384
CURRENT PILING DATE: 1996-11-15
NUMBER OF SEQ ID NOS: 122
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 11
LENGTH: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE: OTHER INFORMATION: Description of Unknown Organism: Primer
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                                                                                                                                                                                                                      DB 1; Length 10;
                                                                                                                                                                                                                                                                               1; Indels
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CURRENT APPLICATION DATA:
FILLOATION NUMBER: US/08/675,816
FILING DATE: 05-JUL-1996
                                                                                                                                                                                                                  Query Match
11.5%; Score 8.4; DB 1;
Best Local Similarity 90.0%; Pred. No. 2e+02;
Matches 9; Conservative 0; Mismatches
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-522-384-11
; Sequence 11, Application US/08522384
; Patent No. 6110667
                                                                                                                         MOLECULE TYPE: DNA (genomic) US-09-008-303-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA ORGANISM: Unknown Organism
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
         10 base pairs
                                      TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                         933 CCTCCTCTTC 942
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                                                                                               linear
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Best Local Similarity
Matches 9; Conserv
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11.5%; Score 8.4; DB 1; Length 10; 90.0%; Pred. No. 2e+02; tive 0; Mismatches 1; Indels
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OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARRS: WOARD FORFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/464,011B
FILING DATE: O5-Jun-1995
CLASSIFICATION: cUnknown-
PRIOR APPLICATION NUMBER: 07/882,438
FILING DATE: May 13, 1993
APPLICATION NUMBER: 08/08,766
FILING DATE: May 13, 1993
APPLICATION NUMBER: 08/06,952
APPLICATION NUMBER: 08/06,952
APPLICATION NUMBER: 08/06,952
APPLICATION NUMBER: 08/06,952
FILING DATE: May 13, 1993
ATTORNEY/AGENT INFORMATION:
NAME: WATDUEY, RICHARD 3, 1327
REFERENCE/DOCKET NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 202/045
TELECOMMUNICATION INFORMATION:
                                                                                   CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 309
US-09-154-750A-4
; Sequence 4, Application US/09154750A
; Patent No. 6432640
; GENERAL INFORMATION;
; APPLICANT: VOGEISTEIN, Bert
; APPLICANT: Kinzler, Kenneth
; APPLICANT: Rogelstein, Bert
; APPLICANT: Rogelstein, Bert
; APPLICANT: Rogelstein, Bert
; APPLICANT: Rollar, Kornelia
; TITLE REFERENCE: 1107.7537
; CURRENT APPLICATION NUMBER: 00/09/154,750A
; CURRENT FILING DATE: 1998-09-17
; PRIOR PRILING DATE: 1998-09-17
; PRIOR FILING DATE: 1998-03-30
; NUMBER OF SEQ ID NOS: 93
; SOFTWARE: RestSEQ for Windows Version 3.0
; LENGTH: 10
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TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-08-464-0118-11
                                Fifth Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHRRACTERISTICS:
LENGTH: 10
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth
Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 90.0
Matches 9; Conservative
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CRGANISM: Homo sapiens
US-09-154-750A-4
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                                                                                             GENERAL INFORMATION:

APPLICANT: Glume, Beatrix
APPLICANT: Blume, Beatrix
APPLICANT: Hamilton, Andrew
APPLICANT: Barry, Cornelius
TITLE OF INVENTION: DNA CONSTITUTE OF INVENTION: DNA CONSTITUTE OF INVENTION: Them
NUMBER OF SIGNINGS: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE Zencea Inc.
STREET: 1800 Concord Pike
COMPUTER: BDS CONCORD PIke
STATE: DB
COUNTRY: USA
ZIP: 19850
COMPUTER: READABLE FORM:
MEDIUM TYPE: FLORPY disk
COMPUTER: EN PC COMPABILIE FORM:
MEDIUM TYPE: PATENTION DATA:
COMPUTER: LINE PATENTION DATA:
FILING DATE: 14-AUG-1997
CUASSITTATION DATA:
APPLICATION NUMBER: GB 95056081.1
FILING DATE: 17-MAR-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 95056081.1
FILING DATE: 17-MAR-1995
ATTORNEY/AGENT INFORMATION:
REFERENCE/DOCKET NUMBER: SEE 45003/UST
TELEPHONE: Globace pairs
TUPPOMATION TOWNER: AND ACCOUNTY
TOPOLOGY: INPORT TOPOLOGY: I
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Patent No. 6568789
GENERAL INFORMATION:
APPLICANT: Wichael D. West
Jerry W. Shay
Woodring E. Wright
TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF CONDITIONS
TELOMERASE ACTIVITY
TELOMERASE ACTIVITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 90.0%; Pred. No. 2e+02;
Matches 9; Conservative 0; Mismatches 1; Indels
                         Sequence 4, Application US/08894324A Patent No. 6204437 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
ORGANISM: TCA MOTIF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 61
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      905 TCATTTTCTT 914
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      US-08-894-324A-4
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OTHER INFORMATION: Theoretical sequence designed to show proper and improper joining OTHER INFORMATION: elements
US-09-914-259-129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                 ; FEATURE:
, OTHER INFORMATION: Hypothetical sequence to demonstrate application.
US-09-709-596A-7
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Pred. No. 2e+02;
0; Mismatches 1; Indels
                                                                                              Sequence 7. Application US/09709596A
Patent No. 6458945
GENERAL INFORMATION:
APPLICANT: Variagenics, Inc.
TITLE OF INVENTION: A Method for Analyzing Polynucleotides
FILE REFERENCE: 258/239
CURRENT APPLICATION NUMBER: US/09/709,596A
CURRENT FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 17
SOFTWARE: Patentin version 3.1
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TITLE OF INVENTION: A Method for Identifying Polymorphisms
FILE REFERENCE: 257/078
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 129, Application US/09914259; Sequence 129, Application US/09914259; Patent No. 6495336; GRNERAL INFORMATION:
APPLICANT: Makowski, Lee
APPLICANT: Williams, Mark
TITLE OF INVENTION: STAGED ASSEMBLY OF NANOSTRUCTURES; FILE REFERENCE: 8471-010-999; CURRENT APPLICATION NUMBER: US/09/914,259; CURRENT FILING DATE: 2000-11-21; NUMBER OF SEG ID NOS: 180; SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-655-104A-7; Sequence 7, Application US/09655104A; Patent No. 6Application US/09655104A; GENERAL INFORMATION:
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90.0%;
                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA ORGANISM: Artificial Sequence
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Matches 9; Conservative
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Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -09-914-259-129
                                                                  RESULT 312
US-09-709-596A-7
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LENGTH: 10
                                                                                                                                                                                                                                                                                                                                 SEQ ID NO.7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; OTHER INFORMATION: Hypothetical sequence to demonstrate application.
US-09-394-457C-7
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                                                                                                                                                                                                                            Sequence 7, Application US/09394457C;
Patent No. 6440705;
Bacter No. 6440705;
GENERAL INFORMATION:
APPLICANT: Variagenics, Inc.
TITLE OF INVENTION: A Method for Analyzing Polynucleotides
FILE REFERENCE: 246/020;
CURRENT FILING DATE: 1999-09-10;
NUMBER OF SEQ ID NOS: 16;
SOFTWARE: Patentin version 3.1;
SEQ ID NO 7;
LENGTH: 10
Score 8.4; DB 1; Length 10;
Pred. No. 2e+02;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 8.4; DB 1; Length 10;
Pred. No. 2e+02;
0; Mismatches 1; Indels
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Pred. No. 2e+02;
0; Mismatches 1; Indels
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Patent No. 6458584
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: MIRZABEKOV, ANDREI
APPLICANT: GUSCHIN, DMITRY Y.
APPLICANT: SHIK, VALENTINE
APPLICANT: PORDSYSHEV, ALEKSEI
APPLICANT: FOTIN, ALEXANDER
APPLICANT: LYSOV, YU
APPLICANT: LYSOV, YU
    11.5%;
90.0%;
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90.0%;
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ORGANISM: Artificial Sequence
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90.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA ORGANISM: Artificial Sequence
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Best Local Similarity 90.0
Matches 9; Conservative
                         Best Local Similarity 90.0
Matches 9; Conservative
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Best Local Similarity 90.0
Matches 9; Conservative
                                                                                         932 CCCTCCTCT 941
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US-09-394-457C-7
         Query Match
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915 TGGTCTTTGC 924

Gaps

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CASOL 319

CASOL 319

CASOL 319

CASOL 319

CASOL 319

CASOL 319

CASOL 310

CORRENT ELU, Qiang

TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE

TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS

FILE REFERENCE: 8325-0011.20 / S11-US2

CURRENT PAPLICATION NUMBER: US/09/989,789

CURRENT FILING DATE: 2002-03-25

NUMBER OF SEQ ID NOS: 4085

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 1659

LENGTH: 10
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. OTHER INFORMATION: Description of Artificial Sequence: example target
.; OTHER INFERMATION: DNA
US-09-989-789-1659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; FEATURE:
; OTHER INFORMATION: Hypothetical sequence to demonstrate application.
US-10-104-818-7
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0
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US-10-14-818-7

i Sequence 7, Application US/10104818

Patent No. 658223

GENERAL INFORMATION:

APPLICANT: VARIGON: A Method for Analyzing Polynucleotides

TITLE OF INVENTION: A Method for Analyzing Polynucleotides

TITLE OF INVENTION: A Method for Analyzing Polynucleotides

CURRENT APPLICATION NUMBER: US/10/104,818

CURRENT FILING DATE: 2092-05-14

PRIOR APPLICATION NUMBER: 09/394,774

NUMBER OF SEQ ID NOS: 16

SOFTWARE: PatentIn Version 3.1

SEQ ID NO 7
                           Score 8.4; DB 1; Length 10;
Pred. No. 2e+02;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 11.5%; Score 8.4; DB 1; Length 10; Best Local Similarity 90.0%; Pred. No. 2e+02; Matches 9; Conservative 0; Mismatches 1; Indels
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                           11.5%;
90.0%;
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA ORGANISM: Artificial Sequence
                           Query Match
Best Local Similarity 90.0
Matches 9; Conservative
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Best Local Similarity 90.0
Matches 9; Conservative
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                                                                                                                                                                1 TATTCCTCCT 10
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                                                                                                                    929 TATCCCTCCT
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, OTHER INFORMATION: Used to demonstrate how indicated aspect of invention works.
US-09-394-467-7
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                                                                                                                                                                                                          OTHER INFORMATION: Hypothetical sequence to demonstrate application.
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; Batent No. 6566059
; GENERAL INFORMATION:
; APPLICANT: Variagenics, Inc.
; TITLE OF INVENTION: A Method for Analyzing Polynucleotides
; FILE REFRENCE: 245/287
; CURRENT APPLICATION NUMBER: US/09/394,467
; CURRENT FILING DATE: 1999-09-10
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Patentin Version 3.0
; SEQ ID NO
; SEQ ID NO
                                                                                                                                                                                                                                                                               Query Match
11.5%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 2e+02;
Matches 9; Conservative 0; Mismatches 1; Indels
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APPLICANT: Generation:
APPLICANT: Generation:
APPLICANT: Finkel, Kevin
APPLICANT: Forkel, Kevin
APPLICANT: Forkel, Kevin
APPLICANT: Lee, Helen H.
TITLE OF INVENTION: HAPLOTYPES OF THE AGTRI GENE
FILE REFERENCE: AGTR1-1136 test
CURRENT FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2000-08-28
NUMBER OF SEQ ID NOS: 27
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2
CURRENT APPLICATION NUMBER: US/09/655,104A CURRENT FILING DATE: 2000-09-05 NUMBER OF SEQ ID NOS: 25 SSOUTHARE: Patentin version 3.1 SEQ ID NO 7 LENGTH: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 22, Application US/09867915
Patent No. 6521747
GENERAL INFORMATION:
                                                                                                                                                              ORGANISM: Artificial Sequence FEATURE:
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Best Local Similarity 90.0
Matches 9; Conservative
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CORGANISM: Homo sapiens
US-09-867-915-22
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                                                                                                                                               TYPE: DNA
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Sequence 25, Application US/08344695

Patent No. 5614398

GENERAL INFORMATION:
APPLICANT: WARREN WILLIAM
APPLICANT: MARREN WILLIAM
APPLICANT: ATKINSON, PETER
TITLE OF INTENTION: A GENE TRANSFER SYSTEM FOR INSECTS
NUMBER OF SEQUENCES:
ADDRESSEE: P.C.
ADDRESSEE: P.C.
STREET: 1755 S. Jefferson Davis Highway, Suite 400
CITY: Arlinginia
STREET: Virginia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 8.4; DB 1; Length 11; Pred. No. 2.2e+02; 0; Mismatches 1; Indels
                   Length 11;
                                                                                1; Indels
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; Sequence 26, Application US/08344695
; Parent No. 5614398
; GENERAL INFORMATION:
APPLICANT: WARREN, WILLIAM
APPLICANT: MARREN, WILLIAM
TITLE OF INVENTION: A GENE TRANSFER SYSTEM FOR INSECTS
NUMBER OF SEQUENCES: 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/344,695
FILING DATE: 18-NOV-1994
ATTORNEY: 536
                   Score 8.4; DB 1;
Pred. No. 2.2e+02;
0; Mismatches 1.
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US-08-344-695-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Kelber, Steven B.
REGISTRATION NUMBER: 30,073
REFERENCE/DOCKET NUMBER: 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 413-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11.5%;
90.0%;
                      Query Match
Best Local Similarity 90.0%;
Matches 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (703) 413-2220
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ouery Match
Best Local Similarity 90.0
Matches 9; Conservative
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EDNESS: unknown
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TOPOLOGY: unknown
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                                                                                                                                                                                                                                                                                                RESULT 321
US-08-344-695-25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
         Sequence 1663, Application US/09989789

Patent No. 6588746
GENERAL INFORMATION:
APPLICANT: LIU, Qiang
TITLE OF INVENTION:
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Patent No. 5614398
GENERAL INFORMATION:
APPLICANT: O'EROCHTA, DAVID
APPLICANT: WARREN, WILLIAM
APPLICANT: WARREN, WILLIAM
APPLICANT: ATKINSON, PETER
ITILE OF INVENTION: A GENE TRANSFER SYSTEM FOR INSECTS
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 8.4; DB 1; Length 10;
Pred. No. 2e+02;
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1755 S. Jefferson Davis Highway, Suite 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/344,695
FILING DATE: 18-NOV-1994
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: unknown
MOLECULE TYPE: other nucleic acid
US-08-344-695-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Kelber, Steven B.
REGISTRATION NUMBER: 30,073
REFERENCE/DOCKET NUMBER: 2747
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 413-3000
                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ouery Match
Best Local Similarity 90.0%;
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELERA: (703) 413-220
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 11 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     nucleic acid
EDNESS: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             933 CCTCCTCTTC 942
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10 CATCCTCTTC 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Arlington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Virginia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       U.S.A.
US-09-989-789-1663/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 320
US-08-344-695-24/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22202
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: V
COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET:
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Sequence 29, Application US/08344695

Patent No. 5614396

GENERAL INFORMATION:
APPLICANT: WARRENTON:
APPLICANT: WARREN, WILLIAM
APPLICANT: WARREN, WILLIAM
APPLICANT: WARREN, WILLIAM
APPLICANT: WARREN, WILLIAM
APPLICANT: WARRENS:
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, ADDRESSEE: P.C.
STREET: 1755 S. Jefferson Davis Highway, Suite 400
CITY: Arlington
STATE: Virginia
CCUTTY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 11.5%; Score 8.4; DB 1; Length 11; Best Local Similarity 90.0%; Pred. No. 2.2e+02; Matches 9; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11.5%; Score 8.4; DB 1; Length 11; 90.0%; Pred. No. 2.2e+02; tive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:

MEDIUM TYPE: R10PQ disk

COMPUTER: BM PC compatible

CLASSIFICATION NUMBER: US/033

REFERENCE/DOCKET NUMBER: 2747-058-27

TELEPHONE: (703) 413-320

               2747-058-27
                                                                                                                                                                                                                                                                                                                                                                                                           other nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: other nucleic acid
       REFERENCE/DOCKET NUMBER: 274
TELEFORMONICATION INFORMATION:
TELEFAX: (703) 413-220
TELEFAX: (703) 413-220
TELEFAX: 24865 OATH UR
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 90.v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: nucleic acid
STRANDEDNESS: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           926 TITIAICCCI 935
                                                                                                                                                                                                                                                                                                                                                                         unknown
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                                                                                                                                                                                                                                                                                                                                                                 ; TOPOLOGY: un;
; MOLECULE TYPE:
US-08-344-695-27
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US-08-344-695-29
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Wis-object 10. Sequence 27, Application US/08344695

Patent No. 5614398

Patent No. 5614398

Patent No. 5614398

PapelICANT: O'BROCHTA, DAVID

APPLICANT: WARREN, WILLIAM

APPLICANT: WARREN, WILLIAM

APPLICANT: ATKINGON, PETER

TITLE OF INVENTION: A GENE TRANSFER SYSTEM FOR INSECTS

NUMBER OF SEQUENCES: 50

CORRESPONDER EDDON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, WAIER & NEUSTADT, ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, WAIER & NEUSTADT, COUNTRY: U.S.A.

STATE: VIRGINIA

COUNTRY: U.S.A.

MEDIUM TYPE: PLOPPY disk

COMPUTER READABLE FORM:

MEDIUM TYPE: PLOPPY disk

COMPUTER: BAP COMPACH:

CORRESTRICATION NUMBER: US/08/344,695

FILING DATE: DATE NOWALION:

ATTORNEY/AGENT INFORMATION:

MAME: Kelber, Steven B.

REGISTRATION NUMBER: 30,073
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, ADDRESSEE: P.C.
STREET: 1755 S. Jefferson Davis Highway, Suite 400
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 11.5%; Score 8.4; DB 1; Length 11; Best Local Similarity 90.0%; Pred. No. 2.2e+02; Matches 9; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                           COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

MEDIUM TYPE: Floppy disk

MEDIUM TYPE: BY FORM:

MEDIUM TYPE: BY FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/NS-DOS

SOFTWARE: BATCHIN Release #1.0, Version #1.30

CURRENT ABPLICATION DATE:

APPLICATION NUMBER: US/08/344,695

FLING DATE: 18-NOV-1994

CLASSIFICATION: 536

ATTORNEY/AGNT INFORMATION:

NAME: Kebber, Steven B.

REGISTRATION NUMBER: 2747-058-27

TELEPHONE: (703) 413-220

TELEPHONE: UNINOWN

TOPOLOGY: unknown

TOPOLOGY: unknown

TOPOLOGY: unknown

TOPOLOGY: UNKNOWN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       926 TITIATCCCT 935
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Score 8.4; DB 1; Length 11; Pred. No. 2.2e+02; 0; Mismatches 1; Indels
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US-08-1714-899-64

Sequence 64, Application US/08173469C

Patent No. 5861244

GENERAL INFORMATION: C. -G.
APPLICANT: HEPBIRN, A. G.
APPLICANT: HEPBIRN, A. G.
APPLICANT: HEPBIRN, A. G.
APPLICANTION: TRIPLE-STRAND FORWATION.
MUMBER OF INVENTION: TRIPLE-STRAND FORWATION.
APPLICANT: HEPBIRN: 365
CORRESPONDENCE ADDRESS: 365
CONRESPONDENCE ADDRESS: 365
COUNTRY: USA
STREET: 510 EAST 73RD STREET,
CITY: NEW YORK
STREET: 510 EAST 73RD STREET,
CONFUTER: USA
ZIP: 10021.
COMPUTER READABLE FORM:
MEDIOW TYPE: 3.5 inch, 1.44Mb storage
COMPUTER: Wordperfect Version 5.1
COMPUTER: Wordperfect Version 5.1
COMPUTER: Wordperfect Version 5.1
CURRENT APPLICATION NUMBER: US/08/173,489C

PILING DATE: 22 DEC 1993
CLASSIFICATION DATA:
APPLICATION NUMBER: US 0.7/968,436
FILING DATE: 29 OCT 1992
ATTORNEY/AGENT INFORMATION:
NAME: Handelmar, Joseph H.
REGISTRALION NUMBER: 26,179
REFERENCE/DOCKER NUMBER: US518-6
                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION UNDER:
FILING DATE: 105/09/152,443A
FILING DATE: 105/09/152,443A
FILING DATE: 105/09/152,443A
FILING DATE: 105/09/1993
CLASSIFICATION: 435
ATTONREY/AGENT INFORMATION:
NAME: LEBINARRY SUSAN K.
REGISTRATION NUMBER: 33,943
REFERENCE/DOCKET UNDER: 33,943
RELEFRATION NUMBER: 33,943
RELEFRATION FOR ST 013,940
TELES: 706141
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 base pairs
TYPE: nucleic acid
STRANDEDNES: single
                                                           ZIP: 94304-1018
COMPUTER READABLE FORM:
CMPUTER PREADABLE FORM:
CMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 90.0%;
Matches 9; Conservative
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California
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US-08-173-489C-64
                                         COUNTRY:
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US-08-122-447A-16/C
; Sequence 16, Application US/08152443A
; Patent No. 5663070
; GENERAL INFORMATION;
APPLICANT: SHAPIRO, JOHN P.
APPLICANT: KIRFER, MILHE J.
APPLICANT: TITLE OF INVENTION: THEREOF
; TITLE OF INVENTION: THEREOF
; CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: BARR, PHILIP J.
APPLICANT: SHAPIRO, JOHN P.
APPLICANT: KIEFER, MICHAEL C.
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION: THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: CALL STATE OF THE STAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11.5%; Score 8.4; DB 1;
90.0%; Pred. No. 2.2e+02;
tive 0; Mismatches 1.
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APPLICATION NUMBER: US 08/152,443
FILING DATE: 15-NOV-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 Page Mill Road
CITY: Palo Alto
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: MORRISON & FOERSTER
STREET: 755 Page Mill Road
CITY: Palo Alto
                                                                                                                                                                               Sequence 16, Application US/08444231
Patent No. 5652210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: LEHNHARDT, SUSAN K.
REGISCRRATION NUMBER: 23 943
REFERENCE/DOCKET NUMBER: 27
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: (415) 813-5600 TELEFAX: (415) 494-0792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (412,
TELEFAX: (412,
TELEX: 706141
INFORMATION FOR SEQ ID NO: 16
SEQUENCE CHARACTERISTICS:
LENGTH: 11 base pairs
"VPE: nucleic acid
"VPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 90.0
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       1 TTTCATCCCT 10
                                                                                                            RESULT 325
US-08-444-231-16/c
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US-08-173-489C-121

SEQUENCE 121, Application US/08173489C

PRECENT NATURE C. -G.

APPLICANT: HERBURN, A. G.

APPLICANT: HERBURN, A. G.

TITLE OF INVENTION: GENETIC SEQUENCE ASSAY USING DNA TITLE OF INVENTION: TALPLE-STRAND FORMATION.

NUMBER OF SEQUENCES: 365

CORRESPONDENCE ADDRESS:

ADDRESSEE: PROFILE DIAGNOSTIC SCIENCES, INC., STREET; 510 EAST 73RD STREET,

CITY: NEW YORK

STREET: SIO RAST 73RD STREET,

COUNTER: NEW YORK

STATE: NEW YORK

COUNTER: USA

INFORMATION OF STATE: WA-DOS version 6.2

COMPUTER: BEADABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44MD storage

COMPUTER: BEADABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44MD storage

COMPUTER: DOS VERSION OF STATE: NOT OF STATE: NOT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
11.5%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 2.2e+02;
Matches 9; Conservative 0; Mismatches 1; Indels
POSITION IN GENOME:
CHROMOSOME/SEGMENT: chromosome 18
MAP POSITION: 18q11.2-12.1
PUBLICATION INFORMATION:
AUTHORS: Macda, S, Mita, S, Araki, S, Shimada, AUTHORS: K.
TITLE: Structure and expression of TITLE: the mutant prealbunin gene associated with TITLE: familial amyloidotic polyneuropathy JOURNAL: Molecular Biological Medicine VOLUME: 3
VOLUME: 3
PAGES: 329-338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RELEVANT RESIDUES IN SEQ ID NO: 99 :FROM 1 TO 11 US-08-173-489C-99
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DESCRIPTION: alpha-2-globin gene (accession
DESCRIPTION: V00516) nucleotides 139 to 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: nucleic acid
STRANDEDNESS: double stranded
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    926 TITTATCCCT 935
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 TTTTCTCCT 10
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DATE: 1986
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Gaps
                                                                                                                                                                                                                                                                          MOLECULE TYPE: other nucleic acid
DESCRIPTION: third strand derived from gamma-
DESCRIPTION: crystallin sequence region in Seq ID No. 586124463
HYPOTHETICAL: Yes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear Molecules Standard Molecules Through Molecules The Second DNA DESCRIPTION: prealbumin gene exons 1 and 2 DESCRIPTION: dacession # M15515) nucleotides 1344 to 1354 HYPOTHETICAL: no ANIT-SENSE: no ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 11.5%; Score 8.4; DB 1; Length 11; Best Local Similarity 90.0%; Pred. No. 2.2e+02; Matches 9; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-173-489C-99

Sequence 99, Application US/08173489C

Sequence 99, Application US/08173489C

Patent No. S861244

GENERAL INFORMATION:
APPLICANT: WANG, C. -G.
APPLICANT: HEPBURN, A. G. -G.
APPLICANT: HEPBURN, A. G. -G.
APPLICANT: HEPBURN, A. GENETIC SEQUENCE ASSAY USING DNA
TITLE OF INVENTION: TRIPLE-STRAND FORMATION.

NUMBER OF SEQUENCES: 365
CORRESPONDENCE ADDRESS:
ADDRESSEE: PROPILE DIAGNOSTIC SCIENCES, INC.,
STREET: 510 EAST 73RD STREET,
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                             HYPOTHERICAL: Yes ANTI-SENSE: No PUBLICATION IN SEQ 11 RELEVANT RESIDUES IN SEQ ID NO: 64 :FROM 1 TO 11 US-08-173-489C-64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44Mb storage COMPUTER: 13.5 inch, 1.44Mb storage COMPUTER: IMPC/XT/AT OPERATING SYSTEM: MS-DOS version 6.2 SOFTWARE: Wordperfect Version 5.1 CURENT APPLICATION DATA: WS/08/173,489C FILING DATE: 22 DEC 1993
CLLASSIFICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION NUMBER: US 07/968,436 FILING DATE: 29 OCT 1992
ATTORNEY/AGENT INFORMATION:
NAME: Handelman, Joseph H. REDISTRATION NUMBER: 29 OCT 1992
ATTORNEY/AGENT INFORMATION:
NAME: Handelman, Joseph H. REDISTRATION NUMBER: 26 OCT 1992
ATTORNEY/AGENT NUMBER: U9518-6
TELECOMMUNICATION INFORMATION:
TELEPHONE: (attorney) (212) 708-1880
TELEPHONE: (attorney) (212) 246-8959
INFORMATION FOR SEQ ID NO: 99:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 base pairs
TYPE: nucleic acid
STRPE: nucleic acid
STRPE: nucleic acid
TYPE: nucleic acid
                                                                            INFORMATION FOR SEQ ID NO: 64:
SEQUENCE CHARACTERISTICS:
LENGHH: 11 bases
TYPE: Nucleic Acid
STRANDEDNESS: single stranded
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               920 TITGCCTTTT 929
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APPLICANT: Woo, Savio L.C.
APPLICANT: Smith, Louis C.
APPLICANT: Smith, Louis C.
APPLICANT: Cristiano, Richard J.
APPLICANT: Gritchalk, Stephen
TITLE OF INVENTION: NUCLEIC ACID TRANSPORTER SYSTEMS AND
TITLE OF INVENTION: METHODS OF USE
NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: "C" stands for 5-methylcytosine
                                                                                                                                                                                                                                                                                                    COUNTRY: CAILLOUTHA
COUNTRY: CAILLOUTHA
COUNTRY: 10.S.A.
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: Storage
COMPUTER: IEM COMPATIBLE
COMPUTER: STORAGE
COMPUTER: IEM COMPATIBLE
COMPUTER: FEST SEQ. for Windows 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/460,890A
FILING DATE: DECEMBER: 08/167,641
FILING DATE: DECEMBER: 07/855,389
FILING DATE: MARCH 20, 1993
APPLICATION NUMBER: 07/855,389
FILING DATE: MARCH 20, 1993
APPLICATION NUMBER: PCT/US93/02725
FILING DATE: MARCH 19, 1993
ATTING DATE: MARCH 19, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: Other nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-460-890A-16
; Sequence 16, Application US/08460890A
; Patent No: 5994109
; GENERAL INFORMATION:
Sequence 2, Application US/08460890A
Patent No. 5994109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REGISTRATION NUMBER: 32,327
REGISTRATION NUMBER: 32,327
REJECOMMUNICATION INFORMATION:
TELEPHONE: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                            ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 90.0
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11 base pairs
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EDNESS: single
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                                                                                                                                                                                                                                                     Query Match
11.5%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 2.2e+02;
Matches 9; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                              RELEVANT RESIDUES IN SEQ ID NO: 121 :FROM 1 TO 11 US-08-173-489C-121
        AUTHORS: Orkin, S H, Goff, S C, Hechtman, R L TITLE: Mutation in an intervening TITLE: sequence splice junction in man JOURNAL: Proceedings of the National Academy of YOLUME: 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: GEOGGE M. Yahwak
REGISTRATION NUMBER: 26,824
REFERENCE/DOCKET NUMBER: Yale
TELECOMUNICATION INFORMATION:
TELEPHONE: (203) 268-1951
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (203)268-1951
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
      ORGANISM: Homo sapiens
PUBLICATION INFORMATION:
AUTHORS: Orkin, S H, C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                     931 TCCCTCCTCT 940
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; MOLECULE TYPE: DNA
US-08-590-571-57
                                                                                                                                                             5041-5045
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Best Local Similarity
Matches 9; Conserv
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US-08-590-571-57/c
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.. 0 Gaps ; 0 11.5%; Score 8.4; DB 1; Length 11; 90.0%; Pred. No. 2.2e+02; tive 0; Mismatches 1; Indels APPLICANT: Woo, Savio L.C.
APPLICANT: Smith, Louis C.
APPLICANT: Cristiano, Richard J.
APPLICANT: Gristiano, Richard
APPLICANT: Gristiano, Richard
TITLE OF INVENTION: NUCLEIC ACID TRANSPORTER SYSTEMS AND

RESULT 331 US-08-460-890A-2

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Sequence 16, Application US/08167641C

Patent No. 6033884

GENERAL INFORMATION:
APPLICANT: Woo, Savio L.C.
APPLICANT: Smitch, Louis C.
APPLICANT: Cristiano, Richard J.
APPLICANT: Gottchalk, Stephen
TITLE OF INVENTION: WETHODS OF USE
NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
CONTAINE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEMTURE:

OTHER INFORMATION: "C" stands for 5-methylcytosine
US-08-167-641C-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 90.0%; Pred. No. 2.2e+02; Matches 9; Conservative 0; Mismatches 1.
          COUNTRY: U.S.A.

ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: Storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS S.O
SOFTWARE: FeatSEQ for Windows 2.O
CURRENT APPLICATION DATA: US/08/167,641C
RILING DATE: December 14, 1993
CLASSIFICATION DATA: US/08/167,641C
RILING DATE: March 20, 1992
RILING DATE: March 20, 1992
RILING DATE: March 20, 1993
FILING DATE: March 19, 1993
RELING DATE: March 19, 1993
APPLICATION NUMBER: PCT/US93/02725
FILING DATE: March 19, 1993
APPLICATION NUMBER: 205/012
FILING DATE: Warch 19, 1993
ATTORNEY/AGENT INFORMATION:
REFERENCE/DOCKET NUMBER: 205/012
FILEBEHOME: (213) 489-1600
TELEBEHOME: (213) 489-1600
TELEBENA: 67-3510
INFORMATION FOR SEQ ID NO: 2:
LENGTH: 11 base pairs
TYPE: mucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: U.S.A.

CUNTRY: U.S.A.

CONFORTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: 3 torage
COMPUTER: IBM COMPACIBLE
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FARSENGE OF WINDOWS 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/167,641C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: Other nucleic acid
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US-08-167-641C-16
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Patent No. 6033884

GENERAL INFORMATION:
APPLICANT: Woo, Savio L.C.
APPLICANT: Smith, Louis C.
APPLICANT: Gritiano, Richard J.
APPLICANT: Gottchark, Stephen
ITTLE OF INVENTION: NUCLEIC FOR USE
NUMBER OF SEQUENCES: 65
CORRESPONDENCE Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11.5%; Score 8.4; DB 1; Length 11; 90.0%; Pred. No. 2.2e+02; tive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; OTHER INFORMATION; "C" stands for 5-methylcytosine US-08-460-890A-16
TITLE OF INVENTION: METHODS OF USE
NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STRRET: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: Journal English
COMPUTER: IBM Compatible
OOPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FestSEQ for Windows 2.0
CURRENT APPLICATION NUMBER: US/08/460,890A
FILING DATE: June 5, 1995
CLASSIFICATION NUMBER: OF/855,389
FILING DATE: December 14, 1993
APPLICATION NUMBER: PCT/0893/02725
FILING DATE: March 10, 1993
APPLICATION NUMBER: PCT/0893/02725
FILING DATE: March 10, 1993
APPLICATION NUMBER: PCT/0893/02725
FILING DATE: March 10, 1993
ATTORNEY/AGENT INFORMATION:
TELEFRAX: 67-310
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH 11 base pairs
TYPE: nucleic acid
STRANDEDNESS: Single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: Other nucleic acid
PEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 11.5
Best Local Similarity 90.0
Matches 9; Conservative
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APPLICANT: Woo, Savio L.C.
APPLICANT: Smith, Louis C.
APPLICANT: Cristiano, Richard J.
APPLICANT: Cristiano, Richard J.
APPLICANT: Gottchalk, Srephen
TITLE OF INVENTION: NUCLEIC ACID TRANSPORTER SYSTEMS AND TITLE OF INVENTION: METHODS OF USE
NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: 633 West Fifth Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: Description of Artificial Sequence:RIBOSOME; OTHER INFORMATION: BINDING SITE (FIGURE 5)
US-08-793-331-15
                                                                                                                     11.5%; Score 8.4; DB 1; Length 11; 90.0%; Pred. No. 2.2e+02; tive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ouery Match 11.5%; Score 8.4; DB 1; Length 11; Best Local Similarity 90.0%; Pred. No. 2.2e+02; Matches 9; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                          Best Local Similarity 90.0
Matches 9; Conservative
                                                                                                                                                                                                                925 CTTTTATCCC 934
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     932 CCCTCCTCTT 941
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                           10 cerrrarce
              ; STRANDEDNESS: sin
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-906-691-44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       90071-2066
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                                                                                                                            Query Match
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US-08-906-61-44/c
Sequence 44, Application US/08906691
Sequence 44, Application US/08906691
Sequence 44, Application US/08906691
Sequence 45, Application US/08906691
Setent No. 606452
SEQUENCE 100.
SEPLICANT: Welseman, Sherman M. APPLICANT: Welseman, Sherman M. APPLICANT: Wallur, Girish N. APPLICANT: Wallur, Girish N. APPLICANT: WILTE OF INVENTION: IDENTIFYING FROTEIN-BINDING SITES FOR DNA-BINDING PROTEINS NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: "C" stands for 5-methylcytosine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRAILING SISIEM:
CURRANT APPLICATION DATA:
CURRANT APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 31-JUL-1997
CLASSIFICATION: 435
ATTONENY/AGENT INPOMATION:
NAME: NO. 6066452tenburg Ph.D., Carol
REGISTRATION NUMBER: 39,317
REFERENCE/DOCKET NUMBER: 39,317
REFERENCE/DOCKET NUMBER: 39,317
REPERENCE/CONTINUMBER: 39,317
REPERENCE/CONTINUMBER: 39,317
RELEPHONE: (206) 622-4900
TELEPHONE: (206) 622-4900
TELEPHONE: (206) 622-6031
INFORMATION FOR SEQ ID NO: 44: SEQUENCE CHARACTERISTICS:
FILING DATE: December 14, 1993
CLASSIFICATION: 435
FRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/855,389
FILING DATE: MARCH 20, 1992
APPLICATION NUMBER: PCT/US93/02725
FILING DATE: MARCH 19, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 205/012
TELEPHONE: (213) 489-1600
TELEPHONE: GAAACTERISTICS:
LENGMATION FOR SEQ IN NO: 16:
SEQUENCE CHARACTERISTICS:
LENGMAT: 11 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 991094
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
MOLECULE TYPE: Other nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 90.0
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         : 11 base pairs
nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          931 TCCCTCCTCT 940
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Seattle
STATE: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-167-641C-16
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Gaps
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APPLICANT: Smith Louis C.
APPLICANT: Smith Louis C.
APPLICANT: Cristiano, Richard J.
APPLICANT: Gristiano, Richard J.
APPLICANT: MUCLEIC ACID TRANSPORTER SYSTEMS AND TITLE OF INVENTION: METHODS OF USE NUMBER OF SEQUENCES: 65
CORRESPONDENCES: 65
ADDRESSEE: Lyon & Lyon
STREET: Suite 4700
CITY: Los Angeles
STREET: California
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 90.0%; Pred. No. 2.2e+02;
Matches 9; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: "C" stands for 5-methylcytosine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY.

COUNTRY.

ZIP: 90071-2066

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 MD
MEDIUM TYPE: storage
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FASTED DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/08/462,040
FILING DATE: June 5, 1995
CLASSIFICATION S.36
PRIOR APPLICATION NUMBER: 08/167,641
APPLICATION NUMBER: 08/167,641
APPLICATION NUMBER: 07/855,389
FILING DATE: MARCH 19, 1993
APPLICATION NUMBER: 07/855,389
FILING DATE: MARCH 10, 1992
APPLICATION NUMBER: PCT/US93/02725
FILING DATE: MARCH 19, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
                        FILING DATE: December 14, 1993
APPLICATION NUMBER: 07,855,389
FILING DATE: March 20, 1992
APPLICATION NUMBER: PCT/1083/02725
FILING DATE: March 19, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 212/063
TELECHONE: (213) 489-1600
TELECHONE: (213) 955-0440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: Other nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-462-040-2
; Sequence 2. Application US/08462040
Patent No. 6177554
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   931 TCCCTCCTCT 940
   APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-460-971A-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
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Sequence 16, Application US/08460971A

Patent No. 6150168

GENERAL INFORMATION:
APPLICANT: Smith, Louis C.
APPLICANT: Grittlann, Richard J.
APPLICANT: Gettelan, Rephen
TITLE OF INVENTION: NUCLEIC ACID TRANSPORTER SYSTEMS AND
TITLE OF INVENTION: NUCLEIC ACID TRANSPORTER SYSTEMS
STREET: SAUTH AND
STREET: SAUTH AND
STREET: SAUTH AND
STREET: SULF 4700
CUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER: ENCOMPATIBE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: BRADABLE FORM:
MEDIUM TYPE: BRADABLE GOMPATA:
COMPUTER: ERSERGE FOR WINGOWS 2.0
CURRENT APPLICATION DATA:
SPRICK APPLICATION DATA:
FILING DATE: JUNE 5, 1995
CLASSIPRCATION DATA:
PRICK APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 90.0%; Pred. No. 2.2e+02;
Matches 9; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; OTHER INFORMATION: "C" stands for 5-methylcytosine US-08-460-971A-2
   COMPUTER: IBM COMPACTLDIE

OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSEQ for Windows 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/460,971A
FILLING DATE: June 5, 1995
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: 08/167,641
FILLING DATE: December 14, 1993
APPLICATION NUMBER: 08/167,641
FILLING DATE: December 14, 1993
APPLICATION NUMBER: 07/855,389
FILLING DATE: March 20, 1992
APPLICATION NUMBER: PCT/US93/02725
FILLING DATE: March 19, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REFERENCE/DOCKET NUMBER: 212/063
TELEFOND: (213) 955-0440
TELEFOND: (213) 955-0440
TELERS: 67-3510
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear MOLECULE TYPE: Other nucleic acid
COMPUTER: IBM Compatible OPERATING SYSTEM: IBM P.C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          931 TCCCTCCTCT 940
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TYPE: DNA ORGANISM: Artificial Sequence
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           LENGTH: 11 base pairs
                                         TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            931 TCCCTCCTCT 940
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       905 TCATTTTTT 914
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US-08-722-015A-4/c
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US-09-358-664-1
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LENGTH: 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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US-08-462-040-16

Sequence 16, Application US/08462040

Sequence 16, Application US/08462040

Patent No. 6177554

GENERAL INFORMATION:
APPLICANT: Woo, Savio L.C.
APPLICANT: Smith, Louis C.
APPLICANT: Cristiano, Richard J.
APPLICANT: Gottchalk, Stephen
TITLE OF INVENTION: METHODS OF USE
NUMBER OF SEQUENCES:
CORRESPONDENCES: 65

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11.5%; Score 8.4; DB 1; Length 11; 90.0%; Pred. No. 2.2e+02; tive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: "C" stands for 5-methylcytosine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 5.50

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/167,641
FILING DATE: December 14, 1993
APPLICATION NUMBER: 07/855,389
FILING DATE: March 20, 1992
APPLICATION NUMBER: PCT/0893/02725
FILING DATE: March 19, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
THEORY AND THE STANDARD 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MIDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSEQ for Windows 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/462,040
FILING DATE: June 5, 1995
CLASSIFICATION: 536
                                                 212/078
                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: Other nucleic acid
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKST NUMBER: 212/(
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERESTICS:
LENGTH: 11 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 90.0
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      931 TCCCTCCTCT 940
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 Trecrecier 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                               linear
                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-462-040-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
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Sequence 4, Application US/08722015A
Patent No. 6379881
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INVESTION:
GENERAL INVESTION:
GENERAL INVESTION:
GENERAL INVESTION:
APPLICANT: Schuitemaker, Johanna
APPLICANT: Schuitemaker, Johanna
TITLE OF INVESTION:
INDUCING AND NON SYNCYTIUM INDUCING VARIANTS OF THE HUMAN IMMUNOI
FILE REFERENCE: 9250.25
CURRENT APPLICATION NUMBER: US/08/722,015A
CURRENT FILING DATE: 1996-11-19
NUMBER OF SEQ ID NOS: 258
SOFTWARE: PatentIn version 3.1
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Batent No. 6495320

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: LOCKHART, DAVID J.
APPLICANT: LAI, CHAO-QIANG
APPLICANT: GUNDERSON, KEVIN
FILE REFERENCE: 23879:0004
CURRENT APPLICATION NUMBER: US/09/358,664
CURRENT FILING DATE: 1999-07-21
NUMBER OF SEQ ID NOS: 1
SOFTWARE: Patentin Ver: 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; OTHER INFORMATION: Description of Artificial Sequence: Homopyrimidine; OTHER INFORMATION: Oligonucleotide
US-09-358-664-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                   Query Match

11.5%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 2.2e+02;
Matches 9; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
11.5%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 2.2e+02;
Matches 9; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11.5%; Score 8.4; DB 1; Length 11;
TOPOLOGY: linear nucleic acid FRATURE: OTHER HONDING "C" stands for 5-methylcytosine US-08-462-040-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide.
US-08-722-015A-4
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RESULT 345
US-08-031-145A-20/c
| US-08-031-147A-20/c
| Sequence 20, Application US/08031147A
| Patent No. 5514577
| GENERAL INFORMATION:
| APPLICANT: Draper et al.
| TITLE OF INVENTION: Modulating the Effects of Herpesviruses |
| TITLE OF INVENTION: Modulating the Effects of Herpesviruses |
| NUMBER OF SEQUENCES: 5 |
| CORRESPONDENCE ADDRESSE: Modelock Washburn Kurtz |
| ADDRESSE: Mackiewicz & No. 5514577ris |
| STREET: One Liberty Place - 46th Floor |
| CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11.5%; Score 8.4; DB 1; Length 12; 90.0%; Pred. No. 2.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MD STORAGE
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: 18M PS/2
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/08/031,147A
FILING DATE: MARCH 12, 1993
CLASSIPICATION DATA:
APPLICATION NUMBER: 485,297
FILING DATE: February 26, 1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 952,132
FILING DATE: SEPEMBER: 954,185
FILING DATE: SEPEMBER: 954,185
FILING DATE: SEPEMBER: 954,185
FILING DATE: SEPEMBER: 954,185
ATTORNEY/AGENT INFORMATION:
NAME: JAH MABER: 1SIS-0469
FELENDAMINICATION INFORMATION:
NAME: JAH MABER: (215) 568-3439
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                        44:
                                                                 INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
LENGTH: 12 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: double
TOPOLOGY: circular
FEATURE:
      202-371-8850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9; Conservative
                                       202-371-8856
                                                                                                                                                                                                                                                                                                        NAME/KEY:
COCATION:
IDENTIFICATION METHOD:
COTHER INFORMATION:
US-07-668-517-44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             905 TCATTTTCTT 914
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 TTATTTTCTT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 9, Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                USA
      TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE: PACCOUNTRY:
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Patent No. 526209

GENERAL INFORMATION:

GENERAL INFORMATION:

GENERAL INFORMATION:

TITLE OF INVENTION:

TITLE OF INV
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                                   Gaps
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Pred. No. 2.2e+02;
0; Mismatches 1; Indels
Best Local Similarity 90.0%; Pred. No. 2.2e+02;
Matches 9; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                 FACESTIANCE NO. 5422251
FACENT NO. 5422251
FACENT NO. 5422251
FATTLE OF INVENTION: TRIPLE-STRANDED NUCLEIC ACIDS
NUMBER OF SEQUENCES: 4
CURRENT APPLICATION DATA:
FILING DATE: 28-JAN-1994
FILING DATE: 28-JAN-1994
FILING DATE: 27-FEB-1992
APPLICATION NUMBER: 841,218
FILING DATE: 27-FEB-1990
APPLICATION NUMBER: 622,330
FILING DATE: 27-NOV-1990
FILING DATE: 09-JUN-1989
FILING DATE: 109-JUN-1989
FILING DATE: 26-NOV-1986
FILING DATE: 26-NOV-1986
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/668,517
FILING DATE: 1991032
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Matthew Jacob
REGISTATION NUMBER: 25,154
REFERENCE/DOCKET NUMBER:
REFERENCE/DOCKET NUMBER: 15,154
RELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 90.0%;
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: ATTORNEY/AGENT INFORMATION:
                                                                                           931 TCCCTCCTCT 940
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   933 CCTCCTCTTC 942
                                                                                                                                  2 TICCICCICT 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID NO:1:
ENGTH: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 344
US-07-668-517-44
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RESULT 347
US-08-173-489C-315/c
Sequence 315, Application US/08173489C
; Patent No. 5861244
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unpublished
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Best Local Similarity
Matches 9; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE: NI
COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz & No. 5593859ris
STREET: One Liberty Place, 46th floor
CITY: Philadelphia
                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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Pred. No. 2.4e+02;
0; Mismatches 1; Indels
                                                                                        11.5%; Score 8.4; DB 1; Length 12; 90.0%; Pred. No. 2.4e+02; cive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Prockep, Darwin J.
APPLICANT: Ala-Kokko, Leena
APPLICANT: Ala-Kokko, Leena
APPLICANT: Fertala, Andrzej
APPLICANT: Sieron, Aleksander
APPLICANT: Kivirikko, Kari I.
APPLICANT: Geddis, Amy
TITLE OP INVENTION: Synthesis of Human Procollagens
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOTTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/211,820
FILING DATE: 11-AUG-1994
CLASSIFICATION A355
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/09061
FILING DATE: 22-OCT-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/780,899
FILING DATE: 23-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: Deluca, Mark
REGISTRATION NUMBER: 33.229
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INF
                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 346
US-08-211-820-5
; Sequence 5, Application US/08211820
; Patent No. 5593859
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 90.0%;
Matches 9; Conservative (
                                                                   Query Match
Best Local Similarity 90.v.
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         899 CCCTGGTCAT 908
                                                                                                                                                                                                                                  899 CCCTGGTCAT 908
                                                                                                                                                                                                                                                                                                  11 CCCCGGTCAT 2
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; LOCATION: 1..1
US-08-211-820-5
; ANTI-SENSE: yes
US-08-031-147A-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AUTHORS: S, Rood, JI.
TITLE: Transfer of Kingella
TITLE: indologenes (Snell and Lapage 1976) to the
TITLE: indologenes (Snell and Lapage 1976) to the
TITLE: indologenes comb nov ransfer of Bacteroides
TITLE: indologenes comb nov transfer of Bacteroides
TITLE: ondosus (Beveridge 1941) to the genus
TITLE: Dichelobacter gen nov as Dichelobacter nodosus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: genomic DNA
DESCRIPTION: 16s rRNA gene from Haemophilus
DESCRIPTION: influenzae (Accession # M35019, M59433 )
DESCRIPTION: nucleotides 406 to 417
HYPOTHETICAL: no
ANTI-SENSE: no
GENERAL INFORMATION:
APPLICANT: WANG, C. -G.
APPLICANT: WANG, C. -G.
APPLICANT: HEBBURN, A. G.
TITLE OF INVENTION: GENETIC SEQUENCE ASSAY USING DNA
TITLE OF INVENTION: TRIPLE-STRAND FORMATION.
NUMBER, OF SEQUENCES: 365
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ); DATE: 1991
; RELEVANT RESIDUES IN SEQ ID NO: 315 :FROM 1 TO 12
US-08-173-489C-315
                                                                                                                                                                                 ADDRÉSSEE: PROFILE DIAGNOSTIC SCIENCES, INC., STREET, 510 BAST 73RD STREET, CITY: NEW YORK STATE: NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REGISTRATION NUMBER: 26,179
REGISTRATION NUMBER: 26,179
REFERENCE/BOCKET NUMBER: U9518-6
TELECOMUNICATION INFORMATION:
TELEPAN: (attorney) (212) 246-8959
INFORMATION FOR SEQ ID NO: 315:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                               COUNTRICE
ZIP: 10021.
COMPUTER READBLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44Mb storage
TOWNSTORE: 1.8M PC/XT/AT
MS-DOS version 6.2
                                                                                                                                                                                                                                                                                                                                                                                                                        CONTINENT AND STATEM OF THE CONTINENT AND SYSTEM OF THE CONTINENT APPLICATION DATA:
APPLICATION NUMBER: US/08/173,489C FILING DATE: 22 DEC 1993
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/968,436
FILING DATE: 29 OCT 1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Haemophilus influenzae PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: nucleic acid
STRANDEDNESS: double stranded
TOPOLOGY: linear
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                   US-01442-809A-27

Sequence 27, Application US/08442809A

Fatent No. 5976873

GENERAL INFORMATION:

APPLICANT: Whitsett, Jeffrey A.

TITLE OF INVENTION: Controlling Lung Cell -
TITLE OF INVENTION: Specific Gene Expression

NUMBER OF SEQUENCES: 76

CORRESPONDENCE ADDRESSE:

ADDRESSEE: Carella, Byrne, Bain, Gilfillan,

ADDRESSEE: Carella, Stewart & Olstein

STREET: Roseland

STREET: Roseland

STATE: New Jersey

COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:

AND OTOSE

COMPUTER READABLE FORM:

MEDUN TYPE: 3.5 inch diskette

COMPUTER: 18P $5/2

COMPUTER: 18P $6/2

FILING DATE: 18P $6/2

ATTORNEY AGENT INFORMATION:

NAME: 0lstein, Elliot M.

REGISTRATION NUMBER: 24/025

REGISTRATION INDER: 24/025

REGISTRATION INFORMATION:

TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-676-782-15
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Best Local Similarity 90.0
Matches 9; Conservative
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        COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8
                                                                                                                    RESULT 348
US-08-403-888A-4/C
US-08-403-888A-4/C
SSEQUENCE 4, Application US/0840388BA
Fatent No. 5952490
GENERAL INFORMATION:
FAPPLICATION:
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Pred. No. 2.4e+02;
0; Mismatches 1; Indels
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Patent No. 5976792
Patent CHEUNG, Ambrose
Papelicant: FISCHETTI, Vincent A.
TITLE OF INVENTION: REGULATION OF EXOPROTEIN IN TITLE OF INVENTION: STAPHYLOCOCCUS AUREUS
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS, L.L.P.
STREET: P.O. Box 1404
CTTY: Alexandria
STREET: Virginia
STAPE: United States
ZIP: 22313-1404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ouery Match
Best Local Similarity 90.0
Best Local Similarity
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; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-403-888A-4
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11 CTTCTTCATT
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US-08-676-782-15
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APPLICANT: Nandabalan, Krishnan
APPLICANT: Nandabalan, Krishnan
APPLICANT: Nandabalan, Matiaa
APPLICANT: Yang, Matiaa
APPLICANT: Yang, Matiaa
APPLICANT: Yang, Matiaa
APPLICANT: Kright, James
APPLICANT: Maticas
TITLE OF INVENTION: PROTEIN INTERACTIONS THAT OCCUR IN POPULATIONS
TITLE OF INVENTION: AND IDENTIFICATION OF INHIBITORS OF THESE INTERACTORS
NUMBER OF SEQUENCES: 122
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ô
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Patent No. 6083693
GENERAL INFORMATION:
APPLICANT: Nandabalan, Krishnan
APPLICANT: Rothberg, Jonathan
TITLE OF INVENTION: INDERNIFICATION AND COMPARISON OF PROTEIN-PROTEIN
TITLE OF INVENTION: INVERACTIONS THAT OCCUR IN POPULATIONS
FILE REFERENCE: 7934-006
CURRENT APPLICATION NUMBER: US/08/663,824
CURRENT PAPLICATION DOWN: 1196
NUMBER OF SEQ ID NOS: 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11.5%; Score 8.4; DB 1; Length 12; 90.0%; Pred. No. 2.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION UNMER: US/08/874,825
FILING DATE: 13-UN-1997
CLASSIPICATION: 435
PRIOR APPLICATION: 435
PRIOR APPLICATION: 1435
PRIOR DATE: 14-UN-1996
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REGISTRATION NUMBER: 18,872
REGISTRATION NUMBER: 18,872
REGISTRATION NUMBER: 7934-045
TELECOMMUNICATION: INFORMATION:
TELEPHONE: 212-790-9090
                                                                 Sequence 89, Application US/08874825
Patent No. 6057101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 212-869-8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 89:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTAIN COUNTAIN COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 90...
Best Local 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                935 TCCTCTTCAT 944
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                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 1155 Ave
CITY: New York
STATE: NY
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-874-825-89
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Patent No. 6001990

GENERAL INFORMATION:
APPLICANT: Warkita, Takaji
APPLICANT: Moradpour, Darius
TITLE OF INVENTION: ANTISENSE INHIBITION OF HEPATITIS C
TITLE OF INVENTION: VIRUS
CORRESPONDENCE ADDRESS: 45

CORRESPONDENCE ADDRESS: 5

ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11.5%; Score 8.4; DB 1; Length 12; 90.0%; Pred. No. 2.4e+02; tive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                    11.5%; Score 8.4; DB 1; Length 12; 90.0%; Pred. No. 2.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 50Z or 55X
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: WORDPEFFECT (Version 5.1)
CURRENT APPLICATION NUMBER: US/08/474,700B
FILING DATE: 07-UNM-1995
PRIOR APPLICATION NUMBER: 08/240,382
FILING DATE: 10 MAY 1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Fraser, Janis K.
REGISTRATION NUMBER: 34,819
REFRENCE/DOCKET NUMBER: 0078
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
                                                                                                                                                                       ; TOPOLOGY: linear
; MOLECULE TYPE: oligonucleotide
US-08-442-809A-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 22: SEQUENCE CHARACTERISTICS: TYPE
TELEPHONE: 201-994-1700
TELEPAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 bases
                                                                                                                                                                                                                                             Query Match 11.5
Best Local Similarity 90.0
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-474-700B-22
                                                                                                                          TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Massachusetts
                                                                                                                                                                                                                                                                                                                                                                 917 GTCTTTGCCT 926
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                                                                                                                                                                                                                                                                                                                                                                                                              3 GTGTTTGCCT 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 351
US-08-474-700B-22
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Gaps

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OTHER INFORMATION: Description of Artificial Sequence: proCaspase-1; OTHER INFORMATION: substrate recognition sequence
US-09-513-783A-55
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| NAME/KET: misc binding | LOCATION: (1) -. (12) | LOCATION: (1) -. (12) | OTHER INFORMATION: synthesized test oligonucleotide for binding | OTHER INFORMATION: studies | US-09-151-8908-39
                                                                             ; OTHER INFORMATION: Description of Artificial Sequence: linker
US-09-231-303-89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Squence 39, Application US/09151890B
Patent No. 6420109
GENERAL INFORMATION:
APPLICANT: Gary P. Schroth
APPLICANT: Thomas Wayne Bruice
TILLE REFERENCE: A600-0128
CURRENT APPLICATION: Nucleic Acid Ligand Interaction Assays
FILE REFERENCE: 1998-09-11
CURRENT APPLICATION NUMBER: US/09/151,890B
CURRENT FILING DATE: 1998-09-11
NUMBER OF SEQ ID NOS: 80
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 12;
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Sequence 55, Application US/09513783A

Sequence 55, Application US/09513783A

PAPLICANT: 6416599

APPLICANT: Giuliano, Kenneth A.

APPLICANT: Rapur, Ravi

TITLE OF TREFERIOR: 97-022-L1

CURRENT APPLICATION NUMBER: US/09/513,783A

CURRENT APPLICATION NUMBER: 2000-02-25

NUMBER OF FILING DATE: 2000-02-25

NUMBER OF FILING PATE: 2000-02-25

SOPTWARE: Patentin Ver. 2.0
                                                                                                                                                   Length
                                                                                                                                                   Query Match
11.5%; Score 8.4; DB 1;
Best Local Similarity 90.0%; Pred. No. 2.4e+02;
Matches 9; Conservative 0; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
11.5%; Score 8.4; DB 1;
Best Local Similarity 90.0%; Pred. No. 2.4e+02;
Matches 9; Conservative 0; Mismatches 1;
     TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQ ID NO 39
LENGTH: 12
TYPE: DNA
ORGANISM: Artificial Sequence
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US-09-151-890B-39/c
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LENGTH: 12
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Fatent No. 6395478
GENERAL INFORMATION:
APPLICANT: Nandabalan, Krishnan
APPLICANT: NEWENTION: IDENTIFICATION AND COMPARISON OF PROTEIN-PROTEIN
FILLE OF INVENTION: IDENTIFICATION OF INHIBITORS OF THESE INTERACTIONS
FILLE REPRENCE: 7934-087
CURRENT APPLICATION NUMBER: 08/663,824
EARLIER PALCATION NUMBER: 08/663,824
NUMBER OF SEQ ID NOS: 118
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 89
LENGTH: 12
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LOCATION: (1) ... (12)
COTHER INFORMATION: synthesized test oligonuclectide for binding
US-09-393-783A-39
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US-09-393-783A-39/c

SQUENCE 39, Application US/09393783A

Patent No. 6355428

GENERAL INFORMATION:

APPLICANT: Schroth, Gary P.

APPLICANT: Sthroth, Gary P.

APPLICANT: Suh, Young J.

TITLE OF INVENTION: Nucleic Acid Ligand Interaction Assays
FILE REFERENCE: 460-0128.30

CURRENT APPLICATION NUMBER: US/09/393, 783A

CURRENT FILING DATE: 1999-10-09

PRIOR FILING DATE: 1998-09-11

NUMBER OF SEQ ID NOS: 80

SOFTWARE: FastSEQ for Windows Version 3.0

LENGTH: 12
                                                                   TYPE: DNA

) ORGANISM: Artificial Sequence

) FEATURE:

) OTHER INFORMATION: Description of Artificial Sequence: linker

US-08-663-824-89
                                                                                                                                                                                                                      Query Match
11.5%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 2.4e+02;
Matches 9; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 8.4; DB 1; Length 12;
Pred. No. 2.46+02;
0; Mismatches 1; Indels
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90.0%;
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SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 89
LENGTH: 12
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Best Local Similarity 90.0
Matches 9; Conservative
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US-09-231-303-89
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Gaps

11.5%; Score 8.4; DB 1; 90.0%; Pred. No. 2.4e+02; Query Match Best Local Similarity

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                                                                                                                                                                                                                                                                                                                                                                                                             Length 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 22, Application PC/TUS9505812
GENERAL INFORMATION:
APPLICANT: Wakita, Takaji
APPLICANT: Wakita, Takaji
TITLE OF INVENTION: ANTISENSE INHIBITION OF
TITLE OF INVENTION: HEPATITIS C VIRUS
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
                                                                                                                                                                                                                                                                                                                                                                                                      Score 8.4; DB 1;
Pred. No. 2.4e+02;
0; Mismatches 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION UNDBER:
APPLICATION NUMBER:
O8/240,382
FILING DATE: 10 May 1994
ATTONNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00786/221001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 502 or 555X
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/05812
                                 ISIS-0469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3: Fish & Richardson
225 Franklin Street
                                                 TELECOMMUNICATION INPORMATION:
TELEPHONE: (215) 568-3100
TELEPAK: (215) 568-3439
INPORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
      32,257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22:
                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 90.0%;
Matches 9; Conservative
REGISTRATION NUMBER: 32 REFERENCE/DOCKET NUMBER:
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 90.0
Matches 9; Conservative
                                                                                                                                                                                                                          TYPE: nucleic acid
STRANDENNES: single
TOPOLOGY: linear
ANTL-SENSE: yes
PCT-US94-02471-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   913 TTTGGTCTTT 922
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STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   single
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                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: MAIT, Indu B.
APPLICANT: DEY, Nrisingha
APPLICANT: BEFERO, Robert J.
TITLE OF INVENTION: USE OF THE FULL LENGTH TRANSCRIPT (FLt) FROM
TITLE OF INVENTION: WRABILIS MOSAIC CAULIMOVIRUS TO EXPRESS CHIMERIC GENES IN PLANT
FILE REFERENCE: 50.29-148
CURRENT APPLICATION NUMBER: US/09/324,803C
CURRENT FILING DATE: 1999-06-03
NUMBER OF SEQ ID NOS: 26
SOFTWARE: Patentin ver. 2.0
SEQ ID NO 7
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PCT-US94-02471-20/C
Sequence 20, Application PC/TUS9402471
General INFORMATION:
TITLE OF INVENTION: Modulating the Effects of Herpesviruses
ITTLE OF INVENTION: Modulating the Effects of Herpesviruses
NUMBER OF SEQUENCES:
ADDRESSEE: Moodcock washburn Kurtz
ADDRESSEE: Moodcock washburn Kurtz
ADDRESSEE: Moodcock washburn Kurtz
ADDRESSEE: Cone Liberty Place - 46th Floor
CITY: Philadelphia
            ..
0
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11.5%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 2.4e+02;
Matches 9; Conservative 0; Mismatches 1; Indels
         1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: PA
COMPUTER: PA
COMPUTER: USA
ZIP: 19103
COMPUTER: EADABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/02471
FILING DATE: Herewith
CLASSIFICATION NUMBER: PCT/US94/02471
FILING DATE: FEBRUARY 26, 1990
FRICK APPLICATION NUMBER: 485,297
FILING DATE: FEBRUARY 26, 1990
FRICK APPLICATION NUMBER: 952,132
FILING DATE: APPLICATION NUMBER: 954,185
FILING DATE: SEPEMBER: 954,185
FILING DATE: JAMES SEPEMBER: 954,185
            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TYPE: DNA (promoter)
; ORGANISM: mirabilis mosaic caulimovirus
US-09-324-803C-7
                                                                                                                                                                                                                                                                     Sequence 7, Application US/09324803C Patent No. 6420547
            9, Conservative
                                                                      908 TITICITIEG 917
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            Matches
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Gaps

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URSULT SET STATES

Sequence 285, Application US/0885954

Patent No. 603855

GENERAL INFORMATION:
PAPLICANT: Hardin, Susan H.
APPLICANT: Hardin, Paul E.
ITILE OF INVENTION: Gene Sequencing and Method Thereof
CONTEXT: Homeyouni, Ramin
APPLICANT: Hardin, Paul E.
ITILE OF INVENTION: Gene Sequencing and Method Thereof
CONTEXT: Housens 56

CONTEXT: ADDRESS:
ADDRESSEE: Fulbright & Jaworski L.L.P.
GITY: Housen
STATE: Texas
CONTEXT: Housen
STATE: Texas
CONTEXT: Housen
STATE: Pack
COMPUTER READABLE FORM:
MEDIUM TYEE: Floppy disk
COMPUTER READABLE FORM:
MEDIUM TYEE: Ploppy disk
COMPUTER: IMP C Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
COMPUTER: Patentin Release #1.0, Version #1.30
CURREWT APPLICATION DATA:
APPLICATION NUMBER: US/08/659,954
FILING DATE:
ATTOMATION TOWBER: US/08/659,954
FILING DATE:
APPLICATION NUMBER: US/08/659,954
FILING DATE:
APPLICATION NUMBER: US/08/659,954
FILING DATE:
APPLICATION NUMBER: US/08/659,954
FILING DATE:
ATTOMATION TOWBER: US/08/659,954
FILING DATE:
APPLICATION NUMBER: US/08/659,954
FILING DATE:
ATTOMATION TOWBER: US/08/659,954
FILING DATE:
APPLICATION NUMBER: US/08/659,954
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
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REGISTRATION NUMBER: 32,714
REFERENCE/DOCKET NUMBER: D-5900
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713/651-5325
TELEPRAX: 713/651-5246
INFORMATION FOR SEQ ID NO: 262:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TYPE: nucleic acid
STRANDEDNESS: single
TYPE: other nucleic acid
DESCRIPTION: /desc = "oligonucleotide"
HYDOTHETICAL: YES
AWIT-SENSE: YES
-08-859-954-2-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "oligonucleotide"
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/desc = "oligonucl
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Best Local Similarity 100...
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TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    935 TCCTCTTC 942
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DESCRIPTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        , ANTI-SENSE;
US-08-859-954-262
                                                                                                                                                                                                                                                                   Sequence 26, Application US/09163485
Patent No. 627571
GENERAL INPORMATION:
APPLICANT: BROADDUS, WILLIAM
APPLICANT: BROADDUS, WILLIAM
APPLICANT: GILLIES, GEORGE
TITLE OF INVENTION: SEQUENTIAL CONSENSUS REGION-DIRECTED AMPLIFICATION OF
TITLE OF INVENTION: NOWN AND NOVEL MEMBERS OF GENE FAMILIES
TITLE OF INVENTION NUMBER: US/09/163,485
CURRENT APPLICATION NUMBER: US/09/163,485
CURRENT FILING DATE: 1998-08-30
SOFTWARE: Patentin Ver. 2.0
SEQ.ID NO. 26
LENGTH: 12
TYPE: DAN
TYP
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US-08-859-554-262/C

Sequence 262, Application US/08859554

Fatent No. 6083659:

APPLICANT: Hardin, Susan H.

APPLICANT: Hardin, Paul E.

TITLE OF INVENTION: Design and Optimized Primer Library for TITLE OF INVENTION: Gene Sequencing and Method Thereof

NUMBER OF SEQUENCES: 56

CORRESPONDENCE ADDRESS:

ADDRESSEE: Fulbright & Jaworski L.L.P.

STREET: 1301 McKinney, Suite 5100

CITY: Houston

STATE: Texas

COMPUTER READABLE FORM:

MEDIUM TYPE: Ploppy disk

COMPUTER: IBM PC Compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

FILING DATE:

APPLICATION NUMBER: US/08/859,954
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
OTHER INFORMATION: oligonucleotide, consensus sequence from human
OTHER INFORMATION: matrix metalloproteinases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ô
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: MOD_RES

: LOCATION: (9)

: OTHER INFORMATION: A, T, C, G, other or unknown
US-09-163-485-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/632,782
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Paul, Thomas D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             930 ATCCCTCCTCTT 941
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Best Local Similarity 58.3
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12 RICHYYCCICCT 1
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COUNTRY: USA
ZIP: 55402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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Matches 8, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         952 ATGTATCG 959
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-021-667A-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                      US-USBSY-309, Application US/0885954
| Sequence 309, Application US/0885954
| Fatent No. 6083695
| GENERAL INFORMATION:
| APPLICANT: Hardin, Susan H. APPLICANT: Hardin, Ramin
| TITLE OF INVENTION: Gene Sequencing and Method Thereof
| TITLE OF INVENTION: Gene Sequencing and Method Thereof
| TITLE OF INVENTION: Gene Sequencing and Method Thereof
| TITLE OF INVENTION: Gene Sequencing and Method Thereof
| TITLE OF INVENTION: Gene Sequencing and Method Thereof
| TITLE OF INVENTION: Gene Sequencing and Method Thereof
| TITLE OF INVENTION: Gene Sequencing and Method Thereof
| TITLE OF INVENTION AND ATE: Texas
| CONFUTER: Texas
| COMPUTER: Texas
| TOTO: 3095 | TO
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100.0%; Pred. No. 1.9e+03;
iive 0; Mismatches 0; Indel
                                                           Query Match
11.0%; Score 8; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 8; Conservative 0; Mismatches 0; Indele
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DESCRIPTION: /desc = "oligonucleotide"
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US-08-021-667A-4/c
; Sequence 4, Application US/08021667A
; Parent No. 5434049
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/632,782
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Paul, Thomas D.
REGISTRATION NUMBER: 32,714
REPRENCE/DOCKET NUMBER: D-590
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713/651-5325
INFORMATION FOR SEQ ID NO: 309:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 11.0
Best Local Similarity 100.
Matches 8; Conservative
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TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            934 CTCCTCTT 941
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US-08-859-954-309
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                                                                                                                                                                                                                                                                                                                                                                                         RESULT 364
US-08-859-954-309
US-08-859-954-285
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APPLICANT: Ranbara, Hidden

HERLICANT: Kanbara, Hidden

HITTE OF INVENTION: DOLYNUCLEDIDE CAPTURING TIP AND

HITTE OF INVENTION: POLYNUCLEDIDE PREPARATIVE NETHOD AND DETECTION

HITTE OF INVENTION: POLYNUCLEDIDE PREPARATIVE NETHOD AND DETECTION

HITTE OF INVENTION: POLYNUCLEDIDE PREPARATIVE NETHOD AND DETECTION

HITTE OF INVENTION: METHOD USING SAME

CITY: Meshington

CITY: Meshington

CONTY: USA

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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Magner, Fred W.
APPLICANT: Regular, Jay
APPLICANT: Henrikeen, Dennis
APPLICANT: Henrikeen, Dennis
APPLICANT: Henrikeen, Dennis
APPLICANT: Marning, Shane
TITLE OF INVENTION: Enzymatic Method for Modification of
TITLE OF INVENTION: Recombinant Polypeptides
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Merchant & Gould
STREET: 3100 No. 5707826west Center
CITY: Minneapolis
STREET: M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11.0%; Score 8; DB 1; Length 9; 100.0%; Pred. No. 1.7e+03; tive 0; Mismatches 0; Indele
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11.0%; Score 8; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 8; Conservative 0; Mismatches 0; Indel:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: ELDEPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
SUBTAME: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/470,220A
FILING DATE: 06-JUN 1995
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: US/08/470,220A
FILING DATE: 20-JUL-1993
ATPORNEY/AGENT INFORMATION:
NAME: NELSON NUMBER: 28,659
REFERENCE/DOCKET NUMBER: 8648.32-US01
TELEPONMICATION NUMBER: 8648.32-US01
TELECOMMUTICATION INFORMATION:
TELECOMMUTICATION INFORMATION:
TELEFRAX: 612-332-9081
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 base pairs
TYPE: MODELOC acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: DNA (genomic)
| IMMEDIATE SOURCE:
| CLONE: Ubiquitin cleaving enzyme
US-08-470-220A-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-470-220A-13/c
; Sequence 13, Application US/08470220A
; Patent No. 5707826
; GENERAL INFORMATION:
                                                                                                                        LENGTH: 9 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: YES
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 100..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              952 ATGTATCG 959
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                                                                                                                                                                                                                                                                                                                                                                        ; ANTI-SENSE: NO
US-08-410-544-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              55402
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US-08-410-544-4/c

US-08-410-544-4/c

US-08-410-544-4/c

US-08-410-544-4/c

US-08-410-544-4/c

Patent No. 5607646

FRINGRAL INPORMATION RAZUNOTI

APPLICANT: KAMBARA, Hideki

TITLE OF INVENTION: POLYNUCLEOTIDE PREPARATIVE METHOD AND DETECTION

TITLE OF INVENTION: POLYNUCLEOTIDE PREPARATIVE METHOD AND DETECTION

TITLE OF INVENTION: METHOD USING SAME

NUMBER OF SEQUENCES: 18

CORRESPONDENCE ADDRESS:

ADDRESSEE: Antonelli, Terry, Stout & Kraus

STREET: Suite 600, 1919 Pensylvania Ave., NW

CITY: MESADELE FORM:

MEDIUM TYPE: FLODY disk

COMPUTER READABLE FORM:

COMPUTER: TEM PC compatible

COMPUTER: TEM 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 8; Conservative 0; Mismatches 0; Indel
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/095,162
FILING DATE: 20-UUL-1993
CLASSIFICATION: NUMBER: 28,659
REGISTRATION NUMBER: 28,659
REFERENCE DOCKET NUMBER: 8648.32-US01
FILEPHONE: 612-332-5300
FILEPHONE: 612-332-9081
FILEPHONE: G12-332-9081
FILEPHONE: G12-338-9081
FILEPHONE: G12-332-9081
FILEPHONE: G12-332-9081
FILEPHONE: G12-332-9081
FILEPHONE: G12-332-9081
FILEPHONE: G12-338-9081
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          933 CCTCCTCT 940
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DB 1; Length 9; . 1.7e+03;
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ZUNTRY: USA
ZUP: 02210.
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATURG SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/680,350
FILING DATE:
TITLE OF INVENTION: with Antisense Oligonucleotides Whyber OF SEQUENCES: 18 CORRESPONSED ADDRESS: ADDRESSEE: Wolf, Greenfield & Sacks PC
                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/680,350
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11.0%; Score 8; DB 1
100.0%; Pred. No. 1.7
:ive 0; Mismatches
                                                               E: Wolf, Greenfield & Sacks PC 600 Atlantic Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 9 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
TOPOLOGY: linear
HYPE: Oligodeoxyribonucleotide
HYPOTHETICAL: YES
                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY AGENT INFORMATION:
NAME: Kindregan, Helen C
REGISTRATION NUMBER: 39,248
REFERENCE/DOCKET NUMBER: W046
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-720-3500
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                         39,248
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ATTORNEY/AGENT INFORMATION:
NAME: Kindregan, Helen C
                                                                                                                                 STATE: MA
COUNTRY: USA
ZIP: 02210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy di
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 100.
Matches 8; Conservative
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                                                                                        STREET: 600 /
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-680-350-8/c
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                                                                                                 RESULT 369
US-08-728-785A-4/C

i Sequence 4, Application US/08728785A

j Patent No. 5817506

d APPLICANT: Okano, Kazunori

APPLICANT: Kambara, Hiddeki

TITLE OF INVENTION: POLYNUCLEOTIDE CAPTURING TIP AND

TITLE OF INVENTION: POLYNUCLEOTIDE PREPARATIVE METHOD AND DETECTION

TITLE OF INVENTION: POLYNUCLEOTIDE PREPARATIVE METHOD AND DETECTION

TITLE OF INVENTION: POLYNUCLEOTIDE REPARATIVE METHOD AND DETECTION

TITLE OF INVENTION: POLYNUCLEOTIDE REPARATIVE METHOD AND DETECTION

TITLE OF INVENTION: POLYNUCLEOTIDE SAME

CORRESPONDENCE ADDRESS:

ADDRESSED: Antonelli, Terry, Stout & Kraus

STREET: Suite 1800, 1300 No. 5817506th Seventeenth St.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
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US-08-680-350-2/c
US-08-680-350-2/c
; Sequence 2, Application US/08680350
; Patent No. 595550
; GENERAL INFORMATION:
; APPLICANT: Levina, Asya
; APPLICANT: Zamecnik, Paul C
; TITLE OF INVENTION: Conjugates of Minor Groove DNA Binders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/728,785A
FILING DATE: 10-OCT 1996
CLASSIFICATION: 435
PRICR APPLICATION DATA:

APPLICATION NUMBER: 08/410,544
FILING DATE: 10-MAR-1995
PRICR APPLICATION DATA:

APPLICATION NUMBER: 08/21,667
FILING DATE: 24-FEB-1993
ATTORNEY/AGENT INFORMATION:
NAME: TEXTY, DAVIG T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   520.31930X00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIF: 22209
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: TEXTY, DAVID TO REGISTRATION NUMBER: 20,178
REFERENCE/DOCKET NUMBER: 520
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-312-6600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: YES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 703-112-6666
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 100.
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 9 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
           933 CCTCCTCT 940
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Gaps

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RESULT 373
US-08-680-350-15/c
| Sequence 15, Application US/08680350
| Partent No. 59555015/c
| Partent No. 59555015/c
| GENERAL INFORMATION:
| APPLICANT: Levina, Asya
| APPLICANT: Zamecnik, Paul C
| TILE OF INVENTION: with Antisense Oligonucleotides
| TILE OF INVENTION: with Antisense Oligonucleotides
| CORRESPONDENCES: 18
| CORRESPONDENCES: ADDRESSEE: Wolf, Greenfield & Sacks PC
| STREET: 600 Atlantic Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .
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US-08-967-374-13/C
US-08-967-374-13/C
Sequence 13, Application US/08967374
Fatent No. 6037143
GENERAL INFORMATION:
APPLICANT: Stout, Jay
APPLICANT: Partisen, Dennis
APPLICANT: Partises, Dennis
APPLICANT: Partises, Dennis
APPLICANT: Partises, Bruce
APPLICANT: Manning, Shane
TITLE OF INVENTION: Recombinant Polypeptides
TITLE OF INVENTION: Recombinant Polypeptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1; Length 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZUET 02210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRATI APPLICATION DATA:
APPLICATION NUMBER: US/08/680,350
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100.0%; Pred. No. 1.7
tive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: KINDREGAN, Helen C
REGISTRATION NUMBER: 39,248
REFERENCE/DOCKET NUMBER: W0461
TELEPCOMMUNICATION INFORMATION:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Merchant & Gould
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 100.
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGIH: 9 base pairs
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  945 TGGTTTAA 952
                                              1 TGGTTTAA
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Retent No. 5955590

GENERAL INFORMATION:
APPLICANT: Levina, Asya
APPLICANT: Lanecnik, Paul C
TITLE OF INVENTION: Conjugates of Minor Groove DNA Binders
TITLE OF INVENTION: with Antisense Oligonuclectides
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESSS:
ADDRESSEE: Wolf, Greenfield & Sacks PC
STREET: 600 Atlantic Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 11.0%; Score 8; DB 1; Length 9; Best Local Similarity 100.0%; Pred. No. 1.7e+03; Matches 8; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                    DB 1; Length 9;
0. 1.7e+03;
ches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Boston
CITY: Boston
CITY: Boston
COUNTRY: USA
COUNTRY: USA
ZIP: 02210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
COMPUTER: IBM FC compatible
COMPUTER: DATEM: PC-DOS/NS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/680,350
                                                                                                                                                                                                                                                                                                                                                                    Query Match 11.0%; Score 8; DB 1
Best Local Similarity 100.0%; Pred. No. 1.7
Matches 8; Conservative 0; Mismatches
REGISTRATION NUMBER: 39,248

REFERENCE/DOCKET NUMBER: W0461/7040
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-720-3500
INFORMATION FOR SEQ 10 NO: 8: SEQUENCE CHARACTERISTICS:
LENGTH: 9 base pairs
LENGTH: nucleic acid
STRANDEDNESS: Single
                                                                                                                                                                              TYPE: nucleic act.
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Oligodeoxyribonucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: Oligodeoxyribonucleotide HYPOTHETICAL: YES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Kindregan, Helen C
REGISTRATION NUMBER: 39,248
REFRENCE/DOCKET NUMBER: W0461
TELEPHONE: 617-720-3500
TELEFAX: 617-720-341
INFORMATION FOR SEQ ID NO: 13: SEQUENCE CHARACTERISTICS:
LENGTH: 9 base pairs
TYPE: nucleic acid
STRANDEDMESS: single
TOPPLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 945 TGGTTTAA 952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9 TGGTTTAA 2
                                                                                                                                                                                                                                                                             HYPOTHETICAL: Y
ANTI-SENSE: NO
US-08-680-350-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 372
US-08-680-350-13
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Mon Oct 18 14:40:17 2004

Query Match

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Pred. No. 1.7e+03;
; Mismatches 0; Indels
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STREET: 3100 No. 6403361west Center
CITY: Minneapolis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/505,991
FILING DATE: 17-Feb-2000
CLASSIFICATION: <UNKNOWN>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/520,485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11.0%; Scc.
100.0%; Pre
100.08;
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ORGANISM: Artificial Sequence
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                              Best Local Similarity 100.
Matches 8; Conservative
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Best Local Similarity 100.
Matches 8; Conservative
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                                                                                                                  930 ATCCCTCC 937
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     955 TATCGCTA 962
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                                                                                                                                                                             1 ATCCCTCC 8
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Sequence 62 Application US/08297395A

GENERAL INFORMATION:
APPLICANT: David A. Hafler

TITLE OF INVENTION: PERTIDES DERIVED FROM IMMUNODMINANT
TITLE OF INVENTION: PERTIDES OF WYELIN BASIC PROTEIN
FILE REFERENCE: 1010/05723US3
CURRENT APPLICATION NUMBER: US/08/297,395A

CURRENT FILING DATE: 1994-08-11

EARLIER FILING DATE: 1993-05-06

EARLIER FILING DATE: 1993-05-06

EARLIER FILING DATE: 1980-03-30

EARLIER FILING DATE: 1980-05-24

EARLIER FILING DATE: 1980-06-24

EARLIER FILING DATE: 1987-06-24

EARLIER FILING DATE: 1987-06-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 11.0%; Score 8; DB 1; Length 9; Best Local Similarity 100.0%; Pred. No. 1.7e+03; Matches 8; Conservative 0; Mismatches 0; Indels
                                                                                                                                           ZIP: 55402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/967,374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8648.32-USD1
                              F: 3100 No. 6037143west Center Minneapolis
                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 08/520,485
FFILIG DATE: 29-40G-1995
ATTORNEY/AGENT INFORMATION:
NAME: Carter, Charles G.
REGISTRATION NUMBER: 35,093
REFERENCE DOCKET NUMBER: 8648.32-TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IMMEDIATE SOURCE:
CLONE: Ubiquitin cleaving enzyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 612-332-9081
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   933 CCTCCTCT 940
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US-08-297-395-62
                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-967-374-13
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US-08-297-395-62
                                                                                                                        COUNTRY:
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                                                                                                                                                                                       Sequence 9, Application US/09063450

Patent No. 6109776

GENERAL INFORMATION:

GENERAL INFORMATION:

TITLE OF INVENTION: Method and System for Computationally Identifying
TITLE OF INVENTION: Clusters Within a Set of Sequences

TITLE OF INVENTION: Clusters Within a Set of Sequences

TITLE OF INVENTION: US/09/063,450

CURRENT FILING DATE: 1998-04-21

NUMBER OF SEQ ID NOS: 38

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 9
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PEATURE:
OTHER INFORMATION: Description of Artificial Sequence:example
OTHER INFORMATION: sequence illustrating a computational methodology
US-09-063-450-9
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Patent No. 4603361
GENERAL INFORMATION:
APPLICANT: Wagner, Fred W.
Stout, Jay
Harriksen, Dennis
Partridge, Bruce
Manning, Shane
TITLE OF INVENTION: Recombinant Polypeptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 55402
COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 8; DB 1; Length 9;
Pred. No. 1.7e+03;
0; Mismatches 0; Indel.
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ATTORNEY/AGENT INFORMATION:
NAME: Carter, Charles G.
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ORGANISM: Artificial Sequence
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US-09-989-789-538/C
US-09-989-789-538/C
| Sequence 538, Application US/09989789
| Patent No. 6588746
| GENERAL INFORMATION:
| TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
| TITLE OF INVENTION: PIPELES BY ZINC FINGERS
| TITLE OF INVENTION: PIPELES BY ZINC FINGERS
| TITLE OF INVENTION: PIPELES BY ZINC FINGERS
| TITLE OF INVENTION: PAGE 001.20 / 511-US2
| CURRENT APPLICATION NUMBER: US/09/989,789
| CURRENT APPLICATION NUMBER: US/09/989,789
| CURRENT APPLICATION NUMBER: US/09/989,789
| SOFTWARE: PATENTING DATE: 2002-03-25
| TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gapa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ) OTHER INFORMATION: Description of Artificial Sequence: example target; OTHER INFORMATION: DNA US-09-989-789-537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 537, Application US/09989789

Sequence 537, Application US/09989789

Patent No. 6588746

GENERAL INFORMATION:
APPLICAMF. LIU, Qiang

TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE

TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS

FILE REPRESENCE: 832-0011.20 / S11-US2

CURRENT APPLICANT. 2002-03-25

CURRENT PILING DATE: 2002-03-25

SOFTWARE: PATENTIN Ver. 2.0

SEQ ID NO 537

LENGTH: 9
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                               8648.32-USD1
                                                                                                                                                                                                                                                                                                                     CLONE: Ubiquitin cleaving enzyme; SEQUENCE DESCRIPTION: SEQ ID NO: 13: US-09-505-991-13
REGISTRATION NUMBER: 35,093
REFERENCE/DOCKET NUMBER: 8648.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-332-9081
INFORMATION FOR SEQ ID NO. 13
SEQUENCE CHARACTERISTICS:
LENGTH: 9 base pairs
TEMPE: nucleic acid
STRANDEDNESS: single
TOPROGY: linear
MOLECULE TYPE: DNA (Genomic)
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 100.
Matches 8; Conservative
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Best Local Similarity
Matches 8; Conserva
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US-09-989-789-537/c
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RESULT 380
PCT-US91-03680-85
Sequence 85, Application PC/TUS9103680
Sequence 85, Application PC/TUS9103680
GENERAL INFORMATION:
APPLICANT: Mateucci, Mark D.
APPLICANT: Mateucci, Mark D.
TITLE OF INVENTION: CROSSLINKING AGENTS WHICH BIND TO THE MAJOR GROOVE OF TITLE OF INVENTION: DUDLEX DNA
TITLE OF INVENTION: DUDLEX DNA
NUMBER OF SEQUENCES: 158
CORRESPONDENCE 158
CORRESPONDENCE MADDRESS:
ADDRESSES:
ADDRESSES:
ADDRESSES:
ATRET: 545 Middlefield Road, Suite 200
CITY: Menlo Park
STARE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
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CTHER INFORMATION: /mod base= OTHER
CTHER INFORMATION: /note= "T-T, linking group o-xyloso (nucleotides OTHER INFORMATION: that have xylose sugar linked via the o-xylene PCT-US91-03680-85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                        Gaps
) OTHER INFORMATION: Description of Artificial Sequence: example target ; OTHER INFORMATION: DNA US-09-989-789-538
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                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                            Length 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
CCMPUTER: IBM PC compatible
CCMPUTER: IBM PC compatible
CCMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
SUFTWARE: Patentin Release #1.0, Version #1.25
SUFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DAM: #35
ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, Kate H.
REGISTRATION NUMBER: 9,959
REFERENCE/DOCKET NUMBER: 
                                                                                                                                                                                   Query Match
11.0%; Score 8; DB 1; Les
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 8; Conservative 0; Mismatches 0;
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LOCATION: 5
LOCATION: 5
OTHER INFORMATION: /mod_base= OTHER
OTHER INFORMATION: /note= "5-methylcytosine"
FEATURE:
NAME/KEY: modified_base
                                                                                                                                                                                                                                                                                                                                                                           935 TCCTCTTC 942
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ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and No. 5641625ris
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and No. 5641625ris
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 43, Application US/08088658
Patent No. 5641625
GENERAL INFORMATION:
APPLICANT: Ecker, David J.
APPLICANT: Buchardt, Ole
APPLICANT: Bedbolm, Michael
APPLICANT: Berg, Rolf H.
APPLICANT: Melsen, Peter E.
APPLICANT: Milegard, Niels E.
TITLE OF INVENTION: HIGH ORDER STRUCTURE AND BINDING OF PEPTIDE
TITLE OF INVENTION: NUCLBIC ACIDS
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11.0%; Score 8; DB 1; Length 10; 100.0%; Pred. No. 2.3e+02; ive 0; Mismatches 0; Indels
                                                                                                                                         COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
CORFWARD SYSTEM: PC-DOS/MS-DOS
SOFTWARD APPLICATION DATA:
APPLICATION NUMBER: US/08/088,658
FILING DATE: 19930702
CLASSIFICATION NUMBER: 08/054,363
FILING DATE: 26-APPLL-1993
ATTONNEY/AGENT INFORMATION:
NAME: Lucci, Joseph
REGISTRATION NUMBER: 33,307
REFERENCE/DOCKET NUMBER: 33,107
REGISTRATION NUMBER: 31,1052
TELEPHONE: 215-568-3100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/088,658
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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Best Local Similarity 100.
Matches 8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
                                                                                                      ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 1993070
CLASSIFICATION: 435
PRIOR APPLICATION DATA
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                                                  STATE: FA
COUNTRY: U.S
TATE: 19103
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PGT-USS6-10108-18/C
Sequence 18, Application PC/TUS9601008
Sequence 18, Application PC/TUS9601008
Settle 18, Application PC/TUS9601008
APPLICANT: Worcester Foundation for APPLICANT: TITLE OF INVENTION: Transcription Inhibitors and Methods of Their Use NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Ecker, David J.
APPLICANT: Buchardt, Ole
APPLICANT: Babolm, Michael
APPLICANT: Nielsen, Peter E.
APPLICANT: Nielsen, Niels B.
APPLICANT: Nielsen, Niels E.
APPLICANT: Milegard, Niels E.
APPLICANT: Milegard, Niels E.
TITLE OF INVENTION: NUCLEIC ACIDS
TITLE OF INVENTION: NUCLEIC ACIDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION:
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INPORMATION:
NAME: Kerner, Ann-Louise
REGISTRATION NUMBER: 33,523
REFERENCE/DOCKET NUMBER: HYZ-037PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-330-1310

TELEPHONE: 617-330-1311

TELEPHONE: 617-330-1311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/01008
                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11.0%; Sc. 100.0%; Pre
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Patent No. 5641625
                                                                                                                                                                                                                                                                                                                                   3: Lappin & Kusmer
200 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 18: SEQUENCE CHARACTERISTICS: LENGTH: 9 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                Massachusetts
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: nucleic acid
STRANDEDNESS: singl
      TTTTCTTT 915
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          945 TGGTTTAA 952
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                                                                                                                                                                                                                                                                                                                                                         STREET: 200 St
CITY: Boston
STATE: Massach
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: line
MOLECULE TYPE: C
HYPOTHETICAL: NC
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                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: U
                                                                                                                                                                                                                                                                                                                                     ADDRESSEE:
      908
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Gaps

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US-08-686-116A-49/c
US-08-686-116A-49/c

US-08-686-116A-49/c

Sequence 49, Application US/08686116A

Patent No. 514331

TITLE OF INVENTION: Peptide Nucleic Acids Having Enhanced
TITLE OF INVENTION: Pinding Affinity, Sequence Specificity

Patent No. 514331

TITLE OP INVENTION: ans Solubility

NUMBER OF SEQUENCES: 53

CORRESPONDENCE ADDRESS:

ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5714331ris LLP

STREET: One Liberty Place - 46th Floor

CITY: Philadelphia

STATE: PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                       Gaps
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US-08-686-116A-51/c
Sequence 1. Application US/08686116A
Patent No. 5714331
GENERAL INFORMATION:
APPLICATION PEDIAGE at 1.
TILLE OF INVENTION: Peptide Nucleic Acids Having Enhanced
TITLE OF INVENTION: Binding Affinity, Sequence Specificity
                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
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Pred. No. 2.3e+02;
Pred. No. 2.3e+02;
Mismatches 0;
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100.0%; Pred. No. ...
... 0; Mismatches
                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: U.S.A.

ZIP: 19103

ZIP: 19103

ZIP: 19103

ZIP: 19104

ZIP: 19103

ZOMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch disk, 1.44 Mb
COMPUTER: IBM PC compacible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Wordberfect 6.1

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/686,116A

FILING DATE: 1011/24, 1996

CLASSIFFCATION: 481

FILING DATE: 22-MOV-1993

ATTORNEY/AGENT INFORMATION:
PREJETRATION NUMBER: 38,325

REFERENCE/DOCKET NUMBER: 38,325

REFERENCE/DOCKET NUMBER: 38,325

REFERENCE/DOCKET NUMBER: 315.2271

TELECOMMUNICATION INFORMATION:
TELEFAX: 215-568-3100

TELEFAX: 215-568-3109

TELEFAX: 215-568-3139

INFORMATION FOR SEQ ID NO: 49:
SEQUENCE FRARACTERISTICS:
LENGTH: 10 bases

LENGTH: 10 bases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ans Solubility
53
  100.08;
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Best Local Similarity 100.
...rhes 8; Conservative
Best Local Similarity 100.
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TYPE: nucleic acid
; STRANDEDNESS: single
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US-08-686-116A-49
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                                                                     906 CATTITCT 913
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TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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US-08-122-433-39/C
US-08-122-433-39/C
Sequence 39, Application US/08122433
Sequence 39, Application US/08122433
Sequence 39, Application US/08122433
Sequence 39, Application US/08122433
SEGUENCE INFORMATION:
TITLE OF INVENTION: OLIGODEOXYNUCLEOTIDES AND
TITLE OF INVENTION: OLIGONUCLEOTIDES USEFUL AS DECOYS FOR PROTEINS WHICH
TITLE OF INVENTION: OLIGONUCLEOTIDES USEFUL AS DECOYS FOR PROTEINS WHICH
TITLE OF INVENTION: SELECTIVELY BIND TO DEFINED DNA SEQUENCES
NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS.
STREET: 444 SOUTH Flower Street, Suite 2000
CITY: Los Angeles
STATE: California
COUNTRY: USA
TITLE OF TABLE CALIFORNIA TOWN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CZPP: 90071

CZPP: 90071

CZPP: 90071

MEDIUM TYPE: Floppy disk
CCMPOTTER: END PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/122,433
FILING DATE: 22-SEP-1993
CLASSTRICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/687,337
FILING DATE: 18-APR-1991
ATTORNEY/AGENT INPORMATION:
NAME: Reflex Reflex: Stephen E.
REGISTRATION NUMBER: 931 9308
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION OF SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 base pairs
TYPE: mocleic acid
TYPE: mocleic acid
TYPE: mocleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1;
                   FILING DATE: 26-ARRIL-1993
ATTORNEY/AGENT INFORMATION:
NAME: Lucci, Joseph
REGISTRATION NUMBER: 33,307
REFERENCE/DOCKET NUMBER: 181S-1052
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-310
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11.0%; Score 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: other nucleic acid US-08-122-433-39
  APPLICATION NUMBER: 08/054,363
                                                                                                                                                                                                                           TYPE: nucleic acid STRANDEDNESS: single ; TOPOLOGY: linear US-08-088-658-43
                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 100.
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 908 TITICITY 915
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S-08-484-51/c
Sequence 51, Application US/08685484
Patent No. 5719260.

Patent No. 5719260.

Patent No. 5719260.

APPLICANT: Buchardt et al.
TITLE OF INVENTION: Peptide Nucleic Acids Having Amino Acid
TITLE OF INVENTION: Side Chains
NUMBER OF SEQUENCES: 53
CORRESPENDENCE ADDRESS:
ADDRESSEE: WOOGCOCK Washburn Kurtz Mackiewicz & No. 5719262ris LLP
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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11.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 8; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1; Length 10; 2.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       11.0%; Score 8; DB 1
100.0%; Pred. No. 2.3
tive 0; Mismatches
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COMPUTER READABLE FORM:

COMPUTER: 19103

COMPUTER: 3.5 inch disk, 1.44 Mb

COMPUTER: 18M PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WordPerfect 6.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/685,484

FILING DATE: 24-JUL-1996

CLASSIFTCATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/108,591

FILING DATE: 22-NOV-1993

ATTONNEY/AGENT INFORMATION:

NAME: Michael P. Straher

REGISTRATION NUMBER: 38,325
38,325
ISIS-2270
                                          REFERENCE/DOCKET NUMBER: ISI
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 bases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: IS
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 51:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                            Ouery Match
Best Local Similarity 100.
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           215-568-3439
                                                                                                                                                                                                                                                                                     TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 10 bases
TYPE: nucleic acid
STRANDEDNESS: single
US-08-685-484-51
                        REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  908 TTTTCTTT 915
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                                                                                                                                                                                                                                                                                                                                                 ; TOPOLOGY: linear
US-08-685-484-49
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Ph
STATE: P
COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         à
              CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5714331ris LLP
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-685-484-49/c
US-08-685-484-49/c
| Sequence 49, Application US/08685484 |
| Parent No. 5719262 |
| TITLE OF INVENTION: Peptide Nucleic Acids Having Amino Acid TITLE OF INVENTION: Side Chains |
| NUMBER OF SEQUENCES: 53 |
| CORRESPONDENCE ADDRESS: ADDRES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                    COMPUTER READBLE FORM:
MEDIUM TYPE: 3.5 inch disk, 1.44 Mb
COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 6.1
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 08/108,591
FILING DATE: 22-NOV-1993
ATTORNEY AGENT INFORMATION:
NAME: MACHAEL P. STRAHER
REGISTRATION NUMBER: 38,325
REFERENCE/DOCKET NUMBER: 1SIS-2271
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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ZIP: 19103.

ZIP: 19103.

COMPUTER READBLE FORM:

MEDIUM TYPE: 3.5 inch disk, 1.44 Mb
COMPUTER: IBM PC compatible

COMPUTER: SYSTEM: PC-DoS/MS-DOS
SOFTWARE: WordPerfect 6.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/685,484
FILING DATE: 24-UUL-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ilarity 100.0%; Pred. Nc
Conservative 0; Mismat
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APPLICATION DATA:
APPLICATION NUMBER: 08/108,591
FILING DATE: 22-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Michael P. Straher
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 51:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  215-568-3439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        908 TTTTCTTT 915
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Best Local Similarity
Matches 8; Conserva
                                                                                                                                                                                   U.S.A.
                                                                                                                                                                                                                  19103
                                                                                                                                                       PA
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US-08-686-116A-51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ΡA
                                                                                                                                                                                   COUNTRY:
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WESULT 391

WESULT 391

WESULT 391

WESULT 391

WESULT 391

WESULT 391

WESULT 301

Sequence 56, Application US/08686113A

Patent No. 576685

TITLE OF INVENTION: Peptide Nucleic Acids Having Enhanced

TITLE OF INVENTION: Affinity And Sequence Specificity

TITLE OF INVENTION: Affinity And Sequence Specificity

TITLE OF INVENTION: Affinity And Sequence Specificity

NUMBER OF SEQUENCES:

ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and No. 5766855ris

STRIE: ADDRESSE: Moodcock Washburn Kurtz Mackiewicz and No. 5766855ris

STRIE: Philadelphia

STRIE: Philadelphia

COMPUTER: DA

ZIP: 19103

COMPUTER: TEM PC compatible

COMPUTER: Norderefect 6.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: 08/108,591

FILING DATE: 22-NOV-1993

ATTORNEY/AGENT INFORMATION:

NAME: Michael P. Straher

NAME: Michael P. Straher

NAME: Wichael P. Straher

REFERENCE/DOCKET NUMBER: 1815-2273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
11.0%; Score 8; DB 1
Best Local Similarity 100.0%; Pred. No. 2.3
Matches 8; Conservative 0; Mismatches
                                                  COMPUTER REDABLE FORM:
MEDIUM TYPE: 3.5 inch disk, 1.44 Mb COMPUTER: IBM PC comparible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: WORTGPE-fect 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/847,108
FILING DATE: 01-MAY-1997
CLASSIFICATION BATA:
APPLICATION NUMBER: 08/686,116
FILING DATE: 10-10, 24, 1996
APPLICATION NUMBER: 08/108,591
FILING DATE: 22-NOV-1993
ATTORNEY/AGENT INFORMATION:
MAME: MECHANER: 38,325
REFERENCE/DOCKET NUMBER: 15IS-2271
TELECOMMUTCATION INPORMATION:
TELEPHONE: 215-568-310
TELEPHONE: 215-568-310
TELEPHONE: 215-568-310
TELEPHONE: 215-568-310
TELEPHONE: 10-568-310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: nucleic acid
STRANDEDNESS: single
                                 ZIP: 19103
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      908 TITICITY 915
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TOPOLOGY: linear
US-08-847-108-51
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U.S.A.
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| Sequence 51, Application US/08847108
| Patent No. 5736336
| GENERAL INFORMATION:
| APPLICANT: Buchardt et al.
| TITLE OF INVENTION: Binding Affinity, Sequence Specificity
| TITLE OF INVENTION: and Solubility
| Patent No. 5736336
| TITLE OF INVENTION: and Solubility
| WUMBER OF SEQUENCES: 53
| CORRESPONDENCE ADDRESS:
| ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5736336ris LLP
| STREET: One Liberty Place - 46th Floor
| CITY: Phladelphia
| STATE: PA
                                                                                            Sequence 49, Application US/08847108
Fatent No. 5736336
GENERAL INFORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION:
FACHER NO. 5736336
FITLE OF INVENTION:
TITLE OF INVENTION:
FATEL OF SEQUENCES:
FATEL OF S
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11.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 8; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Philadelphia
CITY: Philadelphia
STATE: PA
COUNTRY: U.S.A.
ZIP: 19103

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch disk, 1.44 MD
COMPUTER: Wordberfect 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/847,108
FILING DATE: 0.1-MAY-1997
CLASSIFICATION DATA:
APPLICATION NUMBER: 08/686,116
FILING DATE: 0.1-MAY-1997
FILING DATE: 1.1-MAY-1997
FILING DATE: 2.1-MAY-1993
FILING DATE: 2.1-WAY-1993
FILING DATE: 2.1-S68-3439
FILING DATE: 215-S68-3439
FILING DATE: 215-S68-3439
FILING DATE: 215-S68-3439
FILING DATE: 10-DASSES
FREFERENCE CHARACTERISTICS:
FIEUGHER: UNDERSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      908 TTTTCTTT 915
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US-08-847-108-51/c
                                                                               US-08-847-108-49/c
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Gaps

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COUNTRY: U.S.A.
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch disk, 1.44 MD
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/847,095A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ISIS-2270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
CLASSIFICATION
PRICA PEPLICATION DATA:
PRICA PEPLICATION DATA:
APPLICATION NUMBER: 08/685,484
FILING DATE: 24-UUL-1996
APPLICATION NUMBER: 08/108,591
FILING DATE: 22-NOV-1993
ATVOREY/AGATI INFORMATION:
NAME: MICHAEL P. Straher
REGISTRATION NUMBER: 38,325
REBERENCE/DOCKET NUMBER: 1SIS-227
TELEPHONE: 215-568-3100
TELEPHONE: 215-568-3100
INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Fig.
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STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       908 TTTTCTTT 915
                                                                                                                                                                                                                                           STREET: One Libert
CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity Matches 8; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10 Trirchir 3
                       JS-08-847-095A-49/c
                                                                                                                                                                                                                                                                                       STATE: PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-847-095A-49
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Patent No. 5766855
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and No. 5766855ris
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
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; Patent No. 5766855
; GENERAL INFORMATION:
; APPLICANT: Buchardt et al.
; TITLE OF INVENTION: Peptide Nucleic Acids Having Enhanced
; TITLE OF INVENTION: Affinity And Sequence Specificity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11.0%; Score 8; DB 1; Length 10; 100.0%; Pred. No. 2.3e+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                             DB 1; Length 10;
                                                                                                                                                                                                                                           Query Match
11.0%; Score 8; DB 1; Len
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 8; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READBLE FORM:
MEDIUM TYPE: 3.5 inch disk, 1.44 Mb
COMPUTER: 18M PC comparible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/686,113A
FILING DATE: July 24, 1996
CLASSIFICATION NUMBER: US/08/686,113A
FILING DATE: 22-NOV-1993
APTONEY/AGENT INFORMATION:
NAME: MICHAEL STRATION NUMBER: 38,325
REGISTRATION NUMBER: 38,325
REGISTRATION NUMBER: 38,325
RECIERRNCE/DOCKET NUMBER: 1515-2773
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION
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                  TELEPHONE: 215-568-3100
TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 5
SEQUENCE CHARACTERISTICS:
LENGTH: 10 bases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           nucleic acid
EDNESS: single
GY: linear
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                                                                                                                             TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                 908 TTTTCTTT 915
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               908 TTTTCTTT 915
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Best Local Similarity
Matches 8; Conserv
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US-08-686-113A-58/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: U
ZIP: 19103
                                                                                                                                                                            : TOPOLOGY:
US-08-686-113A-56
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Sequence 49, Application US/08847095A
Patent No. 5786461
GENERAL INFORMATION:
APPLICANT: Buchardt et al.
TITLE OF INVENTION: Peptide Nucleic Acids Having Amino Acid
TITLE OF INVENTION: Side Chains
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSER: Woodcock Washburn Kurtz Mackiewicz & No. 5786461ris LLP
STREET: One Liberty Place - 46th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5786461ris LLP
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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Sequence 51, Application US/08847095A
Patent No. 5786461
GENERAL INFORMATION:
APPLICANT: Buchardt et al.
TITLE OF INVENTION: Peptide Nucleic Acids Having Amino Acid
TITLE OF INVENTION: Side Chains
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11.0%; Score 8; DB 1; Length 10; 100.0%; Pred. No. 2.3e+02; tive 0; Mismatches 0; Indels
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MEDIUM TYPE: 3.5 inch disk, 1.44 Mb
COMPUTER: IBM PC compatible
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FEATURE
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US-08-597-467-8/C

i Sequence 8, Application US/08597467

i Patent No. 5824787

i GENERAL INFORMATION:
APPLICANT: SINGER, Paul A.
ITILE OF INVENTION: POLYNUCLEOTIDE SIZING REAGENT
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Spensley Horn Jubas & Lubitz
STREET: 1880 Century Park East, Suite 500
CITY: Los Angeles
STATE: California
COUNTRY: USA

ZIP: 90067
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: PUBPY disk.
MEDIUM TYPE: Floppy disk.
COMPUTER: ENAPPH disk.
COMPUTER: ENAPPH disk.
COMPUTER: ENAPPH disk.
COMPUTER: ENAPPH DECIDOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/597,467
FILING DATE: 03-DEC-1993
APPLICATION NUMBER: US 08/161,901
FILING DATE: 03-DEC-1993
ATYCRNEY/AGENT INFORMATION:
NAME: Wetherell, Jr., Ph.D., John R.
REGISTRATION NUMBER: Ph.D., John R.
REGISTRATION NUMBER: Ph.D., John R.
REGISTRATION NUMBER: Ph.D., John R.
TELEPHON: (619) 455-5110
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 base pairs
TYPE: nucleic acid
                                                                             APPLICATION:
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/685,484
FILING DATE: 24-UUL-1996
APPLICATION NUMBER: 08/108,591
FILING DATE: 22-NOV-1993
ATTORNEY/ACENT INFORMATION:
NAME: Michael P. Straher:
REGISTRATION NUMBER: 38,325
REFERENCE/DOCKET NUMBER: 1815-2270
TELEPONE: 215-568-3100
TELEPONE: 215-568-3101
TELEPONE: 215-568-3101
TELEPAR: 215-568-3101
TELEPAR: 10 bases
INPORMATION FOR SEQ ID NO: 51:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 bases
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
OPERATING SYSTEM: PC-DOS/MS-DOS SUSTEMER: WordPerfect 6.1
SURFENT APPLICATION DATA:
APPLICATION NUMBER: US/08/847,095A
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Best Local Similarity 100.
Matches 8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 396
US-08-590-511-24/C

Sequence 24, Application US/08590571
Patent No. 5861246
GENERAL INFORMATION:
APPLICANT: Sherman Weissman and Girish N. Nallur
ITILE OF INVENTION: MULTIPLE SELECTION PROCESS
NUMBER OF SEQUENCES: 66
CORRESPONDENCES: 66
CORRESPONDENCES: 66
CORRESPONDENCES: ASSOCiates
STREET: 25 SKytop Drive
CITY: Trumbull
STRATE: Connecticut
COUNTRY: USA
ZIP: 06611
STREET: D6611
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: Macintosh
OFFERATION SYSTEM: MS-DOS
SOFTWARE: Microsoft Word 5.1
CURSTRICATION NUMBER: US/08/590,571
FILING SYSTEM: NS-DOS
SOFTWARE: Microsoft Word 5.1
CURSTRICATION NUMBER: US/08/590,571
FILING APPLICATION INFORMATION:
NAME: GGOOTGE NUMBER: Vale
TELEPHONE: (201)268-1951
TELEPHONE: (201)268-1951
TELEPHONE: (201)268-1951
TELEPHONE: LENGTH ON ONE SEQ ID NO: 24:
ETELETAK: (201)268-1951
TELETAK: (201)268-1951
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STRANDEDNESS: single
TOPOLCGY: linear
MOLECULE TYPE: DNA (genomic)
IMMEDIATE SOURCE:
CLONE: ED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              960 CTACCAAC 967
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                                                                                                                                                                                                                       ; NAME/KEY:
; LOCATION:
US-08-597-467-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-590-571-24
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9 TTTTCTTT 2
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Sequence 43, Application US/08471907A

APPLICANT: Ecker, David J.

APPLICANT: Beholm, Michael

APPLICANT: Mielsen, Peter E.

APPLICANT: Milesen, NUCLEIC ACIDS

NUMBER OF SEQUENCES: 56

CORRESPONDENCE ADDRESS:

ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and No. 5986053ris

CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                APPLICANT: Buchardt, Ole
APPLICANT: Egholm, Michael
APPLICANT: Nelsen, Peter E.
APPLICANT: Nelsen, Peter E.
APPLICANT: Milegaard, Niels E.
TITLE OF INVENTION: HICH ORDER STRUCTURE AND BINDING OF PEPTIDE
TITLE OF INVENTION: NUCLEIC ACIDS
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSES: Woodcock Washburn Kurtz Mackiewicz and No. 5986053ris
STREET: One Liberty Place - 46th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471,907A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1; Le:
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100.0%; Pred. No. 2.3
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
CLASSIPFICATION
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/089,658
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
ATTORNEY/ACENT INPORMATION:
NAME: LUCCI, JOSEPH
REGISTRATION NUMBER: 33,307
REFERENCE/DOCKET NUMBER: ISIS
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
David J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
STRANDEDNESS: double
;
TOPOLOGY: linear
US-08-471-907A-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELBFAX: 215-568-3439
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 100.
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                  COUNTRY: U.S.A.
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
Ecker, Dar
Buchardt,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                908 TITICITY 915
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COUNTRY: U.S.A.
ZIP: 19103
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COMPUTER ENABLE PROBE COND.

MEDITAL TPER: PLOUGH COMMENTED.

CONTENTING STEERS. PLOUGH COMMENTED.

CONTENTING STEERS. PLOUGH COMMENTED.

SEPTION ON THE PROBE STEERS. PLOUGH COMMENTED.

FILING DATE.

PRICE AND DATE.

PRICE AND
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GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Deacon, Nicholas J.

APPLICANT: Mechae, Danifer C.

APPLICANT: Cover, Jennifer C.

APPLICANT: Crowe, Suzane

APPLICANT: Crowe, David

TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1

NUMBER OF SEQUENCES: 800

CORRESPONDENCE ADDRESS:

ADDRESSEE: SCULIY, SCOLT, Murphy & Presser

STREE: New York

COUNTY: United States

CITY: Garden City Plaza

CITY: Garden City Plaza

CITY: Garden City Plaza

CONFUTER: New York

CONFUTER: New York

CONFUTER: New York

CONFUTER: IBM PC compatible

OOFERATING SYSTER: PCODS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

MEDICATION NUMBER: 31,346

FILING DATE: 14-FEB-1995

CLASSIFICATION NUMBER: 31,346

FELECOMMUNICATION NUMBER: 9606

TELECOMMUNICATION NUMBER: 9606

T
Sequence 228, Application US/08388353
Patent No. 6010895
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
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11.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 8; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                11.0%; Score 8; DB 1; Length 10; 100.0%; Pred. No. 2.3e+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: Scully, Scott, Murphy & Presser
STREET: 400 Garden City Plaza
CITY: Garden City Plaza
CITY: Garden City
STATE: Nutred States
COUNTRY: United States
COMPUTER: Dispy disk
COMPUTER: FLADABLE FORM:
MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC-DOS/NS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURSTING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURSTING DATE: 14-FEB-1995
CLASSIFICATION: WUMBER: 31,346
REGISTRATION NUMBER: 31,346
REGISTRATION FOR SEQ ID NO: 227:
SEQUENCE CHARACTERISTICS:
LEBRGTH: 10 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Deacon, Nicholas J.
APPLICANT: Dearmont, Jennifer C.
APPLICANT: McPhee, Dale A.
APPLICANT: Crowe, Suzanne
APPLICANT: Crowe, Suzanne
APPLICANT: Cooper, David
TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
NUMBER OF SEQUENCES: 800
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 400
US-08-388-353-227/c
Sequence 227, Application US/08388353
; Fartent No. 6010895
   ; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-388-353-181
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MOLECULE TYPE: DNA (genomic)

US-08-388-353-227
                                                                                                                                                                                                                                                Query Match
Best Local Similarity 100.
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. 0 Gaps 0 Query Match 11.0%; Score 8; DB 1; Length 10; Best Local Similarity 100.0%; Pred. No. 2.38+02; Matches 8; Conservative 0; Mismatches 0; Indels RESULT 402
US-08-388-35-231/C
isequence 231, Application US/0838353
isequence 231, Application US/08453
isequence 231, Appli , MOLECULE TYPE: DNA (genomic) US-08-388-353-228 ZIP: 11530 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk 914 TIGGICIT 921 9 TTGGTCTT 2 linear TOPOLOGY:

914 TIGGICTT 921

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RESULT 401 US-08-388-353-228/c

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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMFUTER: IBM PC Compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURREWY APPLICATION DATA:

APPLICATION NUMBER: US/08/388,353

FILING DATE: 14-FEB1995

CLASSIFICATION NUMBER: US/08/388,353

FLING DATA: 14-78B1995

CLASSIFICATION NUMBER: 9506

TELECOMMUNICATION: RATA 3.3

TELEPRATION NUMBER: 9606

TELECOMMUNICATION INFORMATION:

TELEPRATION NUMBER: 9606

TELECOMMUNICATION INFORMATION:

TELEPRATION SEQ ID NO: 273: SEQUENCE CHARACTERISTICS:

LENGTH: 10 base pairs

TURDIANDENDES: single

STRANDEDNES: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Deacon, Nicholas J.
APPLICANT: Deacon, Nicholas J.
APPLICANT: Learmont, Jennifer C.
APPLICANT: Morbhe, Dale A.
APPLICANT: Croper, Dale A.
APPLICANT: Croper, David
TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
TITLE OF SECURCES: 800
CORRESPONDENCE ADDRESS:
ADDRESSEE: Scully, Scott, Murphy & Presser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Scully, Scott, Murphy & Presser STREET: 400 Garden City Plaza CITY: Garden City STATE: New York COUNTRY: United States
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 273, Application US/08388353
Patent No. 6010895
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 405
US-08-388-353-274/c
; Sequence 274, Application US/08388353
; Patent No. 6010895
; GENERAL INFORMATION:
          ; STRANDEDNESS: single TOPOLOGY: linear COLECULE TYPE: DNA (genomic) US-08-388-353-232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                  Query Match
Best Local Similarity 100.0
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 100.
Matches 8; Conservative
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US-08-388-353-273/c
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MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/388,353
FILING DATE: 14-FEB-1995
CLASSIPICATION: 424
ATTORNEY/AGENT INPORMATION:
NAME: DIGIGILO, Frank S.
REGISTRATION NUMBER: 31,346
REPERENCE/DOCKET NUMBER: 9606
TELEPAX: (516) 742-4343
TELEPAX: (516) 742-4343
TELEPAX: (516) 742-4343
TELEFAX: (516) 742-4345
TELEFAX: (516) 742-4365
TELEFAX: (516) 742
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
SOUTHARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/389,353
FILING DATE: 14-FEB-1995
CLASSFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: DiGABJIO, Frank S.
REGISTRATION NUMBER: 31,346
REFERRNCE/DOCKET NUMBER: 9606
TELECOMMUNICATION INFORMATION:
TELEPRAX: (516) 742-4343
TELEPRAX: (516) 742-4346
TELECOMMUNICATION INCRANTION:
TELEPRAX: (516) 742-4366
TELECOMMUNICATION INCRANTION:
TELEPRAX: (516) 742-4366
TELECOMMUNICATION INCRANTION:
TELEPRAX: (516) 742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 231:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Deacon, Nicholas J.
APPLICANT: Deacon, Jennifer C.
APPLICANT: Merche, Jeale A.
APPLICANT: Crowe, Suzanne
APPLICANT: Crower, David
TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
WUMBER OF SEQUENCES: 800
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AUDRESSE: Scully, Scott, Murphy & Presser STREET: 400 Garden City Plaza CITY: Garden City STATE: New York COUNTRY: United States ZIP: 11530 COMPINED: TO STATE: New York COUNTRY: United States
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 232, Application US/08388353; Patent No. 6010895; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-388-353-231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 100.
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    941 TCATTGGT 948
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100.0%; Pred. No. 2.3
tive 0; Mismatches
          MBER: US/08/388,353
14-FEB-1995
       CURRENT AFFILCATION DATE:

CLASSIFICATION NUMBER: US/08/388, FILING DATE: 14-FEB-195

CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Didiglio, Frank S.
REGISTRATION NUMBER: 31,346
REFRENCE/DOCKET NUMBER: 9606
TELEPHONE: (516) 742-4343
TELEPHONE: (516) 742-4343
TELERX: (516) 742-436
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 308: SEQUENCE CHARACTERISTICS: LENGTH: 10 base pairs
TYPE: nucleic acid
STRANDENESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                          , MOLECULE TYPE: DNA (genomic)
US-08-388-353-308
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nucleic acid
DEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 100.
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              910 TICTITGG 917
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STRANDEDNESS:
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0
          APPLICANT: Learmont, Jennifer C.
APPLICANT: McPhee, Dale A.
APPLICANT: Crowe, Suzanne
APPLICANT: Crowe, Suzanne
APPLICANT: Crowe, Suzanne
APPLICANT: Crowe, David
TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
NUMBER OF SEQUENCES: 800
CORRESPONDERS: 800
CORRESPONDERS: ADDERSS:
ADDRESSEE: Scully, Scott, Murphy & Presser
STRATE: New York
COUNTRY: United States
CITY: Garden City
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPATH:
APPLICATION TYPE: TOPOY Gisk
COMPUTER: LAS ADDRESS: NOS SOFTANCES: 1424
CLASSIFICATION NUMBER: US/08/388,353
FILING DATE: 14-FEB-1995
CLASSIFICATION NUMBER: 31,346
REGISTRATION NUMB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1; Length 10; 2.3e+02;
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Patent No. 6010895
GENERAL INFORMATION
APPLICANT: Learmont, Jennifer C.
APPLICANT: Crowe, Suzanne
APPLICANT: Crowe, Suzanne
APPLICANT: Crowe, Suzanne
TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
NUMBER OF SEQUENCES: 800
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Patentin Release #1.0, Version #1.25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 11.0%; Score 8; DB 1
Best Local Similarity 100.0%; Pred. No. 2.3
Matches 8; Conservative 0; Mismatches
Deacon, Nicholas J.
Learmont, Jennifer C.
McPhee, Dale A.
Crowe, Suzanne
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    908 TTTTCTTT 915
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US-08-488-551B-228/c; Sequence 228, Application US/08488551B; Patent No. 6015661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (516) 742-4366
INFORMATION FOR SEQ ID NO: 227:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear MOLECULE TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10 Trecrer 3
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Best Local Similarity
Matches 8; Conserv
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                                           11.0%; Score 8; DB 1; Length 10; 100.0%; Pred. No. 2.3e+02; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE: GARGEN CALL
STATE: GARGEN CALL
ZIF: 1153-0-0299
COMPUTER: BABDABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: THEN FO Compartible
COMPUTER: THEN FO COMPARISH
SOUTHWARE: PRESENCE #1.0, Version #1.25
COMPUTER: THEN FO COMPARISH
APPLICATION NUMBER: US/08/488,551B
FILING DATE: 14-FEB-1994
APPLICATION NUMBER: PM3864 (AU)
FILING DATE: 11-FEB-1994
APPLICATION NUMBER: PW3024
APPLICATION NUMBER: US 08/383,353
FILING DATE: 17-FEB-1995
APPLICATION NUMBER: US 08/383,353
FILING DATE: 17-MAY-1995
APPLICATION NUMBER: PW3021/95
FILING DATE: 17-MAY-1995
APPLICATION NUMBER: PW3021/95
FILING DATE: 17-MAY-1995
ATCHER FRANK S: DIGIGILO
REFERENCE/DOCKET NUMBER: 9606Z
TELECOMMUNICATION INFORMATION:
FRIEDMANE: FRANK S: DIGIGILO
REFERENCE/FOCKET NUMBER: 9606Z
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Nicholas J. Deacon
APPLICANT: Dale A. McPhee
APPLICANT: David Cooper
TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
NUMBER OF SEQUENCES: 841
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11.0%; Score 8; DB 1; Le. 100.0%; Pred. No. 2.3e+02; tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER STREET: 400 GARDEN GITY PLAZA CITY: GARDEN CITY
                                                                                                                                                                                                                                                 RESULT 408
12.08-488-551B-181/c
15.8equence 181, Application US/08488551B
1 Parent No. 6015661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (516) 742-4366
INFORMATION FOR SEQ ID NO: 181:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (516) 742-4343
                                                              Best Local Similarity 100.
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                    910 TTCTTTGG 917
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  934 CTCCTCTT 941
US-08-388-353-309
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                                           Query Match
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RESULT 409 US-08-488-551B-227/c

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| Sequence 227, Application US/08488551B |
| Patent No. 601561 |
| GENERAL INFORMATION: |
| APPLICANT: Nicholas J. Deacon |
| APPLICANT: David Cooper |
| TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1 |
| NUMBER OF SEQUENCES: 841 |
| CORRESPONDENCE ADDRESS: |
| ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER |
| STREET: 400 GRADEN CITY PLAZA |
| COURTEST |
| COURTEST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 8; DB 1; Length 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE: GARDEN CLII
STATE: MEM YORK
COUNTRY: U.S.A.
21P: 11530-0299
COMPUTER: ELEMPT Compatible
COMPUTER: TEMPT COMPATIBLE
COMPUTER: PATENTIAN NAMER: DATA:
APPLICATION NUMBER: PM364 (AU)
FILING DATE: 12-FEB-1994
APPLICATION NUMBER: PM3021/95
FILING DATE: 12-FEB-1994
APPLICATION NUMBER: US 08/388,353
FILING DATE: 17-ARX-1995
APPLICATION NUMBER: US 08/388,353
FILING DATE: 17-ARX-1995
APPLICATION NUMBER: PM3021/95
FILING DATE: 17-ARX-1995
APPLICATION NUMBER: PM3021/95
FILING DATE: 17-ARX-1995
ATTORNEY/AGENT INFORMATION:
NAME: FRANK S. DIGIGIO
REFERENCE/POCKET NUMBER: 9606Z
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
TELEPHONE: (516) 742-4343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INCRMATION:
APPLICANT: Nicholas J. Deacon
APPLICANT: Daie A. McDer
APPLICANT: Daie A. McDer
APPLICANT: David Cooper
TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
CORRESPONDENCE ADDRESS:
ADDRESSER: SCULLY, SCOTT, MURPHY & PRESSER
STREET: 400 GARDEN CITY PLAZA
CITY: GARDEN CITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SSEE: SCULLY, SCOTT, MURPHY & PRESSER : 400 GARDEN CITY PLAZA GARDEN CITY
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US-US-WES-DAID-434/C

| GENERAL INFORMATION:
| PATENT NO. 601561
| CENERAL INFORMATION:
| APPLICANT: Nicholas J. Deacon
| APPLICANT: David Cooper
| TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
| NUMBER OF SCUENCES: 404.
| CORRESPONDENCE ADDRESS:
| ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
| STREET: GARDEN CITY FLAZA
| CITY: GARDEN CITY FLAZA
| CITY: GARDEN CITY FLAZA
| CITY: GARDEN CITY FLAZA
| COUNTRY: U.S.A.
| COUNTRY: U.S.A.
| STREET: NEW YORK | COOPERATION FREADABLE FOODS // SCOTT // STREET: NEW YORK |
| CONTRY: ISA PC Compatible FOODS // SCOTT // STREET: PATENTIAN PC-DOS/MS-DOS SOFTWARE: PATENTIAN PC-DOS/MS-DOS SOFTWARE: PATENTIAN PC-DOS/MS-DOS SOFTWARE: PATENTIAN DATA: APPLICATION DATA: APPLICATION NUMBER: PRINGO (AU) FILING DATE: 14-FEB-1994 | APPLICATION NUMBER: PRAGO (AU) FILING DATE: 13-DEC-1994 | APPLICATION NUMBER: PRAGO (AU) FILING DATE: 17-PEB-1995 | APPLICATION NUMBER: US 08/388,353 | FILING DATE: 17-PEB-1995 | APPLICATION NUMBER: WAY-1995 | ATTICATION NUMBER: WAY-1995 | ATTICATION NUMBER: WAY-1995 | ATTICATION NUMBER: RANAY-1995 | ATTICATION NUMBER: PRAGO (AU) FILING DATE: 17-PEB-1995 | ATTICATION NUMBER: WAY-1995 | ATTICATION NUMBER: PRAMY S. DIGIGALO. OF ACAPA
| DECENDENT NOTION NUMBER: PRAMY S. DIGIGALO. OF ACAPA
| DECENDENT NOTION NUMBER: PRAMY S. DIGIGALO. OF ACAPA
| DECENDENT NOTION NUMBER: PRAMY S. DIGIGALO. OF ACAPA
| DECENDENT NOTION NUMBER: PRAMY S. DIGIGALO. OF ACAPA
| DECENDENT NOTION NUMBER: PRAMY S. DIGIGALO. OF ACAPA
| DECENDENT NOTION NUMBER: PRAMY S. DIGIGATION N
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Best Local Similarity 100.0%; Pred. No. 2.3
Matches 8; Conservative 0; Mismatches
                                          APPLICATION NUMBER: PM4002 (Au)
FILING DATE: 21-FEB-1994
APPLICATION NUMBER: PN0284 (AU)
FILING DATE: 33-DEC-1994
APPLICATION NUMBER: US 08/388,353
FILING DATE: 14-FEB-1995
APPLICATION NUMBER: US 08/389,353
FILING DATE: 17-MAY-1995
ATTORNEY/AGENT INFORMATION:
NAME: FRANK S. DIGIGILO:
NAME: FRANK S. DIGIGILO:
NAME: FRANK S. DIGIGILO:
NAME: FRANK S. DIGIGILO:
NEPERBENCE/DOCKET NUMBER: 9606Z
TELEGOMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
TELEPHONE: (516) 742-4343
TELEPHONE: (516) 742-4343
TELEPHONE: G16) 742-4366
INFORMATION FOR EQ. ID NO: 231:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-488-551B-231
                                                                                                                                                                                                                                                                         US 08/388,353
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      941 TCATTGGT 948
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 412
US-08-488-551B-232/c
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US-08-488-551B-231/C
Sequence 231, Application US/08488551B
Patent No. 6015661
Sequence 231, Descen
Patent No. 6015661
SEREAL INFORMATION:
APPLICANT: Nicholas J. Deacon
APPLICANT: Dale A. McPhee
APPLICANT: Dale A. McPhee
APPLICANT: Dale A. McPhee
APPLICANT: Dale A. McPhee
APPLICANT: SCOPEX
STATE: OF SEQUENCES: 841
CORRESPONDENCES: SCULY, SCOTT, MURPHY & PRESSER
STATE: 400 GARDEN CITY PLAZA
CITY: GARDEN CITY
STATE: NEW YORK
COUNTRY: U.S.A.
ZIP: 1153-0.259
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
BRING BATE: 14-FEB-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11.0%; Score 8; DB 1; Length 10; 100.0%; Pred. No. 2.3e+02; Live 0; Mismatches 0; Indels
COUNTRY: U.S.A.

ZIP: 11530-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/488,551B
FILING DATE: 07-UN-1995
PRIONE APPLICATION DATA:
APPLICATION NUMBER: PM4002 (AU)
FILING DATE: 21-FEB-1994
APPLICATION NUMBER: PM4002 (AU)
FILING DATE: 12-FEB-1994
APPLICATION NUMBER: PN0284 (AU)
FILING DATE: 14-FEB-1995
APPLICATION NUMBER: PN021/95
FILING DATE: 14-FEB-1995
APPLICATION NUMBER: PN021/95
FILING DATE: 17-MAY-1995
APPLICATION NUMBER: PN021/95
APPLICATION NUMBER: PN021/96

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Best Local Similarity 100.
Matches 8; Conservative
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APPLICANT: Nicholas J. Deacon
APPLICANT: David Cooper
TILLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
CORRESPONDENCE ADDRESS:
ADDRESSE: SCULLY, SCOTT, MURPHY & PRESSER
STREET: 400 GARDEN CITY PLAZA
CITY: GARDEN CITY PLAZA
COUNTRY: U.S.A.
ZIP: 11530-029
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COUNTRY: U.S.A.
SOFTWARE: PRECOUNT MATA:
APPLICATION NUMBER: WAS 4488,551B
FILING DATE: 11-FEB-1994
APPLICATION NUMBER: PRO284 (AU)
FILING DATE: 21-FEB-1994
APPLICATION NUMBER: WO 80/388,353
FILING DATE: 23-DE-1994
APPLICATION NUMBER: WO 80/388,353
FILING DATE: 17-MAY-1995
ATTORNEY/AGENT INFORMATION:
NAME: FRANK S. DIGIGILO
NUMBER: FRANK S. DIGIGILO
NUMBE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11.0%; Score 8; DB 1; Length 10; 100.0%; Pred. No. 2.3e+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                            US-08-488-551B-274/c
) Sequence 274, Application US/08488551B
; Patent No. 6015661
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-488-551B-308/c
; Sequence 308, Application US/08488551B
; Patent No. 6015661
; GENERAL INFORMATION:
; APPLICANT: Nicholas J. Deacon
; APPLICANT: Dale A. McPhee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 100.
Matches 8; Conservative
                                               908 TITICITY 915
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 415
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11.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.38+02;
Matches 8; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                       DB 1; Length 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE: GANDEN CITY
STATE: GANDEN CITY
COUNTRY: U S.A.
ZIP: 11530-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compartible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: U$/08/488,551B
FILING DATE: 07-UN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PW4002 (AU)
FILING DATE: 14-FEB-1994
APPLICATION NUMBER: PW4002 (AU)
FILING DATE: 23-DEC-1994
APPLICATION NUMBER: PW3094
APPLICATION NUMBER: PW3094
APPLICATION NUMBER: PW30195
FILING DATE: 14-FEB-1995
APPLICATION NUMBER: U$ 08/388,353
FILING DATE: 14-FEB-1995
APPLICATION NUMBER: U$ 08/388,353
FILING DATE: 17-MAY-1995
APPLICATION NUMBER: PW3021/95
FILING PATE: 17-MAY-1995
APPLICATION PW3021/95
FILING PATE: 17-MAY-1995
APPLICATION PW3021/95
FILING PW3021/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Nicholas J. Deacon
APPLICANT: Dale A. McPhe
APPLICANT: David Cooper
TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
NUMBER OF SEQUENCES: 841
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
STREET: 400 GARDEN CITY
CITY: GARDEN CITY
                                                                                                                                                                                                                                                                                                                                                                       11.0%; Score B; DB 1
100.0%; Pred. No. 2.3
rative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 413
8.08-488-551B-273/c
; Sequence 273, Application US/08488551B
; Patent No. 6015661
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TELEFAX: (516) 742-4366
INPORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 10 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (516) 742-4366
INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10 base pairs
                                                                                                                                              TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             941 TCATTGGT 948
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               nucleic acid
                                                                                                                                                                                                                         ; TOPOLOGY: linear; MOLECULE TYPE: DNA US-08-488-551B-232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8 TCATTGGT 1
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US-08-488-551B-273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE:
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Gaps

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WS-08-906-691-14/C

| Sequence 14, Application US/08906691
| Sequence 14, Application US/08906691
| Pattent No. 606647
| Pattent No. 606647
| APPLICANT: Weissman, Sherman M. APPLICANT: Walkarni, Prakash
| APPLICANT: Walkarni, Prakash
| TITLE OF INVENTION: IDENTIFYING PROTEIN-BINDING SITES FOR DNA-BINDING PROTEINS |
| TITLE OF INVENTION: DENTIFYING PROTEIN-BINDING SITES FOR DNA-BINDING PROTEINS |
| WINDER OF SEQUENCES: 50 CORRESPONDENCE ADDRESS: |
| ADDRESSES: SEED and BERRY LLP |
| STREET: 6300 Columbia Center, 701 Fifth Avenu |
| STREET: 6300 Columbia Center, 701 Fifth Avenu |
| STREET: 930044 |
| COUNTRY: USA |
| COUNTRY: USA |
| CALPER | COUNTRY: USA | |
| CALPER | COUNTRY: USA |
| CALPER | CALPER | CALPER |
| CALPER | CALPER | CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 8; Conservative 0; Mismatches 0; Indels
                                                    CURRENT APPLICATION DATA:

APPLICATION NUMBER: DATA (AU)
FILING DATE: DATA (AU)
FILING DATE: DATA (AU)
FILING DATE: DATA (AU)
FILING DATE: 12-FEB-194
APPLICATION NUMBER: PM4002 (AU)
FILING DATE: 14-FEB-194
APPLICATION NUMBER: PM0284 (AU)
FILING DATE: 14-FEB-194
APPLICATION NUMBER: DM0284 (AU)
FILING DATE: 14-FEB-195
APPLICATION NUMBER: US 08/388,353
FILING DATE: 14-FEB-195
APPLICATION NUMBER: US 08/388,353
FILING DATE: 17-MAY-195
APPLICATION NUMBER: PM3021/95
FILING DATE: 17-MAY-195
APPLICATION NUMBER: 9606Z
FILING DATE: 17-MAY-195
ATTORNEY/AGENT INFORMATION:
TELEPRAK: (516) 742-4363
INFORMATION FOR SEQ ID NO: 309:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/906,691
FILING DATE: 31-JUL-1997
CLASSIFICATION: 435
ATTORNEY AGENT INFORMATION:
NAME: No. 6066452tenburg Ph.D., Carol
REGISTRATION NUMBER: 39,317
REFERENCE/DOCKET NUMBER: 39,317
TELECOMMULATION INFORMATION:
TELECOMMULATION INFORMATION:
TELECOMMULATION INFORMATION:
TELECOMMULATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             910 TICTITIES 917
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TOPOLOGY: lii
; MOLECULE TYPE:
US-08-488-5518-309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                à
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APPLICANT: David Cooper
TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
NUMBER OF SEQUENCES: 841
CORRESPONDENCE ADDRESS:
ADDRESSEE: ACULLY, SCOTT, MURPHY & PRESSER
CITY: GARDEN CITY
STREET: 400 GARDEN CITY
COINTRY: U.S.A.
ZIP: 11530-0299
COMPUTER REDABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: W4002 (AU)
FILING DATE: 14-FEB-1994
APPLICATION NUMBER: PM0284 (AU)
FILING DATE: 21-FEB-1994
APPLICATION NUMBER: US 08/388,353
FILING DATE: 14-FEB-1995
APPLICATION NUMBER: US 08/388,353
FILING DATE: 17-MAY-1995
ATTORNEY/AGENT INFORMATION:
TELEFORMUNICATION INFORMATION:
TELEFORMUNICATION INFORMATION:
TELEFORM: SEG ID NO: 308:
SEQUENCE CHARRACTERISTICS:
LENGRAL MODEL ACID
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Sequence 319, 3971;
Patent No. 601561
GENERAL INFORMATION
APPLICANT: Dale A. McPhee
APPLICANT: Dale A. McPhee
TITLE OF INVANION: NON-PATHOGENIC STRAINS OF HIV-1
NUMBER OF SEQUENCES: 841
CORRESPONDENCE S. 841
CORRESPONDENCE S. SCULLY, MURPHY & PRESSER
STREET: 400 GARDEN CITY PLAZA
CITY: GARDEN CITY PLAZA
CITY: GARDEN CITY
STATE: NEW YORK
COUNTRY: U.S.A.
ZIP: 11530-0299 disk.
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100.0%; Pred. No. 2.3e+02;
tive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 100.
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              910 TICTITGG 917
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US-08-488-551B-309/c
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OTHER INFORMATION: Description of Artificial Sequence: No. 6228982el Sequence
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GENERAL INVENTION:
GENERAL INVENTION:
APPLICANT: Wittung, Pernilla
APPLICANT: Wittung, Pernilla
APPLICANT: Buchardt, Ole
APPLICANT: Buchardt, Ole
APPLICANT: Bench, Michael
APPLICANT: Berg, Rolf
APPLICANT: Nielsen, Peter E.
FILE REFERENCE: 15151108
CURRENT APPLICATION NUMBER: 08/054,363
PRIOR FILING DATE: 1993-07-02
PRIOR FILING DATE: 1993-07-05
PRIOR FILING DATE: 1992-05-19
NUMBER OF SEQ ID NOS: 42
SOFTWARE: PetentIn Ver. 2.1
SEQ ID NO 20
LENGTH: 10
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GENERAL INFORMATION:
APPLICANT: Wittung, Pernilla
APPLICANT: Buchardt, Ole
APPLICANT: Buchardt, Ole
APPLICANT: Egholm, Michael
APPLICANT: Berg, Rolf
TITLE OF INVENTION: Double-Stranded Peptide Nucleic Acids
FILE REFERENCE: 15181108
CURRENT FILING DATE: 1993-07-02
PRIOR APPLICATION NUMBER: US/08/61F
PRIOR FILING DATE: 1993-04-26
PRIOR FILING DATE: 1993-04-26
PRIOR FILING DATE: 1993-05-19
NUMBER OF SEQ ID NOS: 42
SOFTWARE: PatentIn Ver. 2.1
                     Pred. No. 2.3e+02;
); Mismatches 0; Indels
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100.0%; Pred. No. 2.38+02;
vative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                             US-08-088-661F-20/c
; Sequence 20, Application US/08088661F
; Patent No. 6228982
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; Sequence 22, Application US/08088661F
; Patent No. 6228982
100.0%; Pre-
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ORGANISM: Artificial Sequence
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                        Best Local Similarity 100.
Matches 8; Conservative
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Best Local Similarity 100.
Matches 8; Conservative
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                                                                                                                                                3 CTGGTCAT 10
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LENGTH: 10
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| Sequence 102, Application US/08522384
| Sequence 102, Application US/08522384
| Sequence 102, Application US/08522384
| Patent No. 6110667
| Sequence 102, Application US/08522384
| APPLICANT: LOPEZ-NIETO, CARLOS E
| APPLICANT: NIGAM, SANDAY KUMAR
| TILLE OF INVENTION: CHARACTERIZING NUCLEOTIDE SEQUENCES
| TILLE OF INVENTION: CHARACTERIZING NUCLEOTIDE SEQUENCES
| TILLE OF INVENTION: CHARACTERIZING NUCLEOTIDE SEQUENCES
| CURRENT APPLICATION NUMBER: US/08/522,384
| CURRENT FILING DATE: 1996-11-15
| NUMBER OF SEQ ID NOS: 122
| SEQ ID NO 102
| LENGTH: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NGS-011 410

VIS-08-522-384-74

Sequence 74, Application US/08522384

Sequence 74, Application US/08522384

Sequence 74, Application US/0852384

SERIEM NO. 6110667

SERIEM LINFORMATION: PROCESSES, APPLICANT: LOPEZ-NIETO, CARLOS E

APPLICANT: NIGAM, SANJAY KÜWAR

TITLE OF INVENTION: PROCESSES, APPARATUS AND COMPOSITIONS FOR TITLE OF INVENTION: PROCESSES, APPARATUS AND COMPOSITIONS FOR TITLE OF INVENTION: CHARACTERIZING NUCLEOTIDE SEQUENCES

FILE REFERENCE: 2458-4029

CURRENT FILING DATE: 1996-11-15

NUMBER OF SEQ ID NOS: 122

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 74

LENGTH: 10
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CTHER INFORMATION: Description of Unknown Organism: Primer

US-08-522-384-74
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11.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 8; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                   Length 10;
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                                                                                                                                                                                                                                                                                   DB 1; Len
                                                                                                                                                                                                                                                                                Query Match 11.0%; Score 8; DB 1
Best Local Similarity 100.0%; Pred. No. 2.3
Matches 8; Conservative 0; Mismatches
                             TELEFAX: (206) 682-6031
INPORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Unknown Organism
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA ORGANISM: Unknown Organism
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            901 CTGGTCAT 908
                                                                                                                                nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                      958 CGCTACCA 965
                                                                                                                                                                                                                                                                                                                                                                                                                                      9 CGCTACCA 2
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                                                                                                                                                                                TOPOLOGY: linear / MOLECULE TYPE: DNA US-08-906-691-14
                                                                                                                                                        STRANDEDNESS:
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US-06-156-14

Sequence 14, Application US/08150156A

Setent No. 6357163

GENERAL INFORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
COMPUTER READABLE FORM:
MEDIANT TYPE: Floppy disk
COMPUTER: IRW PC compatible
OPERATING SYSTEM:
SOFTWARE: MORDEFECT 5.1

CURRENT APPLICATION DATA:
CURRENT APPLICATION NUMBER: US/08/150,156A
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11.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 8; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HYPOTHETICAL: NO
ANTI-SENSE: NO
PUBLICATION INFORMATION:
DOCUMENT NUMBER: WO PCT/EP92/01220
US-08-150-156A-5
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/150,156A
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PUBLICATION INFORMATION:
DOCUMENT NUMBER: WO PCT/EP92/01220
                                                                                                                              PRIOR APPLICATION DATA:

APPLICATION NUMBER: DK 0986/91
FILING DATE: 24-MAY-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DK 0987/91
FILING DATE: 24-MAY-1991
FILING DATE: 24-MAY-1991
PRIOR APPLICATION NUMBER: DK 0510/92
FILING DATE: 15-APR-1992
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 10 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
PRICR APPLICATION DATA:
APPLICATION NUMBER: DK 0986/91
FILING DATE: 24-MAY-1991
PRICR APPLICATION NUMBER: DK 0987/91
FILING DATE: 24-MAY-1991
PRICR APPLICATION NUMBER: DK 0987/91
PRICR APPLICATION NUMBER: DK 0987/91
APPLICATION NUMBER: DK 0510/92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 15-APR-1992
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 10 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        908 TITICITY 915
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US-08-150-156A-5/c

### Sequence 5, Application US/08150156A

### Sequence 6, Application US/08150156A

### Sequence 6, Application US/08150156A

### TITLE OF INVENTION: THE USE OF NUCLEIC ACID ANALOGUES IN TITLE OF INVENTION: DIAGNOSTICS AND ANALYTICAL PROCEDURES NUMBER OF SEQUENCES: HOPPY disk

### MEDIUM TYPES: PLOPPY disk

### COMPUTER: IBM PC compatible

### COMPUTER: IBM PC compatible

### OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: THE USE OF NUCLEIC ACID ANALOGUES IN TITLE OF INVENTION: DIAGNOSTICS AND ANALYTICAL PROCEDURES NUMBER OF SEQUENCES: 40
COMPUTER READABLE FORM: 40
COMPUTER READABLE FORM: ABOUTH TYPE: Floppy disk
COMPUTER: IBM PC COMPUTER: DE COMPUTE
                                                                   11.0%; Score 8; DB 1; Length 10; 100.0%; Pred. No. 2.3e+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11.0%; Score 8; DB 1; Length 10; 100.0%; Pred. No. 2.3e+02; tive 0; Mismatches 0; Indels
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PUBLICATION INFORMATION:
DOCUMENT NUMBER: WO PCT/EP92/01220
FILING DATE: 22-MAY-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PFILING DATA:
APPLICATION DATA:
APPLICATION NUMBER: DK 0986/91
PRILING DATE: 24-MAY-1991
PRILING DATE: 24-MAY-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DK 0987/91
FILING DATE: 24-MAY-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DK 0510/92
FILING DATE: 15-APR-1992
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 10 base pairs
TYPE: mucleic acid
STRANDEDNESS: Single
                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-150-156A-2/c; Sequence 2, Application US/08150156A; Patent No. 6357163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
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Best Local Similarity 100.
Matches 8; Conservative
                                                                                                                                          8; Conservative
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                                                                   Query Match
Best Local Similarity
Matches 8; Conserva
                                                                                                                                                                                                                                                                                    9 TTTTCTTT 2
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   US-08-088-661F-22
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100.0%; Pred. No. 2.3e+02;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                     11.0%; Score 8; DB 1; Length 10; 100.0%; Pred. No. 2.3e+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 428
US-09-108-591B-10/C
Sequence 10, Application US/08108591B
Patent No. 6395474
GENERAL INFORMATION:
APPLICANT: Buchardt, Ole
APPLICANT: Egholm, Michael
APPLICANT: Berg, Rolf Henrik
TITLE OF INVENTION: Peter Eigil
APPLICANT: Berg, Rolf Henrik
TITLE OF INVENTION: Peptide Nucleic Acids
FILE REPRENCE: 15150540
CURRENT PELING DATE: 2001-08-13
NUMBER OF SEQ ID NOS: 43
SOOTWARE: PatentIn version 3.1
SEQ ID NO 10
LENGTH: 10
                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 427
US-08-108-591B-9/C
US-08-108-591B-9/C
Sequence 9, Application US/08108591B
Patent No. 6395474
GENERAL INFORMATION:
APPLICANT: Buchardt, Ole
APPLICANT: Bergl, Rolf Henrik
TITLE OF INVENTION: Peptide Nucleic Acids
FILE REFERENCE: ISISOS40
CURRENT APPLICATION NUMBER: US/08/108,591B
CURRENT APPLICATION NUMBER: US/08/108,591B
CURRENT FILING DATE: 2001-08-13
NUMBER OF SEQ ID NOS: 43
SOFTWARE: PatentIN version 3.1
                                                                                                                                                     FEATURE:
; OTHER INFORMATION: No. 6395474el Sequence
US-08-108-591B-8
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CROMINEM: Artificial Sequence
FEATURE:
OTHER INFORMATION: No. 6395474el Sequence
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                  NUMBER OF SEQ ID NOS: 43
SOFTWARE: Patentin version 3.1
                                                                                                           TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Artificial Sequence
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Best Local Similarity 100.0
Matches : 8, Conservative
                                                                                                                                                                                                                                          Query Match
Best Local Similarity 100.
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                   908 TITICITY 915
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CURRENT FILING DATE:
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                                                               SEQ ID NO 8
LENGTH: 10
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                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: THE USE OF NUCLEIC ACID ANALOGUES IN TITLE OF INVENTION: DIAGNOSTICS AND ANALYTICAL PROCEDURES NUMBER OF SEQUENCES: 40
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11.0%; Score 8; DB 1; Length 10; 100.0%; Pred. No. 2.3e+02; Ative 0; Mismatches 0; Indels
                                                               Query Match
11.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 8; Conservative 0; Mismatches 0; Indels
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APPLICANT: Buchardt, Ole
APPLICANT: Bachard, Peter Eigil
APPLICANT: Nielsen, Peter Eigil
APPLICANT: Berg, Rolf Henrik
TITLE OF INVENTION: Peppide Nucleic Acids
FILE REPERENCE: ISISO540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DCS/MS-DOS SOFTWARE: Wordperfect 5.1 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/150,156A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ANTI-SENSE: NO
PUBLICATION INFORMATION:
DOCUMENT NUMBER: WO PCT/EP92/01220
FILING DATE: 22-MAY-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: DK 0986/91
FILING DATE: 24-MAY-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DK 0987/91
FILING DATE: 24-MAY-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DK 0510/92
FILING DATE: 15-APR-1992
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERICS:
LENGTH: 10 Dasse pairs
TYPE: nucleic acid
STRANDENNESS: Single
                                                                                                                                                                                                                                                                                                         Sequence 16, Application US/08150156A; Patent No. 6357163; GENERAL INFORMATION:
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; Sequence 8, Application US/08108591B
; Patent No. 6395474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO
  ; FILING DATE: 22-MAY-1992
US-08-150-156A-14
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                                                                                                                                                          908 TITICITY 915
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Best Local Similarity
Matches 8; Conserv
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                                                                                                                                                                                                                                                                      RESULT 425
US-08-150-156A-16
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US-08-108-591B-10

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US-08-68-1148-56/C

Sequence 56. Application US/08686114B

Patent No. 6414112

GENERAL INFORMATION:
PERIODICANT: Buchardt et al.
TITLE OF INVENTION:
PORTICIONIN: Peptide Nucleic Acids Having 2,6-Diaminopurine Nucleob
NUMBER OF SEQUENCES: 60

CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 6414112ris LLP
CITY: Philadelphia
STARF: PA

COUNTRY: U.S.A.
ZIP: 19103

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 Inch disk, 1.44 Mb

COMPUTER: IBM PC compatible
COMPUTER: U.S.A.
ZIP: 19103

COMPUTER: U.S.A.
ZIP: 19103

COMPUTER: U.S.A.
ZIP: 19103

COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: U.S.A.
ZIP: 19103

COMPUTER: U.S.A.
ZIP: 19103

COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatib
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US-08-686-1148-58/C

Sequence 58, Application US/08686114B

Patent No. 6414112.

GENERAL INFORMATION:

APPLICANT: Buchardt et al.

TITLE OF INVENTION: Peptide Nucleic Acids Having 2,6-Diaminopurine Nucleob NUMBER OF SEQUENCES: 60

CORRESPONDENCE ADDRESS:

ADDRESSE: Woodcock Washburn Kurtz Mackiewicz & No. 6414112ris LLP

STREET: One Liberty Place - 46th Floor

CITY: Philadelphia

STATE: PA

COUNTRY: U.S.A.

ZIP: 1910

MEDIUM TYPE: 3 inch disk, 1.44 Mb

COMPUTER: BAP PC compatible

COMPUTER: IBM PC compatible

COMPUTER: IBM PC COMPATIBLE FORM:

MEDIUM SYSTEM: PC-DOS/MS-DOS
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Best Local Similarity 100.
Matches 8; Conservative
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STRANDEDNESS: single
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                              JS-08-686-114B-56/c
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   Length 10;
                                                             0; Indels
Query Match
11.0%; Score 8; DB 1; Les
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 8; Conservative 0; Mismatches 0;
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Patent No. 6395474
GENERAL INFORMATION:
APPLICANT: Buchardt, Ole
APPLICANT: Eqholm, Michael
APPLICANT: Bergo, Rolf Henrik
TITLE OF INVENTION: Perfer Eigil
APPLICANT: Brog, Rolf Henrik
TITLE OF INVENTION: Peptide Nucleic Acids
FILE REPERENCE: ISISO540
CURRENT APPLICATION UNMER: US/08/108,591B
CURRENT FILING DATE: 2001-08-13
NUMBER OF SEQ ID NOS: 43
SOFTWARE: PatentIn Version 3.1
SEQ ID NO 14
                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
FULL REFERENCE:
GURRENT APPLICATION NUMBER:
GURRENT APPLICATION NUMBER:
GURRENT FILING DATE:
GURRENT FILING DATE:
SOFTWARE:
SOFTWARE:
SOFTWARE:
SEC ID NO:
LENGTH: 10
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US-08-108-591B-14
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US-08-108-591B-12
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA ORGANISM: Artificial Sequence
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US-08-108-591B-12
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US-08-108-591B-14
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APPLICANT: AKSUNIC SURVICHI
APPLICANT: Yasuhiro FURUICHI
APPLICANT: Yuko SHIBATA
APPLICANT: Hiroko FURAKI
APPLICANT: Hiroko FURAKI
APPLICANT: Hiroko FURAKI
APPLICANT: Masanori WATAHIKI
TILLE OF INVENTION: Method for Synthesizing cDNA from mRNA sample
FILE REFERENCE: 00162/HG
CURRENT APPLICATION NUMBER: US/09/508,753B
PRIOR APPLICATION NUMBER: UP 9/270324
PRIOR PILING DATE: 1997-09-18
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APPLICANT: Biji OHARA
APPLICANT: Masanori MATAHTKI
TITLE OF INVENTION: Method for Synthesizing cDNA from mRNA sample
APPLICANT: Eiji OHARA
APPLICANT: Masanori WATAHIKI
TITLE OF INVENTION: Method for Synthesizing CDNA from mRNA sample
FILE REFERENCE: 00162/HG
CURRENT APPLICATION NUMBER: US/09/508,753B
CURRENT FILING DATE: 2000-06-16
PRIOR APPLICATION NUMBER: JP 9/270324
PRIOR PILLING DATE: 1997-09-18
NUMBER OF SEQ ID NOS: 472
SEQ ID NO 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                         .;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; PEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer US-09-508-753B-27
                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 100.0%; Pred. No. 2.38+02;
Matches 8; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 436
US-09-508-753B-50/c
; Sequence 50, Application US/09508753B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: Artificial Sequence
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GENERAL INFORMATION:
APPLICANT: Akira SHIMAMOTO
APPLICANT: Yasuhiro FURUICHI
APPLICANT: Yuko SHIBATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ouery Match
Best Local Similarity 100.
Matches 8, Conservative
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SEQ ID NO 27
LENGTH: 10
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CURRENT FILING DATE: 1998-09-17
PRIOR APPLICATION NUMBER: 60/059,153
PRIOR PILING DATE: 1997-09-17
PRIOR PILING DATE: 1998-03-30
NUMBER OF SEQ ID NOS: 93
SOFTWARE: PESESEQ for Windows Version 3.0
SEQ ID NO 18
LENGTH: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-154-750A-18

Sequence 18, Application US/09154750A

Patent No. 6432640

GENERAL INFORMATION:

APPLICANT: Vogelstein, Bert

APPLICANT: Kinzler, Kenneth

APPLICANT: Rinzler, Kenneth

TILLE OF INVENTION: p33-Induced Apoptosis;

FILE REFERENCE: 1107.75357
                                             FILING DATE: July 24, 1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/108,591
FILING DATE: 22-NOV-1993
ATTORNEY AGENT INFORMATION:
NAME: Michael P. Straher
REGISTRATION NUMBER: 38,325
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
TELEFAX: 215-568-3100
TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 58:
SEQUENCE CHARACTERISTICS:
       CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/686,114B
FILING DATE: July 24, 1996
CLASSIFICATION: 435
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; Sequence 20, Application US/09508753B
; Patent Wo. 65447100;
; APPLICANT: Akira SHIMAMOTO
; APPLICANT: Yasuhiro PURUICHI
; APPLICANT: Yuko SHIBATA
; APPLICANT: Hiroko FUNAKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 11.0
Best Local Similarity 100.
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 10 bases
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Homo sapiens
US-09-154-750A-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               908 TTTTCTTT 915
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Best Local Similarity
Matches 8; Conserva
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
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US-08-686-114B-58
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RESULT 439
US-09-924-346-5
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US-09-508-753B-440/c

Sequence 440, Application US/09508753B.

Patent No. 6544736

GENERAL INFORMATION:
APPLICANT: ARIAE SHIMAMOTO
APPLICANT: Yako SHIBATA
APPLICANT: Yako SHIBATA
APPLICANT: Hiroko FUNAKI
APPLICANT: Hiroko FUNAKI
APPLICANT: Hiroko FUNAKI
APPLICANT: Masanori WaTAHIKI
APPLICANT: Masanori WaTAHIKI
APPLICANTON: Method for Synthesizing CDNA from mRNA sample
TITLE OF INVENTION: Method for Synthesizing CDNA from mRNA sample
CURRENT APPLICATION NUMBER: US/09/508,753B

CURRENT FILING DATE: 2000-06-16
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; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-508-753B-113
                                                                                                                                                                       FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer US-09-508-753B-50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 8; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                       Query Match
11.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 8; Conservative 0; Mismatches 0; Indels
FILE REFERENCE: 00162/HG
CURRENT APPLICATION NUMBER: US/09/508,753B
CURRENT FILING DATE: 2000-06-16
PRIOR APPLICATION NUMBER: UP 9/270324
PRIOR FILING DATE: 1997-09-18
NUMBER OF SEQ ID NOS: 472
LENGTH: 10
                                                                                                                                       TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                        922 TGCCTTTT 929
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patent No. 6613873

APPLICANT: Buchardt. Ole

APPLICANT: Bergholm, Michael

APPLICANT: Nelsen, Peter E.

APPLICANT: Neer No. 1818-3809

CURRENT APPLICANTION: Peptide Nucleic Acids Having 2, 6-Diaminopurine Nucleobases

FILE REFERENCE: ISIS-3809

CURRENT APPLICATION NUMBER: 1896-06-21

PRIOR PILING DATE: 1999-06-21

PRIOR PILING DATE: 1997-05-01

PRIOR PILING DATE: 1996-06-24

PRIOR PLING DATE: 1998-01-24

PRIOR PLING DATE: 1993-11-22

PRIOR FILING DATE: 1991-05-24

PRIOR FILING DATE: 1991-05-24
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                                                                                                                       TYPE: DNA
) ORGANISM: Artificial Sequence
; FRATURE:
; FRATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-508-753B-440
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11.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 8; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                     0; Indels
                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 8; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Squence 5, Application US/09924346
| Patent No. 6555674
| GENERAL INNORMATION:
| APPLICANT: Jens Tornoe
| TILLE OF INVENTION: The JeT Promoter
| FILE REFRENCE: 19313-005
| CURRENT APPLICATION NUMBER: US/09/924,346
| CURRENT FILING DATE: 2001-08-08
| PRIOR PILLING DATE: 2000-08-09
| NUMBER OF SEQ ID NOS: 8
| SOFTWARE: Patentin Ver. 2.1
| SSQ ID NO 5
PRIOR APPLICATION NUMBER: JP 9/270324
PRIOR FILING DATE: 1997-09-18
NUMBER OF SEQ ID NOS: 472
SEQ ID NO 440
LENGTH: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 56, Application US/09337304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       924 CCTTTTAT 931
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US-09-337-304-56/c
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Query Match 11.0
Best Local Similarity 100.
Matches 8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   JS-08-173-489C-73/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-246-373-6
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APPLICANT: Egholm, Michael
APPLICANT: Egholm, Methael
APPLICANT: Nelsen, Peter E.
APPLICANT: Berg, Rolf Henrik
TITLE OF INVENTION: Peptide Nucleic Acids Having 2, 6-Diaminopurine Nucleobases
FILE REFERENCE: ISIS-3809
                                                                                                                                                                                                                                                                                                                                                                                                 ô
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                                                                                                                                                                                                                                                                                                                                                Length 10;
                                                                                                                                                                                                                                                                                                                                             Query Match
11.0%; Score 8; DB 1; Le.
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 8; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILE REFERENCE: LASS-3809
CURRENT APPLICATION NUMBER: US/09/337,304
CURRENT FILING DATE: 1999-06-21
PRIOR APPLICATION NUMBER: 08/847,110
PRIOR PLLING DATE: 1997-05-01
PRIOR PLLING DATE: 1997-05-01
PRIOR PLLING DATE: 1996-07-24
PRIOR PLLING DATE: 1996-07-24
PRIOR PLLING DATE: 1996-07-24
PRIOR PLLING DATE: 1991-05-24
PRIOR PLLING DATE: 1991-05-24
PRIOR PLLING DATE: 1991-05-24
PRIOR PLLING DATE: 1991-05-24
PRIOR APPLICATION NUMBER: 987/91
PRIOR PLLING DATE: 1991-05-24
PRIOR PLLING DATE: 1991-05-24
PRIOR PLLING DATE: 1991-05-24
PRIOR PLLING DATE: 1991-05-24
PRIOR PLING DATE: 1991-05-24
                                                                                                                                                                                               TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
FOTHER INFORMATION: Synthetic Construct
US-09-337-304-56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: Synthetic Construct US-09-337-304-58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Sequence 58, Application US/09337304; Patent No. 6613873; GENERAL INFORMATION:
PRIOR APPLICATION NUMBER: 987/91
PRIOR FLILING DATE: 1991-05-24
PRIOR PLICATION NUMBER: 510/92
PRIOR FILING DATE: 1992-04-15
NUMBER OF SEQ ID NOS: 60
SOFTWARE: Patentin version 3.1
SEQ ID NO 56
LENGTH: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 6, Application US/08246373; Patent No. 5550018 GENERAL INFORMATION: APPLICANT: LEVENBOOK, Inessa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Artificial Sequence
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Best Local Similarity 100.
Matches 8; Conservative
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US-09-337-304-58/c
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US-08-246-373-6/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Pat
SEQ ID NO 58
LENGTH: 10
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Sequence 27, Application US/08910632B

Sequence 27, Application US/08910632B

Sequence 27, Application US/08910632B

SEXELI INFORMATION:
APPLICANT SOOL, ENIC T.
TITLE OF INVENTION: HIGHLY SENSITIVE MULTIMERIC NUCLEIC ACID PROBES
FILE REFERENCE: 220.00010130
CURRENT FILING DATE: 1997-08-13
EARLIER APPLICATION NUMBER: 08/805,631
EARLIER PILING DATE: 1997-02-26

BARLIER PILING DATE: 1995-02-23

EARLIER PILING DATE: 1993-04-15

NUMBER OF SEQ ID NOS: 83

SOFTWARE PRECEIT PRECEIT OF SEQ ID NOS: 83

LENGTH: 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 8; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: other nucleic acid
DESCRIPTION: third strand derived from esterase D
DESCRIPTION: sequence region in Seq ID No. 586124473
HYPOTHEFICAL: Yes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; PUBLICATION INFORMATION:
; RELEVANT RESIDUES IN SEQ ID NO: 74 :FROM 1 TO 11
US-08-173-489C-74
COMPUTER: IBM PC/XT/AT

OPERATING SYSTEM: MS-DOS version 6.2
SOFTWARE: Wordperfect Version 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/173,489C
FILING DATE: 2 DEC 1993
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 07/968,436
FILING DATE: 29 OCT 1992
ATTORNEY/AGENT INFORMATION:
NAME: Handelman, Joseph H.
REGISTRATION NUMBER: U5.179
REFERENCE/DOCKET NUMBER: U9518-6
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (attorney) (212) 708-1880
TELEPHONE: (attorney) (212) 246-8959
INPORMATION FOR SEQ ID NO: 74:
LENGTH: LI DATES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
CTHER INFORMATION: ligation adaptor
US-08-910-632-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: Nucleic Acid
STRANDEDNESS: single stranded
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   908 TITICITI 915
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US-08-910-632-27
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US-08-173-489C-74

i Sequence 7. Application US/08173489C

patent No. 5861244

GENERAL INFORMATION:

APPLICANT: WANG, C. -G.

APPLICANT: WANG, C. -G.

TITLE OF INVENTION: TRIPLE-STRAND FORWATION.

NUMBER OF INVENTION: TRIPLE-STRAND FORWATION.

NUMBER OF INVENTION: TRIPLE-STRAND FORWATION.

STREET: SIO EAST 73RD STREET,

CITY: NEW YORK

CITY: NEW YORK

COUNTRY: USA

ZIP: 10021.

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44Mb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11.0%; Score 8; DB 1; Length 11; 100.0%; Pred. No. 2.6e+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: Genomic DNA
DESCRIPTION: esterase D gene (Accession # M13450)
DESCRIPTION: mucleotides 777 to 787
HYPOTHETICAL: No
ANTI-SENSE: No
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
POSITION IN GENOME:
CHROMOSOME/SEGNENT: chromosome 13
MAP POSITION: 13141.1-q14.2
PUBLICATION: 13141.1-q14.2
AUTHORS: Lee, E Y H P, Lee, W H.
TITLE: Molecular cloning of the
TITLE: molecular cloning of the
TITLE: retinoblastoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ) DATE: 1986
; RELEVANT RESIDUES IN SEQ ID NO: 73 :FROM 1 TO 11
US-08-173-489C-73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Proceedings of the National Academy of Sciences, USA
  OPERATING SYSTEM: MS-DOS version 6.2
SOFTWARE: Wordperfect Version 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/173,489C
FILING DATE: 22 DEC 1993
CLASSIFICATION DATA:
APPLICATION NUMBER: US 07/968,436
FILING DATE: 29 OCT 1992
ATTORNEY/AGENT: US 0CT 1992
REGIGTRATION NUMBER: 26,179
REGIGTRATION NUMBER: 26,179
REGIGTRATION INFORMATION:
TELEFONDE: (attorney) (212) 708-1880
TELEFONDE: (attorney) (212) 246-8959
INFORMATION FOR SEQ ID NO: 73:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: double stranded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 100.
Matches 8; Conservative
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JOURNAL:
VOLUME: 8
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APPLICANT: Garner, Harold R.
APPLICANT: Wren, Jonathan D.
APPLICANT: Wren, Jonathan D.
TITLE OF INVENTION: Polyworphic Repeats in Human Genes
FILE REFERENCE: UTSD0667
CURRENT APPLICATION NUMBER: US/09/475,947A
CURRENT FILING DATE: 1999-12-31
NUMBER OF SEQ ID NOS: 346
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 220.00010140
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-305-1226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear MOLECULE TYPE: DNA (genomic) SEQUENCE DESCRIPTION: SEQ ID NO: 27:
                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: SANDBERG, VICTORIA A.
REGISTRATION NUMBER: 41,287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 230, Application US/09475947A Patent No. 6472154 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 612-305-1228
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 11 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
STRANDEDNESS: single
ZIP: 55401
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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Matches 8; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -09-475-947A-230
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
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TITLE OF INVENTION: CIRCULAR DNA VECTORS FOR SYNTHESIS OF RNA AND
DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                ; Sequence 27; Application US/08805631A
; Patent No. 6096880
; GENERAL INFORMATION:
; APPLICANT: UNIVERSITY OF ROCHESTER
APPLICANT: UNIVERSITY OF ROCHESTER
; TITLE OF INVENTION: CIRCULAR DNA VECTORS FOR SYNTHESIS OF RNA AND
; TITLE OF INVENTION: DNA
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CORRESPONDENCE ADDRESS:
ADDRESSEE: MUETING, RAASCH & GEBHARDT, P.A.
STREET: 119 No. 6368802th Fourth Street, Suite 201
CITY: Minneapolis
STATE: Minnesota
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 8; DB 1; Length 11; Pred. No. 2.6e+02; 0; Mismatches 0; Indels
                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 72
CORRESSPONDENCE ADDRESS.
ADDRESSEE: MUTING, RAASCH & GEBHARDT, P.A.
STREET: 119 No. 6096880th Fourth Street, Suite 201
CITY: Minneapolis
STATE: Minnesota
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER IN PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

SOFTWARE: PALICATION DATA:

APPLICATION NUMBER: US/08/805,631A

FILING DATE: 26-FEB-97

CLASSIPICATION: 536

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/393,439

FILING DATE: 23-FEB-1995

PRIOR APPLICATION NUMBER: US 08/047,860

FILING DATE: 15-APR-1993

ATTORNEY AGENT INFORMATION:

NAME: SANDBERG, VICTORIA A.

REFERENCE/DOCKET NUMBER: 41,287

REFERENCE/DOCKET NUMBER: 220.00010140

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:
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MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 612-305-1228
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                nucleic acid
EDNESS: single
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Best Local Similarity
Matches 8; Conserv
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                                                             US-08-805-631A-27
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0
COMPUTER: IDAPPY disk
COMPUTER: IDAPPY disk
COMPUTER: IDAPPY disk
COMPUTER: IDAPPY disk
COMPUTER: IDAPPE COMPATIBLE
CONFINENT NOT SYSTEM: PC-DOS/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION DATA:
CLASSIFICATION: <Unknown>
PRIOR APPLICATION: <Unknown>
PRIOR APPLICATION: <Unknown>
PRIOR APPLICATION: <Unknown>
PRIOR APPLICATION NUMBER: US 08/805,631
FILING DATE: 26-FEB-97
APPLICATION NUMBER: US 08/393,439
FILING DATE: 12-FEB-1995
APPLICATION NUMBER: US 08/047,860
FILING DATE: 15-APPLICATION NUMBER: US 08/047,860
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 11.0%; Score 8; DB 1; Length 11; Best Local Similarity 100.0%; Pred. No. 2.6e+02; Matches 8; Conservative 0; Mismatches 0; Indels
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| Sequence 251, Application US/09249155A |
| Sequence 251, Application US/09249155A |
| Sequence 251, Application US/09249155A |
| Patent No. 653473 |
| GENERAL INFORMATION: |
| APPLICANT: Heber-Katz, Ellen |
| TITLE OF INVENTION: Compositions and Methods for Wound |
| TITLE OF INVENTION: Healing |
| FILE REFERENCE: 00466.7850A |
| CURRENT APPLICATION NUMBER: US 60/074,737 |
| PRIOR PILING DATE: 1999-02-13 |
| PRIOR FILING DATE: 1998-02-13 |
| PRIOR FILING DATE: 1998-02-14 |
| PRIOR FILING DATE: 1998-09-26 |
| PRIOR FILING DATE: 1998-09-26 |
| NUMBER OF SEQ ID NOS: 346 |
| SOFTWARE: FastSEQ for Windows Version 4.0 |
| LENGTH: 11
APPLICANT: Heber-Katz, Ellen
TITLE OF INVENTION: Compositions and Methods for Wound
TITLE OF INVENTION: Healing
FILE REFERENCE: 00486,78503
CURRENT FILING DATE: 1999-02-12
CURRENT APPLICATION NUMBER: US 60/074,737
PRIOR PILING DATE: 1998-02-13
PRIOR FILING DATE: 1998-02-13
PRIOR FILING DATE: 1998-08-06
PRIOR FILING DATE: 1998-09-26
PRIOR FILING DATE: 1998-09-26
PRIOR APPLICATION NUMBER: US 60/102,051
PRIOR FILING DATE: 1998-09-26
PRIOR FILING DATE: 1998-09-26
PRIOR PLING DATE: 1998-09-26
SOFTWARE: FASTEEQ for Windows Version 4.0
SEQ ID NO 191
LENGTH: 11
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Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 8; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 8; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
CRGANISM: Mus musculus
US-09-249-155A-251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  932 cccrccrc 939
                                                                                                                                                                                                                                                                                                                                                                                                                      ; TYPE: DNA
; ORGANISM: Mus musculus
US-09-249-155A-191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             964 CAACGGTG 971
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 CCCTCCTC 9
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US-09-249-155A-251
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US-09-249-155A-31/C

Sequence 31, Application US/09249155A

Patent No. 6538173

GENERAL INFORMATION:
APPLICANT: Heber-Katz, Ellen
TITLE OF INVENTION: Compositions and Methods for Wound
TITLE OF INVENTION: Healing
FILE REFREENCE: 00486.7853

CURRENT APPLICATION NUMBER: US 60/249,155A

CURRENT PILING DATE: 1999-02-12

PRIOR FILING DATE: 1998-02-13

PRIOR PILING DATE: 1998-02-13

PRIOR PILING DATE: 1998-02-13

PRIOR PILING DATE: 1998-02-18

NUMBER: US 60/102,051

NUMBER: PREFEED TO NUMBER: US 60/102,051

PRIOR FILING DATE: 1998-09-28

NUMBER: PREFEED FREED FREED FOR WINDOWS Version 4.0

SEQ ID NO 31

LENGTH: 11
          RESULT 449
US-09-249-155A-18/C
; Sequence 18. Application US/09249155A
; Patent No. 6538173
; GENERAL INFORMATION:
    APPLICANT: Heber-Katz, Ellen
; TITLE OF INVENTION: Compositions and Methods for Wound; TITLE OF INVENTION: Healing
; FILE REFERENCE: 00486.78503
; CURRENT APPLICATION NUMBER: US/09/249,155A
CURRENT APPLICATION NUMBER: US 60/074,737
; PRIOR PILING DATE: 1999-02-13
; PRIOR PILING DATE: 1998-09-8
; PRIOR PILING DATE: 1998-09-8
; PRIOR FILING DATE: 1998-09-8
; RICK APPLICATION NUMBER: US 60/102,051
; PRIOR FILING DATE: 1998-09-8
; NUMBER OF SEQ ID NOS: 346
; SEQ ID NOS: 346
; SEQ ID NOS: 346
; SEQ ID NOS: 18
; LENGTH: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 8; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 11.0%; Score 8; DB 1; Length 11; Best Local Similarity 100.0%; Pred. No. 2.6e+02; Matches 8; Conservative 0; Mismatches 0; Indels
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US-09-249-155A-191/c
Sequence 191, Application US/09249155A
Parent No. 6538173
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA; CRGANISM: Mus musculus
US-09-249-155A-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
CRGANISM: Mus musculus
US-09-249-155A-18
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RESULT 453
US-07-754-918A-4/C
US-07-754-918A-4/C
Sequence 4, Application US/07754918A
Factor No. 5286484
GENERAL INFORMATION
TITLE OF INVENTION: NUCLEOTIDE SEQUENCE CODING FOR AN
TITLE OF INVENTION: OUTER MEMBRANE PROTEIN FROM NEISSERIA MENINGITIDIS AND USE
TITLE OF INVENTION: OF SAID PROTEIN IN VACCINE PREPARATIONS
NUMBER OF SEQUENCES: 14 ô

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US-08-363-475-27/C

Sequence 27, Application US/08363475
Fabrant No. 5516676;
GENERAL INFORMATION:
APPLICANT: Chiang, Shu-Jen
FAPLICANT: Tonzi, Sean M
TITLE OF INVENTION: PENICILLIN V AMIDOHYDROLASE GENE FROM
TITLE OF INVENTION: PUSARIUM OXYSPORUM
NUMBER OF INVENTION: PUSARIUM OXYSPORUM
NUMBER OF SEQUENCES:
ADDRESSEE: Thomas R. Savitsky
ADDRESSEE: Thomas R. Savitsky
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ..
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Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 8; Conservative 0; Mismatches 0; Indels
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CITY: Princetcon
STREET: New Jersey
COUNTRY: U.S.A.
ZIP: O8543
COMPUTER: EADBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/363,475
FILING DATE: 23-DEC-1994
CLASSIFICATION: 435
ATORNEY/ACENT INFORMATION:
NAME: SAVIESEY, Thomas R.
REGISTRATION NUMBER: 31,661
REPERANCE/DOCKET NUMBER: 0N-0134
TELECHMUNICATION INFORMATION:
TELEPHONE: (609) 252 4956
INFORMATION FOR SED ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 base pairs
LENGTH: 12 base pairs
INFORMATION FOR SED ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 base pairs
INFORMATION FOR SED ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 base pairs
INFORMATION FOR SED ID NO: 27:
SEQUENCE CHARACTERISTICS:
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LENGTH: 12 base pairs
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SEQUENCE CHARACTERISTICS:
LENGTH: 12 base pairs
INFORMATION FOR SED ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: AND SED ID NO: 27:
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                 TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)
US-08-115-497-11
   TELEX: 230 901 SANS UR INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 12 base pairs
                                                                                                                                                                            single
                                                                                                                              TYPE: nucleic acid
STRANDEDNESS: sing
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MOLECULE TYPE: CDNA

US-08-363-475-27
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US-08-280-441-8
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Sequence 11, Application US/08115497

Sequence 11, Application US/08115497

GENERAL INFORMATION:

TITLE OF INVENTION: STEM-LOOP OLIGONUCLEOTIDES CONTAINING

TITLE OF INVENTION: PARALLEL AND ANTIPARALLEL BINDING DOMAINS

NUMBER OF SEQUENCES: 21

CORRESPONDENCE ADDRESS:

ADDRESSEE: Scully, Scott, Murphy & Presser

STREET: 400 Garden City Plaza

CITY: Garden City Plaza

CITY: Garden City Plaza

CONTRY: USA

STRIET: New York

CONTRY: USA

COMPUTER: READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: Patentin Release #1.0, Version #1.25

SOSTWARE: Patentin Release #1.0, Version #1.25

CIRRENT APPLICATION DATE:

FILING DATE:
                        ADDRESSEE: Stanger, Michaelson, Spivak and Wallace, Esq. STREET: Parkway 109 Office Center, 328 Newman Springs STREET: Road, P. O. Box 8489
CITY: Red Bank
STATE: New Jersey
COUNTRY: USA
                                                                                                                                                                                                                      COMPUTER READABLE FORM:

MEDIUM TYPE: 5 1/4" 360KD IBM compatible diskette
COMPUTER: 1BM PS/2 Model 80
OPERATURG SYSTEM: MS-DCS 5.0
SOFTWARE: Microsoft Word 5.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/754,918A
FILING DATE: 19910905
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Michaelson, Peter L.
REGISTRATION NUMBER: 30090
REPRENCE/DOCKET NUMBER: Centro-2R
TELEPHONE: (908)530-6634
INFORMATION FOR SEQ ID NO: TELEPHONE: CHARACTERRESTICS:
INFORMATION FOR SEQ ID NO: 4: SEQUENCE CHARACTERRESTICS:
LENGTH: 12 bases
LENGTH: 12 bases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 8; DB 1; Length 12;
Pred. No. 2.8e+02;
0; Mismatches 0; Indels
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(516) 742-4366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: DiGiglio, Frank S.
REGISTRATION NUMBER: 31,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 100.
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: NUCLEOTIDE
STRANDEDNESS: single
1 TOPOLOGY: linear
US-07-754-918A-4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     925 CTTTTATC 932
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US-08-115-497-11
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TELEFAX: (510)670-9302
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 nucleotides
                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 100.
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                908 TITICITI 915
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
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US-08-410-116B-26
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Sequence 8, Application US/08280441
Patent No. 55522708
GENERAL INFORMATION:
APPLICANT: Sydney Brenner
TITLE OF INVENTION: DNA Sequencing by Stepwise Ligation and Cleavage NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PACEUR NO. 3530031.
APPLICANT: SWITZER, Christopher
TITLE OF INVENTION: NOVEL ANTISENSE OLIGONUCLEOTIDES
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSE: Townsend and Townsend Khourie and Crew
STREET: Steuart Street Tower, One Market Plaza
CITY: San Francisco
STATE: California
COMPUTER: California
COMPUTER: Plopy disk
COMPUTER READABLE FORM:
MEDIUM TYPE: Flopy disk
COMPUTER: Plopy disk
COMPUTER: Pacentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
PLING DATE: 18-MAR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 12;
                                                                                                                                                                                                                                                                                                     CORRECTION SYSTEM: Windows 3.1/DOS 5.0
SOFTWARE: Microsoft Word for Windows, vers. 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/280,441
FILING DATE:
CLASSIFICATION 1435
PRIOR APPLICATION NUMBER: 08/222,300
FILING DATE: 04-APR-94
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1; Ler
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 11.0%; Score 8; DB 1
Best Local Similarity 100.0%; Pred. No. 2.6
Matches 8; Conservative 0; Mismatches
                                                                                                                                                                                                              COUNTRI:
ZIP: 95014
COMPUTER READABLE FORM:
MEDLUM TYPE: 3.5 inch diskette
MEDLUM TYPE: 3.5 inch diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-214-603-11/c
; Sequence 11, Application US/08214603
; Patent No. 5596091
                                                                                                                                 ADDRESSEE: Stephen C. Macevicz
STREET: 21890 Rucker Drive
CITY: Cupertino
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                935 TCCTCTTC 942
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 18
CLASSIFICATION:
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US-08410-116B-26
US-08410-116B-26
Sequence 26, Application US/08410116B
Patent No. 5599675
GENERAL INFORMATION:
APPLICANT: Sydney Brenner, Glenn Albrecht, Andrew J. Blasband
APPLICANT: Sydney Brenner, Glenn Albrecht, Andrew J. Blasband
APPLICANT: Applicant 40
COMPRESPONDENCE ADDRESS:
ADDRESSEE: Stephen C. Macevicz, Lynx Therapeutics, Inc.
STREET: 3832 Bay Center Place
CITY: Hayward California
COUNTRY: USA
COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11.0%; Score 8; DB 1; Length 12; 100.0%; Pred. No. 2.8e+02; tive 0; Mismatches 0; Indels
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HATTORNEY/AGENT INFORMATION:

NAME: Kezer, William B.

REGISTRATION NUMBER: 37,369

REFERENCE/DOCKET NUMBER: 2307E-052100US

TELECOMMUNICATION INFORMATION:
TELEFANCE: (415) 543-9600

TELEFAX: (415) 543-5043

INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 base pairs
LENGTH: 12 base pairs
TOPOLOGY: linear

MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "Oligodeoxynucleotide"
US-08-214-603-11
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Gaps
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APPLICANT: KOOL, ETIC T.
TILLE OF INVENTION: STEM-LOOP AND CIRCULAR OLIGONUCLEOTIDES
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSED: Scully, Scott, Murphy & Presser
STREET: 400 Ganden City Plaza
CITY: Garden City
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 11.0%; Score 8; DB 1; Length 12; Best Local Similarity 62.5%; Pred. No. 2.8e+02; Matches 5; Conservative 3; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11.0%; Score 8; DB 1; Length 12;
                                    OPERATION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PPETENTIN Release #1.0, Version #1.25
SUFWARE: PPETENT NELSE #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/408,656
FILING DATE: 21-MAR-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Didiglio, Frank S.
REGISTRATION NUMBER: 93.73
TELEPRAYION NUMBER: 93.73
TELEPRAYION NUMBER: 93.73
TELEPRAY: (516) 742-434
TELEPRAX: (516) 742-434
TELEPRAX: (516) 742-436
TELEPRAX: (516) 742-436
TELEPRAX: (510) NO: 2:
SEQUENCE CHARACTERISTICS:
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            IBM PC compatible SYSTEM: PC-DOS/MS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (516) 742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 12 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: nucleic acid
STRANDEDNESS: single
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STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          931 TCCCTCCT 938
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
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                COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 461
US-08-408-656-3/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TOPOLOGY:
US-08-408-656-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-408-656-3
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            Gaps
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Patent No. 5574683
GENERAL INFORMATION:
APPLICANT: Kool, Eric T.
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSES: Scully, Scott, Murphy & Presser
STREET: 400 Garden City Plaza
CITY: Garden City
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 460
US-08-408-656-2
Sequence 2, Application US/08408656
Patent No. 5674683
GENERAL INFORMATION:
APPLICANT: KOOL, Eric T.
TILE OF INVENTION: STEM-LOOP AND CIRCULAR OLIGONUCLEOTIDES
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Scully, Scott, Murphy & Presser
STREET: 400 Garden City Plaza
CITY: Garden City
CITY: Garden City
            0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
11.0%; Score 8; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 8; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE: Mew York
COUNTRY: U.S.A.
ZIP: 11530-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: INP PC COMPALISH
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Parentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/408,656
FILING DATE: 21-MR-1995
CLASSIFCATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Digillo, Frank S.
REFERENCE/DOCKET NUMBER: 93.346
REFERENCE/DOCKET NUMBER: 91.346
REFERENCE/DOCKET NUMBER: 93.33
TELECOMMUNICATION NUMBER: 91.346
REFERENCE/GOTE NUMBER: 93.346
REFERENCE/GOTE NUMBER: 91.346
REFERENCE/GOTE NUMBER: 91.346
REFERENCE/GOTE NUMBER: 93.33
TELECOMMUNICATION NUMBER: 93.33
TELECOMMUNICATION NUMBER: 93.346
REFERENCE/GOTE NUMBER: 93.33
TELECOMMUNICATION NUMBER: 93.33
    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: U.S.A.
ZIP: 11530-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 12 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: nucleic acid
STRANDEDNESS: single
                                                                        935 TCCTCTTC 942
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           931 TCCCTCCT 938
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US-08-408-656-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New York
                                                                                                                                                                                                                                                             RESULT 459
US-08-408-656-1
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Matches
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USS-ULT 46-413-613

USS-ULT 46-413-613-30

Sequence 30, Application US/08413813

Patent No. 568394

TITLE OF INTENTION:

TITLE OF INTENTION: SINGLE-STRANDED, CIRCULAR OLIGONUCLEOTIDES

NUMBER OF SEQUENCES: 44 Oct., Murphy & Presser

CORRESPONDENCE ADDRESS:

ADDRESSES Scully, Scott, Murphy & Presser

CITY: Garden City
STREET: New York

CUNTRY: USA

ZIP: 11530

COMPUTER: New York

COUNTRY: USA

ZIP: 11530

COMPUTER: EMP PC Compatible

OCMPUTER: IBM PC Compatible

OCMPUTER: IBM PC Compatible

OCMPUTER: Detentin Release #1.0, Version #1.25

CURRENT APPLICATION NUMBER: US/08/413,813

FILING DATE:

ATPLICATION NUMBER: US/08/413,813

FILING DATE: BACHALL REPREMATION:

ATPLICATION NUMBER: 31,346

REGISTRATION NUMBER: 31,346

REGISTRATION NUMBER: 31,346

REGISTRATION NUMBER: 31,346

RELEPRANCE (516) 742-4343

TELEPRANCE (516) 742-4343

TELEPRANCE (516) 742-4343

TELEPRANCE (516) 742-4343

TELEPRANCE (516) 742-4343

TELERANCE (516) 742-4343

TELERANCE (516) 742-4345

TELERANCE (516) 742-4345

TELERANCE (516) 742-4345

TELERANCE (516) 742-4345

TELERANCE (516) 742-4343

TELERANCE (516) 742-4343

TELERANCE (516) 742-4343

TELERANCE (516) 742-4345

TELERANCE (516) 742-4343

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100.0%; Pred. No. 2.8e+02;
tive 0; Mismatches 0; Indels
                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRATI APPLICATION DATA:
APPLICATION NUMBER: US/08/413,813
                                                                                                                                                                                                                                                                                                                                                                FILING DATE:

CLASSIFICATION: 536

TCLASSIFICATION: 536

ATTORNEY/AGENT INFORMATION:
NAME: Didiglio, Frank S.
REGISTRATION NUMBER: 31,346

REFERENCE/DOCKET NUMBER: 31,346

TELEPAN: (516) 742-4343

TELEPAN: (516) 742-4343

TELEPAN: (516) 742-436

TELEPAN: 20 901 SANS UR

INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 base pairs
TYPE: nucleic acid
STRANBEDNESS: single

STRANBEDNESS: single
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Best Local Similarity 100.
Matches 8; Conservative
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STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        908 TITICITI 915
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                                                                                                                     Gaps
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US-08-413-813-13/c
US-08-413-813-13/c
US-08-413-813-13/c
Sequence 13, Application US/08413813
Patent No. 5683874
Fatent No. 5683874
TITLE OF INVENTION: SINGLE-STRANDED, CIRCULAR OLIGONUCLEOTIDES
CORRESPONDENCE ADDRESS:
ADDRESSEE: Scully, Scott, Murphy & Presser
STREET: 400 Garden City Plaza
COUNTRY: USA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    % Sequence 1.2 Application US/08413813

| Sequence 1.2 Application US/08413813
| Patent No. 5633874
| GENERAL INFORMATION:
| APPLICANT: KOOJ, Eric T. TILE OF INVENTION: SINGLE-STRANDED, CIRCULAR OLIGONUCLEOTIDES
| NUMBER OF SEQUENCES: 44
| CORRESPONDENCE ADDRESS: 5cully, Scott, Murphy & Presser STREET: 400 Garden City Plaza
| CITY: Garden City Plaza | COUNTRY: USA | COUNTRY: USA
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                                                    Pred. No. 2.8e+02;
; Mismatches 0; Indels
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ATTORNEY/AGENT INFORMATION:
NAME: Diddiglio, Frank S.
REGISTRATION NUMBER: 31,346
REFRENCE/DOCKET NUMBER: 8085ZX
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
TELEPHONE: (516) 742-4343
TELERAX: (516) 742-4346
TELERAX: 0901 SANS UR
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 base pairs
TYPE: nucleic acid
STREET INFORMATION: 12:
SEGUENCE CHARACTERISTICS:
LENGTH: 12 base pairs
TYPE: nucleic acid
STREET INFORMATION: 12:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
SEGUENCE CH
100.08; Pre-
                                              Best Local Similarity 100.
Matches 8; Conservative
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Best Local Similarity 100.
Matches 8; Conservative
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COMPUTER READABLE FORM:
                                                                                                                                                                                                             931 TCCCTCCT 938
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TITLE OF INVENTION: RNA APTAMERS BASED ON SHAPE SELECTION NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSE: Schwegman, Lundberg, Woessner & Kluth, P.A. STREET: P.O. Box 2938
CITY: Minneapolis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11.0%; Score 8; DB 1; Length 12; 100.0%; Pred. No. 2.8e+02; trive 0; Mismatches 0; Indels
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/466,670
                                                                                                                                                                                                                    COUNTY: USA
ZIF: 55402
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/662,335A
FILING DATE: 12-JUN-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: NO. 5792613e
FILING DATE:
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423.001US1
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REGISTRATION NUMBER: 30,440
REFERENCE/DOCKET NUMBER: 42
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
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TELEFAX: 612-339-3061
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SEQUENCE CHARACTERISTICS:
LENGTH: 12 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 11.0
Best Local Similarity 100.
Matches 8, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: nucleic acid
STRANDEDNESS: single
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CLASSIFICATION:
PRIOR APPLICATION DATA:
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; MOLECULE TYPE: CDNA
US-08-662-335A-16
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COUNTRY:
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                                                                                                                                                                                                                                                                                                                      Sequence 26, Application US/08667689A
Patent No. 5714330
GENERAL INVARIATION:
APPLICANT: Sydney Brenner, Robert B. DuBridge
TITLE OF INVENTION: DNA Sequencing by Stepwise Ligation and Cleavage NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESS:
ADDRESSEE: Stephen C. Macevicz, Lynx Therapeutics, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
              Query Match 11.0%; Score 8; DB 1; Length 12; Best Local Similarity 12.5%; Pred. No. 2.8e+02; Matches 1; Conservative 7; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: USA

ZIP: 94545

ZIP: 94545

COMPUTER READABLE FORM:
MEDIUM TYPE: 0.5 inch diskette
COMPUTER: IBM compatible
OPERATING SYSTEM: Windows, vers. 2.0
SOFTWARE: Microsoft Word for Windows, vers. 2.0
SOFTWARE: MICROSOFT WINDER: US/08/667,689A
FILING DATE: 21-JUN-1996
CLASSIFICATION NUMBER: 08/410,116
FILING DATE: 24-MAR-95
PRIOR APPLICATION NUMBER: 08/22,300
FILING DATE: 04-APR-94
PRIOR APPLICATION NUMBER: 08/22,300
FILING DATE: 04-APR-94
FILING DATE: 04-APR-94
FILING DATE: 04-APR-94
FILING DATE: 25-JUL-94
ATTORNEY/AGENT INFORMATION:
NAME: Stephen C. Macevicz
REGISTRATION NUMBER: 30,285
REFERENCE/DOCKET NUMBER: 801-06
TELECOMMUNICATION INFORMATION:
THELECOMMUNICATION INFORMATION:
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Patent No. 5792613
GENERAL INFORMATION: Schmidt, Francis J.
TITLE OF INVENTION: METHOD FOR OBTAINING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (510) 670-9365
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TELEFAX: (510) 670-9302
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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EDNESS: single
                                                                                                                               908 TTTTCTTT 915
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STATE: California
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US-08-667-689A-26
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Gaps
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US-08-466-670-11
; Sequence 11, Application US/08466670
; Patent No. 5808036
; GENERAL INFORMATION:
; APPLICANT: Kool, Eric T.
; TITLE OF INVENTION: PARALLEL AND ANTIPARALLEL BINDING DOMAINS; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS: 2
; ADDRESSEE: Scully, Scott, Murphy & Presser
; CITY: Garden City Plaza
; CUNTRY: USA
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0; Indels
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100.0%; Pred. No. 2.8e+02;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch diskette
COMPUTER: 18M compatible
OPERATING SYSTEM: Windows 3.1/DOS 5.0
CURRENT APPLICATION DATA:
APPLICATION NOMBER: US/08/712,011
FILING DATE: 11-SPE-96
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RIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 08/410,116
FILING DATE: 24 MAR.95

RIOR APPLICATION DATA:
APPLICATION NUMBER: 08/22,300
FILING DATE: 04.APR.94

PRIOR APPLICATION NUMBER: 08/280,441
FILING DATE: 25-JUL-94
ATTORNEY/AGENT INFORMATION:
NAME: Stephen C. Macevicz
REGISTRATION NUMBER: 30,285
REFERENCE/OCKET NUMBER: 81c3c2
TELEPRONE: (510) 670-9365
TELEPRONE: (510) 670-9365
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APPLICANT: Wu, Fred
APPLICANT: Kealey, James T.
APPLICANT: PRUZAN, RONALd
APPLICANT: PRUZAN, RONALD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12 nucleotides
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Best Local Similarity 100.
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: nucleic acid
STRANDEDNESS: single
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                                   924 CCTTTTAT 931
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US-08-712-011-26
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APPLICANT: Mohr, Ian J.
APPLICANT: Gluzman, Yakov
TITLE OF INVENTION: Avirulent Herpetic Viruses Useful as
TITLE OF INVENTION: Tumoricidal Agents and Vaccines
VUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: American Cyanamid Company
STREET: One Cyanamid Plaza
CITY: Wayne
STRIE: New Jersey
COUNTRY: United States
ZIP: 07470-8426
COMPUTER: READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: OF COMPATIBLE
COMPATIBLE OF COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
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11.0%; Score 8; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 8; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1; Length 12; . 2.8e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
CLASSIFICATION: 424
ATTORNEY/AGENT INPORMATION:
NAMB: Barnhard, Blizabeth M.
REGISTRATION NUMBER: 31,088
REPERENCE/DOCKET NUMBER: 33,161-00
TELECOMMUNICATION INPORMATION:
TELEPHONE: 201-831-3365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11.0%; Score 8; I
100.0%; Pred. No.
APPLICATION NUMBER: 08/115,497
                   FILING DATE:
ATTORNEY/ACENT INFORMATION:
NAME: DIGGGLIO, Frank S.
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 8771
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-434
TELEFAX: 230 901 SANS UR
INFORMATION FOR SEC ID NO: 11: SEQUENCE CHARACTERISTICS:
LENGTH: 12 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
STRANDEDNESS: single
STRANDEDNESS: single
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Patent No. 5824318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 , MOLECULE TYPE: DNA (genomic)
US-08-466-670-11
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MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 100.
Matches 8; Conservative
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SEQUENCE CHARACTERISTICS:
LENGTH: 12 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      908 TTTTCTTT 915
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-686-631-7
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US-08-712-011-26

| Sequence 26, Application US/08712011
| Sequence 26, Application US/08712011
| Patent No. 5831065
| Patent No. 5831065
| Patent No. 5831065
| TITLE OF INVENTION:
| APPLICANT: Sydney Brenner
| TITLE OF INVENTION: Kits for DNA Sequencing by Stepwise Ligation and Cleavage NUMBER OF SEQUENCES: 40
| CORRESPONDENCE ADDRESS: ADDRESSEE: Stephen C. Macevicz, Spectragen, Inc. STREET: 3312 Bay Center Place CITY: Hayward CITY: Hayward STATE: California Gaps ö

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US-08-173-489C-83/c

Sequence 83, Application US/08173489C

Sequence 83, Application US/08173489C

Sequence 83, Application

Sequence 83, Application

Parent No. 5861244

APPLICANT: WANG, C. -G.

APPLICANT: HEPBURN, A. G.

ITLE OF INVENTION: TRIPLE-STRAND FORMATION.

ITLE OF INVENTION: TRIPLE-STRAND FORMATION.

NUMBER OF SEQUENCES: 365

CORRESPONDENCE ADDRESS: 365

STREET: PROFILE DIAGNOSTIC SCIENCES, INC.,

STREET: SIO EAST 73RD STREET,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11.0%; Score 8; DB 1; Length 12;
100.0%; Pred. No. 2.8e+02;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            retinoblastoma gene (Accession # M33647, J02994) nucleotides 1842 to 1853
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44Mb storage COMPUTER: 1BM FC/XT/AT COMPUTER: 1BM FC/XT/AT COMPUTER: 1BM FC/XT/AT CORRATING SYSTEM: MS-DOS version 6.2 SOFTWARE: Wordperfect Version 5.1 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/173,489C FILING DATE: 2 DEC 1993 CLASSIFICATION DATA: APPLICATION DATA: APPLICATION NUMBER: US 07/968,436 FILING DATE: 29 OCT 1992 ATTORNEY AGENT INFORMATION: NAME: Handelman, Joseph H. REFERENCE/DOCKET NUMBER: US-179 REFERE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (attorney) (212) 708-1880
httorney) (212) 246-8959
SEQ ID NO: 83:
FILING DATE: 04-APR-94
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/280,441
FILING DATE: 25-JUL-94
ATTORNEY/AGENT INFORMATION:
NAME: Stephen C. Macevicz
REGISTRATION NUMBER: 30,285
REGISTRATION NUMBER: 30,285
REBERENCE/DOCKET NUMBER: 31,301
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 nucleotides
TYPE: nucleic acid
STRANDENNESS: single
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TYPE: Nucleic Acid
STRANDEDNESS: double stranded
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 100.
Matches 8; Conservative
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DESCRIPTION:
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TOPOLOGY:
US-08-478-239A-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: NEW
STATE: NE
COUNTRY:
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       TITLE OF INVENTION: Methods for Detecting the RNA Component of TITLE OF INVENTION: Telomerase
NUMBER OF SEQUENCES: 26
CORRESPONDENCES. ADDRESSES: ADDRESSES: TOWNSEND and TOWNSEND and CREW LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
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MEDIUM TYPE: 3.5 inch diskette
COMPUTER: 18M compatible
COMPUTER: 18M compatible
COMPUTER: 18M compatible
OPERATING SYSTEM: Windows 3.1/DOS 5.0
SOFTWARE: Microsoft Word for Windows, vers. 2.0
CURRENT APPLICATION NUMBER: US/08/478,239A
FILING DATE: 07-JUN-95
CLASSIFICATION NUMBER: 08/410,116
FILING DATE: 24-MAR-95
PRIOR APPLICATION NUMBER: 08/410,116
FILING DATE: 24-MAR-95
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/222,300
                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

MEDIUM TYPE: Floppy disk

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/770,565

FILING DATE: 20-DEC-1996

CLASSIFICATION: 435

ATTONREY/AGENT INPORMATION:

NAME: Storella, John R:

REGISTRATION NUMBER: 32,944

REGISTRATION NUMBER: 32,944

RELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-478-239A-26

Sequence 26, Application US/08478239A

Patent No. 5856093

GENERAL INFORMATION:
APPLICANT: Sydney Brenner
ITILE OF INVENTION: Method of Determining Zygosity
NUMBER OF SEQUENCES: 40

CORRESPONDENCE ADDRESS:
ADDRESSEE: Stephen C. Macevicz, Spectragen, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: Stephen C. Macevicz, Spectragen, Inc. STREET: 3812 Bay Center Place CITY: Hayward STATE: California COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11.0%; Score 8; DB 1; Le
100.0%; Pred. No. 2.8e+02;
ative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 4: SEQUENCE CHARACTERISTICS: LENGTH: 12 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           935 TCCTCTTC 942
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4 TCCTCTTC 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 8; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-770-565-4
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Gaps
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APPLICANT: Kool, Eric T.
APPLICANT: Kool, Eric T.
TITLE OF INVENTION: SINGLE-STRANDED, CIRCULAR OLIGONUCLEOTIDES
NUMBER OF SUCURNES: 44
CORRESPONDENCE ADDRESS:
ADDRESSEE: Soully, Scott, Murphy & Presser
STREET: 400 Garden City Plaza
CITY: Garden City
STATE: New York
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  %30.8-467.346-30

Sequence 30, Application US/08467346

Parent No. 587210.8

CORRESPONDENCE ADDRESS:

ADDRESSEE: Scully, Scott, Murphy & Presser
                                                                                   11.0%; Score 8; DB 1; Length 12; 100.0%; Pred. No. 2.8e+02; tive 0; Mismatches 0; Indels
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Pred. No. 2.8e+02;
0; Mismatches 0; Indels
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APPLICATION NUMBER: US/08/467,346
FILING DATE: 06-JUN-1995
CLASSIFICATION NUMBER: US/08/467,346
FILING DATE: 06-JUN-1995
CLASSIFICATION NUMBER: US/08/413,813
APPLICATION NUMBER: US 08/413,813
ATTORNEY/AGENT INFORMATION:
NAME: DiGiglio, Frank S.
REGISTRATION NUMBER: 8085ZYX
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                US-08-467-346-13/c
; Sequence 13, Application US/08467346
; Patent No. 5872105
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Best Local Similarity 100.0%; P
Matches 8; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: New York
COUNTRY: USA
ZIP: 11530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4366
TELEK: 230 901 SANS UF
INFORMATION FOR SEQ ID NO: 13
SEQUENCE CHARACTERISTICS:
                                                                            Query Match
Best Local Similarity 100.
Matches 8; Conservative
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STRANDEDNESS: single
                                                                                                                                                                                                                    908 TTTTTTT 915
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                 US-08-467-346-12
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| Sequence 12, Application US/08467346
| Patent No. 587210.
| GENERAL INFORMATION:
| APPLICANT: Kool, Eric T.
| TITLE OF INVENTION: SINGLE-STRANDED, CIRCULAR OLIGONUCLEOTIDES NUMBER OF SEQUENCES: 44
| CORRESPONDENCE ADDRESS: ADDRESSE: Scully, Scott, Murphy & Presser STRET: 400 Garden City Plaza STRET: 400 Garden City Plaza COUNTRY: Garden City
| STRIE: New York COUNTRY: USA
ANTI-SENSE: No
ORGANISM: Homo sapiens
MAP POSITION: 13244.2
PUBLICATION INFORMATION:
AUTHORS: Wang X P, Bogenmann, E, Li, F P, Weinberg, AUTHORS: R A

ITILE: Deletions of a DNA sequence
TITLE: Organization of the sequence and its encoded
TITLE: protein
JOURNAL: Sciences, USA
WANTIONAL: Sciences, USA
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Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 8; Conservative 0; Mismatches 0; Indels
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MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,346
FILING DATE: 06-UN-1995
PRIOR APPLICATION: 536
PRIOR APPLICATION NUMBER: US/08/413,813
FILING DATE: 30-MAR-1995
ATOMNEY/AGENT INFORMATION:
NAME: DIGGGJIO, FRANK S.
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 31,346
REFERENCE/DOKET NUMBER: 31,346
REGISTRATION INFORMATION:
TELEFAX: (516) 742-4343
TELEFAX: (516) 742-4343
TELEFAX: (516) 742-436
TELEFAX: (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DATE: 1987; RELEVANT RESIDUES IN SEQ ID NO: 83 :FROM 1 TO 12 US-08-173-489C-83
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PAGES:
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19-08-654-823B-655

19-08-654-823B-655

19-08-654-823B-655

19-08-654-823B-655

19-08-654-825B-655

19-08-654-825B-654

19-08-
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Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 8; Conservative 0; Mismatches 0; Indels
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Best Local Similarity 100.0%; Pred. No. 2.6
Matches 8; Conservative 0; Mismatches
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NAME: Misrock, S. Leslie
RECISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 7934-
TELEPHONE: (212) 790-990
TELEPHONE: (212) 869-9741/8864
                         TELEPHONE: (703) 205-8000
TELEPAX: (703) 205-8050
INFORWATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 65:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           948 TITAATGI 955
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-663-823B-65
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                                                                                                                                                          COMPUTER: 11330
COMPUTER: Floppy disk
COMPUTER: Floppy disk
COMPUTER: Floppy disk
COMPUTER: Floppy disk
COMPUTER: Patentin Release #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,346
FLING DATE: 06-UN-1995
PRIOR APPLICATION: 536
PRIOR APPLICATION NUMBER: US 08/413,813
FILING DATE: 30-MAR-1995
ATTORNEY AGENT INFORMATION:
NAME: Digiglio, Frank S:
REGISTRATION NUMBER: 8085ZXX
TELEGRACE/DOCKET NUMBER: 8085ZXX
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: (516) 742-4343
TELEFAX: (516) 742-4346
TELEFAX: (516) 742-4346
TELEFAX: SO 901 SANS UR
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 Dase pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: NAKATANI, TOMOYUKI
APPLICANT: GOMI, HIDEYUKI
APPLICANT: WIJDENES, JOHN
APPLICANT: NOGUCHI, HIROSHI
TITLE OF INVENTION: HUMANIZED B-B10
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH
STREET: PO BOX 747
CITY: FALLS CHURCH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: USA

ZIF: 22040-0747

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,081B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: SVENSSON, LEONARD REGISTRATION NUMBER: 30,330
REFERENCE/DOCKET NUMBER: 20-3484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 476
US-08-232-081B-33/c
; Sequence 33, Application US/08232081B
; Patent No. 5886152
STREET: 400 Garden City Plaza
CITY: Garden City
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: nucleic acid
STRANDEDNESS: single
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Sequence 86, Application US/08874825

Patent No. 6057101

GENERAL INFORMATION:
APPLICANT: Nandabalan, Krishnan
APPLICANT: Rothberg, Jonathan
APPLICANT: Rang, Meijia
APPLICANT: Kanght, James
APPLICANT: Kalbfleisch, Theodore
TITLE OF INVENTION: IDENTIFICATION AND COMPARISON OF
TITLE OF INVENTION: AND IDENTIFICATION OF INHIBITORS OF THESE INTERACTORS
ITLE OF INVENTION: AND IDENTIFICATION OF INHIBITORS OF THESE INTERACTORS
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11.0%; Score 8; DB 1; Length 12; 100.0%; Pred. No. 2.8e+02; tive 0; Mismatches 0; Indels
              COMPUTER READABLE FORM:
MEDIUM TYPE: FIDDPY disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/779,355
PLING DATE: 06-JAN-1997
CLASSIFICATION: 435
PLING APPLICATION WHERE: US/08/775,993
FILING DATE: 03-JAN-1997
ATPONER' APPRICATION NUMBER: 36,576
REFERENCE/DOCKET NUMBER: 36,576
REFERENCE/DOCKET NUMBER: 36,576
REFERENCE/COMPATION: NUMBER: 36,576
REFERENCE/COMPATION: NUMBER: 36,576
REFERENCE/COMPATION NUMBER: 13,536
TELEFRAX: (202)628-8844
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 base pairs
LEUGHER: 12 base pairs
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COMPUTER: IBM COMPATIBLE
SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION NUMBER: US/08/874,825
FILING DATE: 13-UNN-1997
CLASSIFICATION: 435
PRIOR APPLICATION: 435
PRIOR APPLICATION: 435
PRIOR APPLICATION: 08/663,824
FILING DATE: 14-UNN-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-779-355-10
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Best Local Similarity 100.
Matches 8; Conservative
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      935 TCCTCTTC 942
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 USA
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COUNTRY:
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                                                                                           Sequence 13, Application US/08507032

APPLICANT: Planagan, William A. APPLICANT: Crabtree, Gerald R. TITLE OF INVENTION: Screening Methods for Immunosuppressive TITLE OF INVENTION: Agents

NUMBER OF SEQUENCES: 19

CORRESPONDENCE: 19

STREET: One Market Plaza, Steuart Tower, Suite 2000

CITY: San Francisco

STREET: One Market Plaza, Steuart Tower, Suite 2000

CITY: San Francisco

STATE: California

COMUTRY: USA

ZIP: 94105

MEDIUM TYPE: READABLE FORM:

MEDIUM TYPE: PLOPDY disk

COMPUTER: IBM PC Compatible

COMPUTER: IBM PC Compatible

COMPUTER: IBM PC Compatible

COMPUTER: PRESPONDENCE

SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
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US-08-79-355-10
US-08-79-355-10
Sequence 10, Application US/08779355
Patent No. 6017701
GENERAL INFORMATION:
APPLICANT: Mullinax, Rebecca L.
TITLE OF INVENTION: METHODS AND ADAPTORS FOR GENERATING TITLE OF INVENTION: SPECIFIC NUCLBIC ACID POPULATIONS NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: Evenson, McKeown, Edwards & Lenahan P.L.L.C.
STREET: D.C.
STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 1; Length 12; . 2.8e+02;
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Best Local Similarity 100.0%; Pred. No. 2.8
Matches 8; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
CLASSIPECATION:
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/08/228,944
FILING DATE:
APPLICATION NUMBER: US 07/749,385
FILING DATE: 22-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
RECISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 5490A-89
TELECOMMUNICATION INFORMATION:
TELEPAX: 415-326-2402
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/507,032
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      nucleic acid
EDNESS: single
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                                                RESULT 478
US-08-507-032-13/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-507-032-13
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Gaps

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Sequence 112 Application US/08874825
Patent No. 6657101
GENERAL INFORMATION:
APPLICANT: Nandabalan, Krishnan
APPLICANT: Rothberg, Jonathan
APPLICANT: Raight, James
APPLICANT: Kaight, James
APPLICANT: Kaight, James
TITLE OF INVENTION: IDENTIFICATION AND COMPARISON OF
TITLE OF INVENTION: PROTEIN-PROTEIN INTERACTIONS THAT OCCUR IN POPULATIONS
TITLE OF INVENTION: AND IDENTIFICATION OF INHIBITORS OF THESE INTERACTORS
NUMBER OF SEQUENCES: 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ô
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                                                        11.0%; Score 8; DB 1; Length 12; 100.0%; Pred. No. 2.8e+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPTRY: USA

ZIP: 10036/2711

COMPUTER REDABLE FORM:
MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSEQ Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/97

FLING DATE: 13-UN-1997

FLING APPLICATION DATA:

APPLICATION NUMBER: 08/63,824

FILING DATE: 14-UN-196

ATTORNEY AGENT INFORMATION:
NAME: Misrock, S. Leslie

REGISTRATION NUMBER: 18,872

REGISTRATION NUMBER: 18,872

REGISTRATION NUMBER: 13,872

REGISTRATION NUMBER: 13,872

REGISTRATION NUMBER: 13,872

REFERENCE/DOCKET NUMBER: 7934-045

TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STAIE: NY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 483
US-08-938-835A-10
; Sequence 10, Application US/08938835A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 212-869-8864
TELEX: 66141 PENNIE
INPORMATION POS SEQ ID NO: 112:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 base pairs
                                                                                  Best Local Similarity 100.
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                          937 CICITCAI 944
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US-08-874-825-112
                                                                                                                                                                                                                                                                                                     US-08-874-825-112
               US-08-874-825-87
                                                             Query Match
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US-08-874-825-87
i Sequence 87, Application US/08874825
i Patent No. 6057101
j GENERAL INFORMATION:
APPLICANT: Nandabalan, Krishnan
APPLICANT: Rothberg, Jonathan
APPLICANT: Kalbfleisch, Theodore
i APPLICANT: Kalbfleisch, Theodore
ITILE OF INVENTION: IDENTIFICATION AND COMPARISON OF
ITILE OF INVENTION: AND IDENTIFICATION OF INHIBITORS OF THESE INTERACTORS
ITILE OF INVENTION: AND IDENTIFICATION OF INHIBITORS OF THESE INTERACTORS
CORRESPONDENCE ADDRESS:
ADDRESSE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY. New York
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COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0
CURSENT APPLICATION DATA:
APPLICATION NUMBER: US/08/874,825
FILING DATE: 13-UN-1997
CLASSIFICATION NUMBER: 08/63,824
FILING DATE: 14-UN-1996
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 7934-045
TELECHONE: 212-790-9090
TELECHONE: 212-790-9090
TELEFAX: 212-869-8864
INFORMATION FOR SEQ ID NO: 87:
                                                           7934-045
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 7934-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-790-9090
TELEFAX: 212-868-8864
TELEX: 6141 PENNIE
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 12 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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LENGTH: 12 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLLOGY: linear
MOLECULE TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 100.
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   937 CTCTTCAT 944
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4 CTCTTCAT 11
                                                                                                                                                                                                                                                                                                     ; TOPOLOGY: linear; MOLECULE TYPE: DNA US-08-874-825-86
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STATE: NY
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Gaps

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JACKENT NO. 80.7 (1008)

JACKENT NOOL, ERIC T.

APPLICANT: KOOL, ERIC T.

TITLE OP INVENTION: HIGHLY SENSITIVE MULTIMERIC NUCLEIC ACID PROBES
FILE REFERENCE: 220.00010.30

CURRENT APPLICATION NUMBER: U$ (08/09/910, 632B)

CURRENT APPLICATION NUMBER: U$ (08/05, 631)

BARLIER APPLICATION NUMBER: 08/05.631

BARLIER PILING DATE: 1997-02-26

EARLIER PILING DATE: 1995-02-23

BARLIER PILING DATE: 1995-04-15

NUMBER OF SEQ ID NOS: 83

SOFTWARE: PATENTING DATE: 1993-04-15

NUMBER OF SEQ ID NOS: 83

SOFTWARE: PATENTING DATE: 2.0

SEQ ID NO 11

LENGTH: 12
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TITLE OF INVENTION: HIGHLY SENSITIVE MULTIMERIC NUCLEIC ACID PROBES TITLE OF INVENTION: HIGHLY SENSITIVE MULTIMERIC NUCLEIC ACID PROBES FILE REFERENCE: 220.00010130.

CURRENT APPLICATION NUMBER: US/08/910,632B

CURRENT FILING DATE: 1997-08-13

EARLIER PRILING DATE: 1997-02-26

EARLIER FILING DATE: 1997-02-23

EARLIER FILING DATE: 1993-04-15

NUMBER: OF SEQ ID NOS: 83

SOFTHARE: PATENTING DATE: 1993-04-15

NUMBER: OF SEQ ID NOS: 83

SOFTHARE: PATENTING DATE: 1003-04-15

SOFTHARE: PATENTING DATE: 1003-04-15
                                                                                                                                                                  Query Match
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 8; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11.0%; Score 8; DB 1; Length 12; 100.0%; Pred. No. 2.8e+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                         US-08-910-632-11/c
; Sequence 11, Application US/08910632B
; Patent No. 6077668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CTHER INFORMATION: desired oligomer US-08-910-632-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 36, Application US/08910632B Patent No. 6077668 GENERAL INFORMATION:
; SEQ ID NO 8

; LENGTH: 12

TYPE: DNA

ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: linear sequence
US-08-910-632-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 100.
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               908 TITICITY 915
                                                                                                                                                                                                                                                                908 TTTTCTTT 915
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TITLE OF INVENTION:
APPLICANT: KOOL, ERIC T.
TITLE OF INVENTION:
HIGHLY SENSITIVE MULTIMERIC ACID PROBES
CURRENT APPLICATION NUMBER: US/08/910,632B
CURRENT FILING DATE: 1997-08-13
EARLIER APPLICATION NUMBER: 08/805,631
EARLIER FILING DATE: 1995-02-26
EARLIER FILING DATE: 1995-02-23
EARLIER APPLICATION NUMBER: 08/33,439
EARLIER APPLICATION NUMBER: 08/33,439
EARLIER APPLICATION NUMBER: 08/33,439
EARLIER PILING DATE: 1993-04-15
NUMBER OF SEQ ID NOS: 83
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                      GENERAL INFORMATION:
APPLICANT: SORGE, Joseph A.
APPLICANT: MULINAX, Rebecca L.
TITLE OF INVENTION: METHODS AND ADAPTORS FOR GENERATING
TITLE OF INVENTION: SPECIFIC NUCLEIC ACID POPULATIONS
NUMBER OF SEQUENCES: 69
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Parabow, Garrett &
ADDRESSE: Dunner, L.L.P.
STREET: 1300 I Street, N.W.
CITY: Washington
STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                          Score 8; DB 1; Le
Pred. No. 2.8e+02;
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                                                                                                                                                                                                                                                                                COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 484
US-08-910-632-8/c
: Sequence 8, Application US/08910632B
; Patent No. 6077668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
11.0%; Soc
Best Local Similarity 100.0%; Pi
Matches 8; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-938-835A-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  935 TCCTCTTC 942
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         Patent No. 6060245
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937 CTCTTCAT 944
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STATE: Minnesota
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4 CTCTTCAT 11
  4 CTCTTCAT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                            Sequence 86, Application US/08663824

Batent No. 6083693

GENERAL INFORMATION:
GANEALINFORMATION:
GANEALINFORMATION:
APPLICANT: Nandabalan, Krishnan
APPLICANT: Nandabalan, Krishnan
APPLICANT: NOTEMPTION: IDENTIFICATION AND COMPARISON OF PROTEIN-PROTEIN
TITLE OF INVENTION: INTERACTIONS THAT OCCUR IN POPULATIONS
FILE REFERENCE: 7994-006
CURRENT APPLICATION NUMBER: US/08/663,824
CURRENT FILING DATE: 1996-06-14
NUMBER OF SEQ ID NOS: 118
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Nandabalan, Krishnan
APPLICANT: Scriberg, Jonachan
APPLICANT: Scriberg, Jonachan
TITLE CANT: TECTE OF INVENTION: IDENTIFICATION AND COMPARISON OF PROTEIN-PROTEIN
TITLE OF INVENTION: INTERACTIONS THAT OCCUR IN POPULATIONS
FILE REFERENCE: 7934-006
CURRENT APPLICATION NUMBER: US/08/663,824
CURRENT PILING DATE: 1996-06-14
NUMBER OF SEQ ID NOS: 118
SOFTWARE: Patentin Ver. 2.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; OTHER INFORMATION: Description of Artificial Sequence: linker US-08-663-824-87
                                                                                                                  DB 1; Length 12;
. 2.8e+02;
ches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 11.0%; Score 8; DB 1; Length 12; Best Local Similarity 100.0%; Pred. No. 2.8e+02; Matches 8; Conservative 0; Mismatches 0; Indels
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                                                                                                                  Query Match
11.0%; Score 8; DB 1
Best Local Similarity 100.0%; Pred. No. 2.8
Matches 8; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Sequence 87, Application US/08663824
; Patent No. 6083693
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
ORGANISM: Artificial Sequence
                                           ) OTHER INFORMATION: primer US-08-910-632-36
                                                                                                                                                                                                                   908 TTTTCTTT 915
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     937 CTCTTCAT 944
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                                                                                                                                                                                                                                                               11 TTTTCTT 4
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US-08-663-824-87
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LENGTH: 12
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WESULT 489

19-68-65-124-112

Sequence 112, Application US/08653824

Sequence 112, Application US/08653824

Sequence 112, Application US/08653824

Sequence 112, Application US/08653824

APPLICANT NANDAMBLAIN, THERACTIONS THAT OCCUR IN POPULATIONS

TILLE REFERENCE 7934-006

CURRENT PAPLICATION WINDER: US/08/663,824

SOUTHAR SEQUENCE 7934-006

SOUTHAR SEGUENCE 7034-006

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ABELICANT: UNIVERSITY OF ROCHESTER
APPLICANT: UNIVERSITY OF ROCHESTER
TITLE OF INVENTION: CIRCULAR DNA VECTORS FOR SYNTHESIS OF RNA AND
TITLE OF INVENTION: DNA
NUMBER OF SEQUENCES: 72
CORRESPONDENCES: 72
CORRESPONDENCES: ADDRESS:
STREET: MINNESOLE: MUETING, RAASCH & GEBHARDT, P.A.
STREET: Minnespolis
STREET: Minnespolis
STATE: Minnespolis
STATE: MINNESOLE
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM:
OPERATING SYSTEM:
CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER:
FLING DATE: 26-FEB-97
CLASSIFICATION S36
PRIOR APPLICATION NUMBER: US/08/805,631A
APPLICATION NUMBER: US/08/805,631A
APPLICATION NUMBER: US/08/393,439
FILING DATE: 23-FEB-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/393,439
FILING DATE: 15-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: SANDBERG, VICTORIA A.
REGISTRATION NUMBER: 41,287
REFERENCE/DOCKET NUMBER: 220.00010140
TELECOMMULCATION NUMBER: 41,287
REFERENCE/DOCKET NUMBER: 220.00010140
TELECOMMULCATION INFORMATION:
TELECOMMULCATION NUMBER: 220.00010140
TELECOMMULCATION S50.1226
INFORMATION FOR SEQ ID NO: 36: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                          US-08-805-631A-36/c
; Sequence 36, Application US/08805631A
; Patent No. 6096880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 55401
COMPUTER READABLE FORM:
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: UNIVERSITY OF ROCHESTER
TITLE OF INVENTION: CIRCULAR DNA VECTORS FOR SYNTHESIS OF RNA AND
TITLE OF INVENTION: DIA
NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
ADDRESSEE: MUETINO, RAASCH & GEBHARDT, P.A.
STREET: 119 No. 6096880th Fourth Street, Suite 201
CITY: Minneapolis
STRTE: Minneapolis
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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100.0%; Pred. No. 2.8e+02;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                     0; Indels
                                                                                                                                                                                                                                                     Score 8; DB 1; Length 12;
Pred. No. 2.8e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: USA
ZIP: 55401
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBN PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/805,631A
FILING DATE: 26-FEB-97
FILING DATE: 23-FEB-1995
FILING DATE: 13-6-FEB-1995
FILING DATE: 13-48-1993
FILING DATE: 15-APR-1993
APPLICATION NUMBER: US 08/047,860
FILING DATE: 15-APR-1993
ATTORNEY/AGENT INFORMATION:
ARPLICATION NUMBER: 41,287
REGISTRATION NUMBER: 220.00010140
TELEPHONE: 612-305-1226
TELEPHONE: 612-305-1226
TELEPHONE: 612-305-1226
TELEPHONE: G12-305-1226
TELEPHONE: G12-305-12
                                                                                                                                                                                                                                 11.0%; Scott 100.0%; Pred. No. ...
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US-08-805-631A-11/c
; Sequence 11, Application US/08805631A
; Patent No. 6096880
                                                                                                                            TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)
US-08-805-631A-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: DNA (genomic)
SEQUENCE CHARACTERISTICS:
LENGTH: 12 base pairs
                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 100.
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 100.
Matches 8; Conservative
                                 LENGTH: 12 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     908 TITICITY 915
                                                                                                                                                                                                                                                                                                                                                                                 908 TITICITI 915
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Sequence 45, Application US/09593323

Batent No. 6265213

GENERAL INFORMATION:
APPLICANT: Morgan, Antony R.
APPLICANT: Severini, Alberto
TITLE OF INVENTION: Compositions and Methods for Determining the Activity
TITLE OF INVENTION: of DNA-Binding Proteins and of Initiation of
TITLE OF INVENTION: Transcription
FILE REFERENCE: DNAB-02921
CURRENT APPLICATION NUMBER: US/09/593,323
CURRENT FILING DATE: 2000-06-13
PRIOR APPLICATION NUMBER: 09/344,300
PRIOR FILING DATE: 1999-06-24
11.0%; Score 8; DB 1; Length 12; 100.0%; Pred. No. 2.8e+02;
                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQ ID NOS: 72
PatentIn Ver. 2.0
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SOFTWARE:
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Sequence 59, Application US/09354231B
Sequence 59, Application US/09354231B
Sequence 59, Application US/09354231B
GENERAL INFORMATION:
APPLICANT: DeBonte, Lorin R.
APPLICANT: Shorrosh, Basil S.
TITLE OF INVENTION: FATTY ACID DESATURASES AND MUTANT SEQUENCES THEREOF
TITLE OF INVENTION: FATTY ACID DESATURASES AND MUTANT SEQUENCES THEREOF
CURRENT APPLICATION NUMBER: US/09/354,231B
CURRENT FILING DATE: 1999-07-16
PRIOR APPLICATION NUMBER: US 08/874,109
PRIOR APPLICATION NUMBER: US 08/874,109
NUMBER OF SEQ ID NOS: 69
SEQ ID NO S9
LENGTH: 12
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                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Morgan, Antony R.
APPLICANT: Morgan, Antony R.
APPLICANT: Severini, Alberto
TITLE OF INVENTION: Compositions and Methods for Determining the Activity
TITLE OF INVENTION: of DNA-Binding Proteins and of Initiation of
TITLE OF INVENTION: Transcription
FILE REFERENCE: DNAB-0291
CURRENT APPLICATION NUMBER: US/09/344,300B
CURRENT FILING DATE: 1999-06-24
NUMBER OF SEQ ID NOS: 72
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 45
LENGTH: 12
                                                                                                                               Gaps
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; OTHER INFORMATION: Description of Artificial Sequence: Synthetic US-09-344-300-45
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                                                                        Query Match
11.0%; Score 8; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 8; Conservative 0; Mismatches 0; Indels
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11.0%; Score 8; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 8; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                               Sequence 45, Application US/09344300B
Patent No. 6297013
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA ORGANISM: Phaseolus vulgaris
       OTHER INFORMATION: Primer
                                                                                                                                                                              954 GTATCGCT 961
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Best Local Similarity
Matches 8; Conserv
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               US-09-281-418-185
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APPLICANT: Inoue, Takakazu
TITLE OF INVENTION: Method of Amplifying DNA Fragment, Apparatus for Amplifying DNA F
TITLE OF INVENTION: agenet, Method of Assaying Microorganisms, Method of Analyzing Mi
TITLE OF INVENTION: agenet, Method of Assaying Microorganisms, Method of Analyzing Mi
TITLE OF INVENTION: nisms and Method of Assaying Contaminant
TITLE OF INVENTION: 1992-03-7
CURRENT PAPLICATION NUMBER: 1999-03-30
EARLIER APPLICATION NUMBER: 1999-03-31
EARLIER PILING DATE: 1999-03-16
EARLIER FILING DATE: 1999-03-16
NUMBER OF SEQ ID NOS: 216
SEQ ID NO 185
LENGTH: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 45, Application US/09594108
| Patent No. 628448|
| Patent No. 628448|
| GENERAL INFORMATION:
| APPLICANT: Morgan, Antony R. APPLICANT: Severini, Alberto | TITLE OF INVENTION: Compositions and Methods for Determining the Activity | TITLE OF INVENTION: Transcription | TITLE OF INVENTION: Transcription | TITLE OF INVENTION: Transcription | FILE REFERENCE: DNAB-02921 | CURRENT APPLICATION NUMBER: US/09/594,108 | PRIOR APPLICATION NUMBER: 09/344,300 | PRIOR PILING DATE: 1999-06-13 | PRIOR PILING DATE: 1999-06-24 | NUMBER OF SEQ ID NOS: 72 | SOFTWARE: PatentIn Ver. 2.0
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                                                                                                        , OTHER INFORMATION: Description of Artificial Sequence: Synthetic US-09-593-323-45
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Patent No. 6287769
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100.0%; Pre
SEQ ID NO 45
LENGTH: 12
TYPE: DNA
ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA ORGANISM: Artificial Sequence
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Best Local Similarity 100.
Matches 8; Conservative
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US-09-281-418-185/c
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US-09-594-108-45/c
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LENGTH: 12
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APPLICATION NUMBER: US 08/805,631
FILING DATE: 26-FEB-97
APPLICATION NUMBER: US 08/393,439
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Best Local Similarity luv.
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Sequence 11, Application US/09569344
Patent No. 6368802
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: UNIVERSITY OF ROCHESTER
TITLE OF INVENTION: CIRCULAR DNA VECTORS FOR SYNTHESIS OF RNA AND DNA
                                            Sequence 8, Application US/09569344

Sequence 8, Application US/09569344

Patent No. 6368802

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: UNIVERSITY OF ROCHESTER
TITLE OF INVENTION: CIRCULAR DNA VECTORS FOR SYNTHESIS OF RNA AND DNA
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CORRESPONDENCE ADDRESS:
ADDRESSEE: MUETING, RAASCH & GEBHARDT, P.A.
STREET: 119 No. 6368802th Fourth Street, Suite 201
CITY: Minneapolis
STATE: Minnesota
                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: MUETING, RAASCH & GEBHARDT, P.A.
STREET: 119 No. 6368802th Fourth Street, Suite 201
CITY: Minneapolis
STATE: Minnesota
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11.0%; Score 8; DB 1; Length 12; 100.0%; Pred. No. 2.8e+02; ative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                   ZIP: 55401

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: 1BM PC compatible
OPPUTER: SYSTEM: PC-DOS/MS-DOS
OPPETATION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/569,344
FILING DATE: 11-MAY-2000
CLASSIFICATION: cUnknown>
PRIOR APPLICATION: cUnknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/393,439
FILING DATE: 26-FEB-97
APPLICATION NUMBER: US 08/393,439
FILING DATE: 23-FEB-1995
APPLICATION NUMBER: US 08/047,860
FILING DATE: 15-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: SANDERG, VICTORIA A.
REGISTRATION NUMBER: 41,287
REFERENCE/DOCKET NUMBER: 220.00010140
TELECOMMUNICATION INFORMATION:
TELEFAX: 612-305-1226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 8:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 12 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 100.
Matches 8; Conservative
                                                                                                                                                                                                 NUMBER OF SEQUENCES:
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RESULT 498
US-09-569-344-8/c
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RESULT 500
US-09-569-344-36/c
US-09-569-344-36/c
; Sequence 37, Application US/09569344
; Patent No. 6368802
; GENERAL INFORMATION:
; GENERAL INFORMATION:
; TITLE OF INVENTION: CIRCULAR DNA VECTORS FOR SYNTHESIS OF RNA AND
TITLE OF INVENTION: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
COUNTER: COLUTER: COLUTER: SA401

COMPUTER READALBE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IDB PC compatible
COMPUTER: Datenin Release #1.0, Version #1.30
SOFTWARE: Patenin Release #1.0, Version #1.30
CURRITY APPLICATION NUMBER: US (08/05,631
FILING DATE: 11-MAY-2000
FILING DATE: 26-FEB-97
FILING DATE: 27-FEB-1995
FILING DATE: 15-APR-1993
ATTORNEY AGENT INCRMATION:
NAME: SANDBERG, VICTORIA A.
REGISTRATION NUMBER: 41,287
FILING DATE: 41,287
FILING DATE: 12-305-1226
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LEBNOTH: 12 base pairs
THENOTH FOR SEC ACID
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CORRESPONDENCE ADDRESS: 72
CORRESPONDENCE ADDRESSE: MUSTING, RAASCH & GEBHARDT, P.A.
STREET: 119 No. 6368802th Fourth Street, Suite 201
CITY: Minneapolis
STATE: Minneapolis
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYRE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/569,344
FILING DATE: 11-May-2000
CLASSIFCATION: cURKNOWN>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 11:
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Page 180

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; FILE REFERENCE: 7934-087
; CURRENT APPLICATION NUMBER: US/09/231,303
; CURRENT FILING DATE: 1999-01-12
; EARLIER APPLICATION NUMBER: 08/663,824
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: Patentin Ver. 2.0
; SRQ ID NO 87
; LENGTH: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                             TYPE: DNA ORGANISM: Artificial Sequence
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Best Local Similarity 100.
Matches 8, Conservative
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Sequence 86, Application US/09231303

Patent No. 6395478

GENERAL INFORMATION:

APPLICANT: Nandabalan, Krishnan

APPLICANT: Nandabalan, Krishnan

TITLE OF INVENTION: IDENTIFICATION AND COMPARISON OF PROTEIN-PROTEIN

TITLE OF INVENTION: IDENTIFICATION OF INHIBITORS OF THESE INTERACTIONS

FILE REPRENCE: 7934-087

CURRENT APPLICATION NUMBER: US/09/231,303

CURRENT FILING DATE: 1999-01-12

EARLIER PAPLICATION NUMBER: 08/663,824

BARLIER PAPLICATION NUMBER: 08/663,824

NUMBER OF SEQ ID NOS: 118

SOFTWARE: PATENTING DATE: 1996-06-14

NUMBER OF SEQ ID NOS: 118

SOFTWARE: PATENTING DATE: 1996-06-14

SOFTWARE: PATENTING DATE: 1996-06-14
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Sequence 87, Application US/09231303
Sequence 87, Application US/09231303
GENERAL INFORMATION:
APPLICANT: Nondabalan, Krishnan
APPLICANT: Sothberg, Jonathan
TITLE OF INVENTION: IDENTIFICATION AND COMPARISON OF PROTEIN-PROTEIN
TITLE OF INVENTION: IDENTIFICATION OF INHIBITORS OF THESE INTERACTIONS
TITLE OF INVENTION: IDENTIFICATION OF INHIBITORS OF THESE INTERACTIONS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
11.0%; Score 8; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 8; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11.0%; Score 8; DB 1; Length 12; 100.0%; Pred. No. 2.8e+02; tive. 0; Mismatches 0; Indels
                                                       FILING DATE: 15-APR-1993
ATTORNEY/AGBNT INFORMATION:
NAME: SANDBERG, VICTORIA A.
REGISTRATION NUMBER: 41,287
REFERENCE/DOCKET NUMBER: 220.00010140
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-305-1226
TELEPHONE: 612-305-1226
          FILING DATE: 23-FEB-1995
APPLICATION NUMBER: US 08/047,860
                                                                                                                                                                                                                                                                                                               LENGTH: 12 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECTLE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 36:
                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 36: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 100.
Matches 8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-569-344-36
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US-09-231-303-86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-231-303-86
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Sequence 112. Application US/09231303

Patent No. 6395478

GENERAL INFORMATION:

APPLICANT: Nandablan, Krishnan

TITLE OF INVENTION: IDENTIFICATION AND COMPARISON OF PROTEIN-PROTEIN

TITLE OF INVENTION: INTERACTIONS THAT OCCUR IN POPULATIONS AND

TITLE OF INVENTION: IDENTIFICATION OF INHIBITORS OF THESE INTERACTIONS

FILE REFERENCE: 7934-087

CURRENT APPLICATION NUMBER: US/09/231,303

CURRENT FILING DATE: 1999-01-12

CURRENT APPLICATION NUMBER: 08/663,824

EARLIER FILING DATE: 1996-06-14

NUMBER OF SEQ ID NOS: 118

SEQ ID NO 112
                                                                                                                                Gaps
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; OTHER INFORMATION: Description of Artificial Sequence: linker US-09-231-303-87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: Description of Artificial Sequence: linker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 504
US-09-475-947A-19
is Sequence 19, Application US/09475947A
j Patent No. 6472154
j GENERAL INFORMATION:
APPLICANT Garner, Harold R.
APPLICANT: Wren, Jonathan D.
J TITLE OF INVENTION: Polymorphic Repeats in Human Genes
FILE REFERENCE: UTSD0667
CURRENT APPLICATION NUMBER: US/09/475,947A
CURRENT FILING DATE: 1999-12-31
j SDQ ID NO 19
                                                                         11.0%; Score 8; DB 1; Length 12;
100.0%; Pred. No. 2.8e+02;
vative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11.0%; Score %; DB 1; Length 12; 100.0%; Pred. No. 2.8e+02; attive 0; Mismatches 0; Indels
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Gaps
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FORTHER DEPLICATION PC/TUS9503602

Sequence 1, Application PC/TUS9503602

Sequence 1, Application PC/TUS9503602

SEQUENCE 1 INFORMATION:

TITLE OF INVENTION:

TITLE OF INVENTION:

TITLE OF INVENTION:

TOWNERS OF SEQUENCES:

ADDRESSE:

SCHEET: 400 Garden City Plaza

CITY:

CONTYR: 0.2.A.

ZIP: 11530-029

COMPUTER: IBM PC Compatible

COMPUTER: PLOST MRS-DCS/MS-DOS

SOFTWARE: PATENTIN Release #1.0, Version #1.25

CILASIFICATION NUMBER: PCT/US95/03602

FILING DATE: 21-MAR-1995

CLASSIFICATION NUMBER: 31,346

REFERENCE/COKET NUMBER: 31,346

REGISTRATION NUMBER: 31,346

REGISTRATIO
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GENERAL INPORMATION:
APPLICATE Research Corporation Technologies, Inc.
TITLE OF INVENTION: STEM-LOOP AND CIRCULAR OLIGONUCLEOTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
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                                                                                                                                                                                                                                                                                 1; Indels
                                                                                                                                                                                                                 Score 8; DB 1; Length 12;
Pred. No. 2.8e+02;
1; Mismatches 1; Indels
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OTHER INFORMATION: /note= "5-methylcytosine"
                                                                                                             /mod_base= OTHER
/note= "5-methylcytosine"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
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Pred. No.
                                                                                                                                                                                                                             11.0%;
                           FEATURE:
NAME/KEY: modified_base
COCATION: 11
OTHER INFORMATION: /mod
CTHER INFORMATION: /note
PCT-US91-03680-93
                                                                                                                                                                                                                          Query Match
Best Local Similarity 80.0
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 100.
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Research Co
TITLE OF INVENTION: ST
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                              933 CCTCCTCTTC 942
                                                                                                                                                                                                                                                                                                                                                                               2 MCTTCTCTTC 11
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PCT-US95-03602-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PCT-US95-03602-2
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Sequence 93, Application PC/TUS9103680

GENERAL INFORMATION:

APPLICANT: Matteucci, Mark D.

APPLICANT: Krawczyk, Steven

TITLE OF INVENTION: SEQUENCE-SPECIFIC NONPHOTOACTIVATED

TITLE OF INVENTION: DUPLEX DNA

NUMBER OP SEQUENCES: 158

CORRESPONDENCE ADDRESS:

ADDRESSEE: Mortison & Poerster

STREET: 545 Middlefield Road, Suite 200

CITY: Meallo Park

STATE: California

COUNTRY: USA
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                                                                                                                                              11.0%; Score 8; DB 1; Length 12; 100.0%; Pred. No. 2.8e+02; tive 0; Mismatches 0; Indels
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MEDIUM TYPE: Floppy disk
COMPUTER IBM PC compatible
COMPUTER: IBM PC compatible
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US91/03680
FLING DATE: 19910524
CLASSITCATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 4610-0011.40
REGISTATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 4610-0011.40
TELERPAX: 415-327-7250
TELERPAX: 415-327-7250
TELERY: 706141
INFORMATION FOR SEQ ID NO: 93:
SEQUENCE CHARACTER: STICS:
LENGTH: 12 base pairs
TYPE: NUCLEIC ACLD
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION: 3
OTHER INFORMATION: /mod_base= OTHER
OTHER INFORMATION: /note= "5-methylcytosine"
FEATURE:
NAME/KEY: modified_base
LOCATION: 6
OUTHER INFORMATION: /mod_base= OTHER
OTHER INFORMATION: /note= "5-methylcytosine"
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FEATURE:
NAME/KEY: modified_base
LOCATION: 2
OTHER INFORMATION: /mod_base= OTHER
OTHER INFORMATION:
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LOCATION: 8
OTHER INFORMATION: /mod_base= OTHER
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                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                  908 TITICITY 915
                                                                                                                                                 Query Match
Best Local Similarity
Matches 8; Conserv
      ; LENGTH: 12
; TYPE: DNA
; ORGANISM: human
US-09-475-947A-19
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Pred. No. 2.8e+02;
0; Mismatches 2; Indels
                                                                                                                                                                                                                     Query Match
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 8; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Alexander-Bridges, Maria C.
APPLICANT: Alexander-Bridges, Maria C.
APPLICANT: Alexander-Bridges, Maria C.
APPLICANT: Alexander-Bridges, Maria C.
TITLE OF INVENTION: HUHBITION OF INSULIN-INDUCED TITLE OF INVENTION: ADIPOSIS
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 502 or 553X
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
FILING DATE: US/08/242,409
FILING DATE: CLASSIFICATION: 514
PRIOR APPLICATION NUMBER: US/08/242,409
FILING DATE: APPLICATION DATA:
APPLICATION NUMBER: MS/08/242,409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            00786/238001
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ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 0078(
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEPAX: (617) 542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2, Application US/08049283A Patent No. 5502176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-242-409-2; Sequence 2, Application US/08242409; Patent No. 5496831
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10.7%;
81.8%;
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 81.8
Matches 9; Conservative
           12 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      929 TATCCCTCCTC 939
                                          ; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
PCT-US95-03602-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Boston
STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 Trrccccccrc 11
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US-08-049-283A-2/c
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PCT-US95-01602-1/C
; Sequence 3, Application PC/TUS9503602
; Sequence 3, Application
; TILE OF APPLICANT: Research Corporation Technologies, Inc.
; TILLE OF INVENTION: STEM-LOOP AND CIRCULAR OLIGONUCLEOTIDES
; WUMBER OF SEQUENCES:
; RORRESPONDENCE ADDRESS:
; CORRESPONDENCE ADDRESS:
; STREET: 400 Garden City Plaza
CITY: Garden City Plaza
CITY: Garden City
; STATE: New York
COMPTRY: US.A.
; COMPTRY: NEADABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPTRE: PROPHY READABLE FORM:
; APPLICATION NUMBER: PCT/US95/03602
; FILLING DATE: 21-MAR-1995
; PURCHARM TANDONEY NATHER THEODALE NUMBER: PCT/US95/03602
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .
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                                                                                                 STATE: OLD 
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11.0%; Score 8; DB 1; L.
Best Local Similarity 62.5%; Pred. No. 2.8e+02;
Matches 5; Conservative 3; Mismatches 0
ADDRESSEE: Scully, Scott, Murphy & Presser
STREET: 400 Garden City Plaza
CITY: Garden City
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: DIGIGGIO., FRANK S.
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 9373
TELECOMMUNICATION INFORMATION:
TELEFAN: (516) 742-4343
TELEFAX: (516) 742-4343
TELEFAX: (516) 742-4366
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: DiGiglio, Frank S.
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 9373
TELECOMMUNICATION INFORMATION:
TELERRY: (516) 742-4343
TELERRY: (516) 742-4346
TELERRY: (516) 742-4346
TELERS: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 3:
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PCT-US95-03602-2
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APPLICANT: Ecker, David J.
APPLICANT: Ecker, David J.
APPLICANT: Bruice, Thomas A.
APPLICANT: Bruice, Thomas A.
APPLICANT: Driver, Vickie
APPLICANT: Hanecak, Ronnie C.
APPLICANT: Vickers, Timothy A.
APPLICANT: Vickers, Timothy A.
APPLICANT: Vickers, Timothy A.
APPLICANT: Vickers, Timothy A.
APPLICANT: Watt, Jaqueline
TITLE OF INVENTION: Synthetic Unrandomization of Oligomer
TITLE OF INVENTION: Pragments
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSER: Woodcock Washburn Kurtz Mackiewicz and No. 5672472ris
STREET: One Liberty Place - 46th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cuery Match
10.7%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 2.8e+02;
Matches 9; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: FACTORIANCE OF THE COUNTRY: U.S.A.

ZIP: 19103
COMPUTER READABLE FORM:
MEDLUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/196,103A
FILING DATE: February 22, 1994
CLASSIFICATION DATA:
APPLICATION NUMBER: US 749,000
FILING DATE: 23-AQG-1991
ATTORNEY/AGENT INFORMATION:
NAME: GAUMOND, Rebecca R.
                   COMPUTER: 150. LISECTE, 1.44 FID BUDINGS FOR THE STATEM TO BE STATEM TO SYSTEM: 1BM P.C. DOS (Version 5.0) SOFTWARE: Wordberfect (Version 5.1) CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/435,350 FILING DATE: 05-MAY-1995 CLASSIFICATION NUMBER: 05/09/35,310 FILING DATE: AND TA: APPLICATION NUMBER: 07/936,531 FILING DATE: AND TA: ARCHARGE SOFTWARE SOFTWARE
3.5" Diskette, 1.44 Mb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 13, Application US/08196103A
Patent No. 5672472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     916 GGTCTTTGCCT 926
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-435-350-109
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US-08-196-103A-13
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                       APPLICANT: Tenen, Daniel G.
APPLICANT: Pahl, Heike L.
APPLICANT: Bahl, Heike L.
TINGON: Cell Specific Promoter and Uses Thereof
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
CITY: Lexington
STATE: Massachusetts
CCUNTRY: USA
ZIP: 02173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ..
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                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: PLOPPY disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRANT APPLICATION DATA:
APPLICATION NUMBER: US/08/049,283A
FILING DATE: 14-APR.1993
CLASSIFICATION TAIS
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/020,465
FILING DATE: 19-FEB-1993
CLASSIFICATION 135
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/837,776
FILING DATE: 13-FEB-1992
CLASSIFICATION NUMBER: 22,592
ATTOREY/AGENT INFORMATION:
REFERENCE/DOCKET NUMBER: BIH91-03'A
TELECOMMUNICATION NUMBER: 22,592
REFERENCE/COCKET NUMBER: BIH91-03'A
TELECOMMUNICATION NUMBER: 21,594
TELEPHONE: (617) 861-6240
INFORMATION FOR SED ID NO: 2:
SEQUENCE CHARACTERISTICS:
TENRANTI 11 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-435-350-109/c

Sequence 109, Application US/08435350

Sequence 109, Application US/08435350

Patent No. 5599704

GENERAL INFORMATION:
APPLICANT: James D. Thompson
APPLICANT: Asmeth G. Draper
TITLE OF INVENTION: METHOD AND REAGENT FOR
TITLE OF INVENTION: TREATMENT OF BREAST CANCER
NUMBER OF SEQUENCES: 118

CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 611 West Sixth Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 10.7%; Score 7.8; DB 1; Best Local Similarity 81.8%; Pred. No. 2.8e+02; Matches 9; Conservative 0; Mismatches 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; MOLECULE TYPE: DNA (genomic)
US-08-049-283A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 11 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       919 CTTTGCCTTTT 929
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 90017
COMPUTER READABLE FORM:
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CITY: Los Angeles
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
       GENERAL INFORMATION:
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Watt, Jacqueline
APPLICANT: Wogesh S. Sanghvi
TITLE OF INVENTION: Improved Methods for Synthetic Unrandomization
TITLE OF INVENTION: of Oligomer Fragments
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and No. 5698391ris
STREET: One Liberty Place - 46th Floor
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0
                        Score 7.8; DB 1; Length 11; Pred. No. 2.8e+02; 0; Mismatches 2; Indels
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Pred. No. 2.8e+02;
3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA: NA
APPLICATION NUMBER: US/08/357,396
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CLASSIFICATION: 436
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
FILING DATE: 23-AUG-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 196,103
FILING DATE: 22-FEB-1994
ATONEV/AGENT INFORMATION:
NAME: RAIDH, Rebecca L.
REGISTRATION NUMBER: 35,152
REBERBENG-DOCKET NUMBER: 1515-174
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: U.S.A.
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                         RESULT 514
US-08-357-396-13
; Sequence 13, Application US/08357396
; Patent No. 5698391
; GENERAL INFORMATION:
APPLICANT: Philip Dan Cook
                                                                                                                                                                                                                                                                                                                                                        Philip Dan Cook
Beker, David J.
Anderson, Kevin
Bruice, Thomas A.
Davis, Peter
Driver, Vickie
Freier, Susan, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear

MOLECULE TYPE: RNA (genomic)
US-08-357-396-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hanecak, Ronnie C
Vickers, Timothy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 54.5%;
Matches 6; Conservative
                           Query Match
Best Local Similarity 81.8%;
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 215-566-3439
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 base pairs
                                                                                                                         958 CGCTACCAACG 968
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   932 CCCTCCTCTTC 942
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                      11 CGGTACCAAGG 1
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US-08-314-3109A-34/C
; Sequence 34, Application US/08314309A
; Patent No. 56/7141
; GENERAL INFORMATION:
APPLICANT: ISOGAI, TAKAO
; APPLICANT: FUKAGWA, MASAO
APPLICANT: FUKAGWA, MASAO
APPLICANT: TRAMONI, ICHIRO
APPLICANT: TRAMONI, ICHIRO
APPLICANT: KOJO, HITOSHI
ITILE OF INVENTION: PROCESS FOR PRODUCING 7-AMINOCEPHEM
ITILE OF INVENTION: COMPOUND OR SALTS THEREOF
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                  Score 7.8; DB 1; Length 11; Pred. No. 2.8e+02; 3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OBLON, SPIVAK, McCLELLAND, MAIER & NEUSTADT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1755 S. Jefferson Davis Highway, Suite 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER EADABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: IBM NOWER: US (00 / 631,906

PILNG APPLICATION NOWER: US (00 / 631,906

ATTORNEY/AGENT INFORMATION:

NAME: Oblon, No. 5677141man F.

REGISTRATION NUMBER: 18-63-0 CONT

TELERRALION NUMBER: 24,618

REPERENCE/DOCKET NUMBER: 18-863-0

TELERRALION NUMBER: 24,618

REPERENCE/CONCET NUMBER: 18-863-0

TELERRALION NUMBER: 13-3000

TELERRALION NUMBER: 13-3200

TELERRALION FOR SEQ ID NO: 34:

SEQUENCE CHARACTERISTICS:

LEMMTH: 11 has a paire
REGISTRATION NUMBER: 35,152
REFERENCE/DOCKET NUMBER: ISIS-0678
TELECOMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: Other nucleic acid,
DESCRIPTION: synthetic DNA
                                                                                                                                                                                                                                         ; TOPOLOGY: linear
; MOLECULE TYPE: RNA (genomic)
US-08-196-103A-13
                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 54.5%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 11 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                   932 CCCTCCTCTTC 942
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: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Arlington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE:
ADDRESSEE:
STREET: 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-314-309A-34
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SEE: PROFILE DIAGNOSTIC SCIENCES, INC., 1510 EAST 73RD STREET, NEW YORK
                                                                                                                     COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44Mb storage COMPUTER: IBM FOLYN/AT OPERATING SYSTEM: MS-DOS version 6.2 SOFTWARE: Wordperfect Version 5.1 CURRENT APPLICATION DATA:

CLASSIFICATION DATA: 2.2 DEC 1993
CLASSIFICATION NUMBER: US/08/173,489C
FILING DATE: 2.2 DEC 1993
CLASSIFICATION NUMBER: US/08/136
FILING DATE: 2.9 OCT 1992
ATTORNEY/AGENT INFORMATION:
NAME: Handelman, Joseph H. REFERENCE/DOCKET NUMBER: US/186
TELEFORMUNICATION INFORMATION:
TELEFORMUNICATION INFORMATION:
TELEFORMUNICATION INFORMATION:
TELEFORMUNICATION INFORMATION:
TELEFORMUNICATION INFORMATION:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 bases
TYPE: Nucleic Acid
STRANDEDURSS: single stranded
STRANDEDURSS: single stranded
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RELEVANT RESIDUES IN SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 81.8%;
Matches 9; Conservative (
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                                                                     NEW YORK
                                                                                             USA
                                                                                                                10021
       ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-173-489C-60
                                                                                      COUNTRY:
ZIP: 100:
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                                                                                                                                                                            APPLICANT: Ecker, David J.
APPLICANT: Ecker, David J.
APPLICANT: Davis, Peter
APPLICANT: Vickers, Timothy A.
TITLE OF INVENTION: IMMUNOABSORBANT SCREENING ASSAY FOR TRANSCRIPTION
TITLE OF INVENTION: EATTORS AND OTHER BIOMOLECULE BINDING
TORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and
ADDRESSEE: No. 57472531is
STREET: One Liberty Place - 46th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ..
0
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Pred. No. 2.8e+02;
3; Mismatches 2; Indels
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US-08-173-489C-60
S-08-173-489C-60
Pacter No. 5861244
GENERAL INFORMATION:
APPLICANT: WANG, C. -G.
TITLE OF INVENTION:
TITLE OF INVENTION: GENETIC SEQUENCE ASSAY USING DNA TITLE OF INVENTION: TRIPLE-STRAND FORMATION.
NUMBER OF SEQUENCES: 365
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/386,141
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/032,852
FILING DATE: 16 MAR 1993
APPLICATION NUMBER: US/07/749,000
FILING DATE: 23-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: Gaumond, Rebecca R.
REGISTATION NUMBER: 35,152
REFERENCE/DOCKET NUMBER: ISIS-0653
TELECOMMUNICATION: INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE: PA
COUNTRY: U.S.A.
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                         Sequence 13, Application US/08386141
Patent No. 5747253
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear

MOLECULE TYPE: RNA (genomic)
US-08-386-141-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: 215-568-3400
TELEPAX: 215-568-3439
INPORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 54.5%;
Matches 6; Conservative
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                                                                                               US-08-386-141-13
       엄
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RESULT 517
US-08-173-489C-138
; Sequence 138, Application US/08173489C
; Patent No. 5861244
; GENERAL INFORMATION:
; APPLICANT: WANG, C. -G.
; TITLE OF INVENTION: GENETIC SEQUENCE ASSAY USING DNA; TITLE OF INVENTION: TRIPLE-STRAND FORMATION.
; TITLE OF SEQUENCES: 365; CORRESPONDENCE ADDRESS:
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PROFILE DIAGNOSTIC SCIENCES, INC.,
STREET: "" VORK
                                                                                                                                                                                                                                      Length 11;
                                                                                                                                                                                                                                   Score 7.8; DB 1; Length 11 Pred. No. 2.8e+02; 0; Mismatches 2; Indels
TODGLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: third strand derived from HER-2
DESCRIPTION: sequence region in Seq ID No. 586124459
                                                                                                                                                                    60 :FROM 1 TO 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: USA
ZIP: 10021.

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44Mb storage
COMPUTER: IBM PC/XT/AT
OPERATING SYSTEM: MS-DOS version 6.2
SOFTWARE: Wordperfect Version 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/173,489C
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Gaps ö

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TOPOLOGY: linear MOLECULE TYPE: other nucleic acid DESCRIPTION: third strand derived from Hepatitis B DESCRIPTION: isolate ayw sequence region in Seq ID No. 5861244149 HYPOTHETICAL: yes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: genomic DNA
DESCRIPTION: 23s rRNA gene from Escherichia coli
DESCRIPTION: (Accession # M25458) nucleotides 982 to 992
                                                                                                                                                                                                                                                                                                                                                    Score 7.8; DB 1; Length 11;
Pred. No. 2.8e+02;
                                                                                                                                                                                                                                                                                                                                                                                                      2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-173-489C-221/C

Sequence 221, Application US/08173489C

Patent No. 5861244

GENERAL INFORMATION:
APPLICANT: WANG, C. -G.
APPLICANT: HERBURN, A. G.
TITLE OF INVENTION: GENETIC SEQUENCE ASSAY USING DNA
TITLE OF INVENTION: TRIPLE-STRAND FORMATION.
NUMBER OF SEQUENCES: 365
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                   ANTI-SENSE: no'
PUBLICATION INFORMATION:
RELEVANT RESIDUES IN SEQ ID NO: 150 :FROM 1 TO 11
US-08-173-4805-150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROFILE DIAGNOSTIC SCIENCES, INC.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44Mb storage
COMPUTER: IBM PC/XT/AT
CORRETING SYSTEM: MS-DOS version 6.2
SOFTWARE: Wordperfect Version 5.1
CURRENT APPLICATION DATA:
APPLICATION UNMBER: US/08/173,489C
FILING DATE: 22 DEC 1993
CLASSIFICATION NUMBER: US/08/173,489C
FILING DATE: 29 DEC 1993
CLASSIFICATION NUMBER: US/08/436
FILING DATE: 29 OCT 1992
ATTORNEY/AGENT INFORMATION:
NAME: HAndelman, JOSeph H.
REFERENCE/DOCKET NUMBER: U9518-6
TELECOMMUNICATION INFORMATION:
REFERENCE/DOCKET NUMBER: U9518-6
TELEPHONE: (ALLORINGY) (212) 70.0000
                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   y) (212) 708-1880
(212) 246-8959
O: 221:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO. 221:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 base pairs
TYPE: nucleic acid
STRANDEDNESS: double stranded
                                                                   TYPE: nucleic acid
STRANDEDNESS: single stranded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     : 510 EAST 73RD STREET
NEW YORK
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ORIGINAL SOURCE:
ORGANISM: Escherichia coli
STRAIN: MRE600
                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 81.8%;
Matches 9; Conservative
                         SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                   931 TCCCTCCTCTT 941
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10021
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      ਨੇ
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                                                                                                                                                                                                                                                                                                                                                                        TYPE: nucleic acid STRANDENNESS: single stranded STRANDENNESS: single stranded TOPOLOGY: linear MOLECULE TYPE: other nucleic acid DESCRIPTION: third strand derived from Hepatitis B DESCRIPTION: isolate adr sequence region in Seq ID No. 5861244137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ouery Match
10.7%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 2.8e+02;
Matches 9; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 150, Application US/08173489C
Patent No. 5861244
GENERAL INFORMATION:
APPLICANT: WANG, C.-G.
APPLICANT: WANG, C.-G.
TITLE OF INVENTION: GENETIC SEQUENCE ASSAY USING DNATITLE OF INVENTION: TRIPLE-STRAND FORMATION.
NUMBER OF SEQUENCES: 365
CORRESPONDENCE ADDRESS:
ADDRESSEE: PROFILE DIAGNOSTIC SCIENCES, INC.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PUBLICATION INFORMATION:

RELEVANT RESIDUES IN SEQ ID NO: 138 :FROM 1 TO 11
US-08-173-489C-138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: PROFILE DIAGNOSTIC SCIENCES, INC., STREET: 510 EAST 73RD STREET, CITY: NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PHPLACE

RIGHOR DATE: ...
CLASSIFICATION DATA:
APPLICATION NUMBER: US 07/968,436
FILING DATE: 29 OCT 1992
ATTORNEY/AGENT INFORMATION:
NAME: Handelman, Joseph H.
REPERRNEZ/DOCKET NUMBER: 26,179
REPERRNEZ/DOCKET NUMBER: U9518-6
TELECOMMUNICATION INFORMATION:
TELEPHONE: (attorney) (212) 708-1880
TELEPHONE: (attorney) (212) 708-1880
FILING DATE: 22 DEC 1993
CLASSIFICATION: 435
PRICR APPLICATION DATA:
APPLICATION NUMBER: US 07/968,436
FILING DATE: 29 OCT 1992
ATTORNEY/AGENT INFORMATION:
NAME: Handedlman, Joseph H.
REGISTRATION NUMBER: 26,179
REFERENCE/DOCKET NUMBER: U9518-6
TELECOMOUNICATION INFORMATION:
TELEPAX: (attorney) (212) 708-1880
TELEFAX: (attorney) (212) 246-8959
INFORMATION FOR SEQ ID NO: 138:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 bases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44Mb storage
COMPUTER: IBM PC/XI/AT
OFBEATING SYSTEM: MS-DOS version 6.2
SOFTWARE: Wordperfect Version 5.1
CURRENT APPLICATION DATA:
RPLING DATE: 22 DEC 1993
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COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 518
US-08-173-489C-150
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; PUBLICATION INFORMATION:
; RELEVANT RESIDUES IN SEQ ID NO: 226 :FROM 1 TO 11
US-08-173-489C-226
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                                                                                                   10.7%;
81.8%;
                                                                                              Query Match
Best Local Similarity 81.8
Matches 9; Conservative
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Pred. No. 2.8e+02;
0; Mismatches 2; Indels
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MEDIUM TYPE: 3.5 inch, 1.44Mb storage
COMPUTER: BM PC/XT/AT
COMPUTER: Mordperfect Version 6.2
SOFTWARE: Wordperfect Version 5.1
SOFTWARE: Wordperfect Version 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/173,489C
FILING DATE: 2.2 DEC 1993
CLASSIFICATION: 435
FILING DATE: 2.2 DEC 1993
CLASSIFICATION: A35
FILING DATE: 2.9 OCT 1992
ATTORNEY/AGENT INFORMATION:
MAME: Handelman, Joseph H.
REGISTRATION NUMBER: 26,179
REFERENCE/DOCKET NUMBER: 26,179
REFERENCE/DOCKET NUMBER: 26,179
REFERENCE/COCKET NUMBER: 26,179
TELEPHONE: (attorney) (212) 246-8959
INFORMATION FOR SEQ ID NO: 226:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 bases
TYPE: nucleic acid
STRANDEDNESS: single stranded
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: third strand derived from H. morrhuae
DESCRIPTION: third strand derived and DESCRIPTION: 133 region in Seq ID No. 5861244225
                               Machatt, M, A,
Edwards, K, Koessel,
                                                                                                                                                                                                                                                                                                                                                                                                                                              2; Indels
                                                                                              Primary and secondary structures of Escherichia coli MRE 600 235 structures of Escherichia coli MRE 600 235 secondary structure for maize chloroplast 235 rRNA and for large portions of mouse and human 165 mitochondrial rRNAs Nucleic Acids Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 226, Application US/08173489C
Patent No. 5861244
GENERAL INFORMATION:
APPLICANT: WANG, C.-G.
APPLICANT: HEPBURN, A. G.
TITLE OF INVENTION: TRIPLE-STRAND FORMATION.
NUMBER OF SEQUENCE. 365
CORRESPONDENCE ADDRESS:
ADDRESSES: PROFILE DIAGNOSTIC SCIENCES, INC.,
                                                                                                                                                                                                                                                                                                                                 221 :FROM 1 TO 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: PROFILE DIAGNOSTIC SCIENCES, INC. STREET, 510 EAST 73RD STREET, CITY: NEW YORK STATE: NEW YORK
PUBLICATION INFORMATION:
AUTHORS: Branlant, C, Krol, A, Mac AUTHORS: Bruyet, J, Ebel, J P, Ed AUTHORS: H.
TITLE: Primary and secondary
TITLE: structures of Escherichia col TITLE: ribosomal RNA Comparison with TITLE: recondary structure for maize TITLE: rRNA and for large portions of TITLE: 165 mitochondrial rRNAs JOURNAL: Nucleic Acids Research
                                                                                                                                                                                                                                                                                                      DATE: 1981
; RELEVANT RESIDUES IN SEQ ID NO:
US-08-173-489C-221
                                                                                                                                                                                                                                                                                                                                                                                                h 10.7%;
Similarity 81.8%;
9; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            929 TATCCCTCCTC 939
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Best Local Similarity
Matches 9; Conserv
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US-08-173-489C-226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
                                                                                                                                                                                                                                                                                  PAGES:
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Gaps
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DESCRIPTION: 23s rRNA gene from Rhodobacter
DESCRIPTION: capsulatus (Accession # X06485) nucleotides
DESCRIPTION: 1038 to 1048
HYPOTHETICAL: no
ANTI-SENSE: no
ORIGINAL SOURCE:
ORRANISM: Rhodobacter capsulatus
        Length 11;
                                                                                                                                                                                                                                                                                                                                                  RESULT 521
UG-06-173-499C-265/C

Sequence 265, Application US/08173489C

Fatent UN- S861244

GENERAL INFORMATION:
FATILE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TRIPLE-STRAND FORWATION:
OF SEQUENCES:
ADDRESSES:
                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN: dsm 938
PUBLICATION INFORMATION:
AUTHORS: Regenburger, A. Ludwig, W. Frank, R., AUTHORS: Bloecker, H. Schleifer, K. H.
TITLE: Complete nucleotide sequence
TITLE: of a 23s ribosomal RNA gene from Rhodobacter
TITLE: oc apsulatus
Score 7.8; DB 1; Li
Pred. No. 2.8e+02;
0; Mismatches 2;
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Sequence 18, Application US/08227180B
Patent No. 5866698
GENERAL INFORMATION:
APPLICANT: Ecker et al.
TITLE OF INVENTION: Modulation of Gene Expression
TITLE OF INVENTION: Through Interference with RNA Secondary Structure
NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
ADDRESSEE: Jane Massey Licata, Esq.
STREET: 210 Lake Drive East, Suite 201
CITY: Cherry Hill
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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0
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Pred. No. 2.8e+02;
0; Mismatches 2; Indels
Score 7.8; DB 1; Length 11; Pred. No. 2.8e+02; 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MIDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE COMPUTER: 18M 486
OPPRATING SYSTEM: WINDOWS FOR WORKGROUPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 91320-1789
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 in., DS, 1.4 MB
                                                                                                                                                                                                        US-001.282-383-2
Sequence 2, Application US/08282383
Fetent No. 5864031
CENERAL INFORMATION:
APPLICANT: Sandra E. Russo-Rodriguez
APPLICANT: Tapper M. Koga
TITLE OF INVENTION: 5'-Dithio-Modified
TITLE OF INVENTION: 01/gonucleotides
TITLE OF SEQUENCES:
ADDRESSEE: Amgen Inc.
STREET: 1840 Dehavilland Dr.
CITY: Thousand Oaks
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh OS 7.0
SOFTWARE: Microsoft Word Version 5.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/282,383
FILING DATE: 29UUL1994
CLASSIFICATION: 536
CLASSIFICATION: 536
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: other nucleic acid
  10.7%;
81.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10.7%;
81.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 81.0
    Query Match 10.7
Best Local Similarity 81.6
Matches 9/ Conservative
                                                                                        935 TCCTCTTCATT 945
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              911 TCTTTGGTCTT 921
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 Trraregrerr 11
                                                                                                                             11 rccccrrcrrr 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Thousand Oak
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 11 bases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               08002
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MOLECULE TYPE: genomic DNA
DESCRIPTION: 16s rMA gene from Chlamydia psittaci
DESCRIPTION: (Accession # M13769) nucleotides 203 to 213
                                                                                        10.7%; Score 7.8; DB 1; Length 11; 81.8%; Pred. No. 2.8e+02; Live 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                          RESULT 522
US-08-173-489C-295/C
US-08-173-489C-295/C
Patent No. 5861244
GENERAL INFORMATION:
APPLICANT: WANG, C. -G.
TITLE OF INVENTION: GENETIC SEQUENCE ASSAY USING DNA TITLE OF INVENTION: TRIPLE-STRAND FORMATION.
NUMBER OF SEQUENCES: 365
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             295 :FROM 1 TO 11
                              265 : FROM 1 TO 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SSEE: PROFILE DIAGNOSTIC SCIENCES, INC.,
I: 510 EAST 73RD STREET,
NEW YORK
NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 22 DEC 1993
CLASSIFICATION. 435
FRIOR APPLICATION DATE: 30 PCT 1993
ATTORNEY FABOR THORNATON:
NAME: Handelman, Joseph H.
REGISTRATION NUMBER: 26,179
REFERENCE/DOCKET NUMBER: 96,179
REFERENCE/DOCKET NUMBER: 19518-6
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION SEQ 10 NO: 295:
SEQUENCE CHARACTERISCICS:
LENGTH: 11 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: 3.5 inch, 1.44Mb storage COMPUTER: IBM PC/XT/AT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Chlamydia psittaci
PUBLICATION INFORMATION:
AUTHORS: Weisburg, W G, Hatch, T P,
TITLE: Eubacterial Origin of
TITLE: Chlamydiae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OPERATING SYSTEM: MS-DOS version 6.2 SOFTWARE: Wordperfect Version 5.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/173,489C
FILING DATE: 22 DEC 1993
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     JOURNAL: Journal of Bacteriology VOLUME: 167
        DATE: 1988
RELEVANT RESIDUES IN SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; RELEVANT RESIDUES IN SEQ ID NO: US-08-173-489C-295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               nucleic acid
FDNESS: double stranded
                                                                                        Query Match
Best Local Similarity 81.8
Matches 9; Conservative
                                                                                                                                                                           929 TATCCCTCCTC 939
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 10021.
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inc.
                                                                                                                                                                                                                 11 Triccircric 1
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STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ANTI-SENSE: no
ORIGINAL SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HYPOTHETICAL:
                                                  US-08-173-489C-265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE:
STREET: 51
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COUNTRY:
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Sequence 7, Application US/08991830A
Patent No. 6027892
GENERAL INFORMATION:
APPLICANT: Chang, Esther H.
APPLICANT: Chang, Esther F.
TITLE OF INVENTION: Compositions and Methods for Reducing Radiation and Drug Resis NUMBER OF SEQUENCES: 9
CORRESPONDENCES: 9
CORRESPONDENCES: Sana A. Pratt
STREET: 10821 Hillbrooke Lane
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                                                                                                                                                                                                                                                               Score 7.8; DB 1; Length 11;
Pred. No. 2.8e+02;
0; Mismatches 2; Indels
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Pred. No. 2.8e+02;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 10821 Hillbrooke Lane
CITY: Potomac
STRIE: MARYLAND
COUNTRY: USA
ZIP: 20854
COMPUTER: READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OFREATING SYSTEM: Macintosh
OFTWARE: Microsoft Word 6.0
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/08/991,830A
FILING DATE: 16 December 1997
CLASSIFICATION DATA:
APPLICATION NUMBER: 60/034,160
FILING DATE: 30 December 1996
ATTORNEY/AGENT INFORMATION:
NAME: Sana A. Pratt
REGISTRATION NUMBER: 39,441
REFERENCE/DOCKET NUMBER:
TELEPHONE: (301) 294-9171
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 base pairs
TYPE: Nucleic acid
STRANDEDNESS: Single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 527
US-09-105-515-3
; Sequence 3, Application US/09105515
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81.8%;
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Best Local Similarity 81.8%;
Matches 9; Conservative
             ; SEQUENCE CHARACTERISTICS:
; LENGTH 11 base pairs
; TYPE: Nucleic acid
; STRANDEDNESS: Single
; MOLECULE TYPE: DNA
US-08-991-830A-6
                                                                                                                                                                                                                                       928 TTATCCTCCT 938
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MOLECULE TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-991-830A-7
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APPLICANT: Chang, Esther H.
APPLICANT: Chang, Esther H.
APPLICANT: Chang, Esther H.
APPLICANT: Pirollo, Kathleen F.
TITLE OF INVENTION: Compositions and Methods for Reducing Radiation and Drug Resis NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS: 9
CORRESPONDENCE ADDRESS: 9
CORRESPONDENCE ADDRESS: 1
ADDRESSEE: Sana A. Pract
STREET: 10821 Hillbrooke Lane
CITY: Potomac
STREET: 10821 Hillbrooke Lane
CITY: Potomac
STREET: 10821 Hillbrooke Lane
COUNTRY: USA
ZIF: 20854
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh
OPERATING SYSTEM: Macintosh
OPERATING SYSTEM: Macintosh
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Wacintosh
SOFTWARE: Microsoft Word 6.0
CURRENT APPLICATION NUMBER: US/08/991,830A
FILING DATE: 16 December 1997
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Pred. No. 2.8e+02;
3; Mismatches 2;
CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

FILING DATE: APAT1 13, 1994

CLASSIFICATION: 435

CLASSIFICATION: 435

FILING DATE: APAT3: 1994

APPLICATION DATA:

APPLICATION NUMBER: 07/518,929

FILING DATE: MAY 4, 1990

APPLICATION NUMBER: 07/801,168

FILING DATE: MAP 4, 1991

APPLICATION NUMBER: 07/801,168

FILING DATE: NPO. 586698ember 20, 1991

APPLICATION NUMBER: 15, 1991

APPLICATION NUMBER: 15, 1991

APPLICATION NUMBER: 15, 1991

ATTORNEY/AGENT INFORMATION:

NAME: Jane Massey Licata

REGISTRATION NUMBER: 32,257

REFERENCE/DOCKET NUMBER: 151S-1420

TELEPAX: (215) 568-3100

TELEPAX: (215) 568-3100

INFORMATION FOR SEQ ID NO: 18:

LENGTH: LENG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 525
US-08-991-830A-6
; Sequence 6, Application US/08991830A
; Patent No. 6027892
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APPLICATION NUMBER: 60/034,160
FILING DATE: 30 December 1996
ATTORNEY/AGENT INFORMATION:
NAME: Sana A. Pratt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REGISTRATION NUMBER: 39,441
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 294-9171
TELEFAX: (301) 294-7357
INFORMATION FOR SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 54.5%;
Matches 6; Conservative
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STRANDEDNESS: single
TOPOLOGY: linear
NATI SENSE: yes
US-08-227-180B-18
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US-09-487-130-11

is Sequence 11, Application US/09487130

is Sequence 11, Application US/09487130

is Patent No. 61562322

is GENERAL INFORMATION:
is APPLICAMY: GARY, DONALD M.
is TITLE OF INVENTION: DUPLEX
is TITLE OF DATE: 2000-01-19
is PRIOR APPLICATION NUMBER: US/09/487,130
is PRIOR APPLICATION NUMBER: US/09/487,130
is PRIOR FILING DATE: 1999-07-20
is NUMBER OF SEQ ID NOS: 17
is SEQ ID NO 11
is LENGTH: 11

                                                                                                                                                               Sequence 9, Application US/09487130

Fatent No. 6362323

Fatent No. 6362323

FAPLICANT: GRAY. DONALD M.

APPLICANT: HASHEW, GIHAN M.

TITLE OF INVENTION: CONVERSION OF A WATSON-CRICK DNA TO A HOOGSTEEN-PAIRED

TITLE OF INVENTION: UDPLEX.

FILE REPERENCE: 91556/663851P

CURRENT APPLICATION NUMBER: US/09/487,130

FRIOR APPLICANTION NUMBER: 09/357,424

FRIOR APPLICANTION NUMBER: 09/357,424

FRIOR APPLICATION NUMBER: 09/357,424

FRIOR APPLICATION NUMBER: 09/357,424

FRIOR APPLICATION NUMBER: 09/357,424

FRIOR PLINTO DATE: 1999-07-20

NUMBER OF SEQ ID NOS: 17

SEQ ID NO 9

LENGTH: 11
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; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: nucleic acid
US-09-487-130-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: Description of Artificial Sequence: synthetic OTHER INFORMATION: nucleic acid
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Pred. No. 2.8e+02;
5; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            JO.7%; Score 7.8; DB 1;
Local Similarity 36.4%; Pred. No. 2.8e+02;
hes 4; Conservative 5; Mismatcher
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: RNA
ORGANISM: Artificial Sequence
FEATURE:
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ORGANISM: Artificial Sequence
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Matches 4, Conservative
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11 TCTTTTGTCAT 1
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Matches
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US-08-679-493A-67/c

Sequence 67, Application US/08679493A

Patent No. 6303295

GENERAL INFORMATION:

PAPLICAMI: TAylor, Ethan W.

TITLE OF INVENTION: SELENOPROTEINS, CODING SEQUENCES AND METHODS

FILE REPRENCE: 55-95

CURRENT APPLICATION NUMBER: US/08/679,493A

CURRENT PILING DATE: 1996-07-12

PRIOR APPLICATION NUMBER: 60/001203

PRIOR FILING DATE: 1995-07-14

PRIOR APPLICATION NUMBER: 60/003,112

PRIOR FILING DATE: 1995-09-01

NUMBER OF SEQ ID NOS: 2.0

SOFTWARE: Patentin Ver. 2.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 7.8; .DB 1; Length 11;
Pred. No. 2.8e+02;
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                                                                                                                                                                                                                                                                                                            STATE: IL
COUNTRY: US
ZIP: 60601-6780

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/105,515
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: RNA
ORGANISM: Human immunodeficiency virus type 1
                                          SMERAL INFORMATION:
APPLICANT: BROUGH, DOUGLAS B.
TITLE OF INVENTION: RECOMBINANT ADENOVIRUS
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                             ADDRESSEE: LEYDIG, VOIT & MAYER, LID.
STREET: TWO PRUDENTIAL PLAZA, SUITE 4900
CITY: CHICAGO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: KILYK JR., JOHN
REGISTRATION NUMBER: 30763
REFERENCE/DOCKET NUMBER: 8382
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-616-5600
TELEPHAX: 312-616-5600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 312-616-5700 INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: DNA (genomic)
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Best Local Similarity 81.8%;
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          nucleic acid
EDNESS: unknown
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Best Local Similarity
Matches 9; Conserv
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911 TCTTTGGTCTT 921

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Gaps

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RESULT 531

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Query Match
Best Local Similarity 81.8
Matches 9; Conservative
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Best Local Similarity
Matches 9; Conserv
                                                                                                      LENGTH: 11
TYPE: DNA
ORGANISM: human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA ORGANISM: human
                                                                                                                                                                   US-09-475-947A-167
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                                                                   APPLICANT: DUTTA, Sukanta K.
APPLICANT: DUTTA, Sukanta K.
APPLICANT: DUTTA, Sukanta K.
APPLICANT: BISWAS, Biswajit
APPLICANT: BISWAS, Biswajit
APPLICANT: BISWAS, Biswajit
APPLICANT: BISWAS, BISWAS, BIZE-VARIABLE STRAIN-SPECIFIC PROTECTIVE ANTIGEN FOR TITLE OF INVENTION: POTOMAC HORSE FEVER
FILE REFERENCE: 8172-9016
CURRENT APPLICATION NUMBER: US/09/157,257
CURRENT FILING DATE: 1998-09-18
EARLIER APPLICATION NUMBER: 60/059,252
EARLIER PILING DATE: 1997-09-18
SOUNDER OF SEQ ID NOS: 48
SOFTWARE: PATENTIN Ver. 2.0
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Pred. No. 2.8e+02;
0; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-475-947A-167/c

Sequence 167, Application US/09475947A

Sequence 167, Application US/09475947A

Setent No. 6472154

GRNERAL INFORMATION:
APPLICANT: Wren, Jonathan D.
APPLICANT: Minna, John D.
TITLE OF INVENTION: Polymorphic Repeats in Human Genes
FILE REFERENCE: UTSD0667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Generical Application US/09748044
Fatent No. 6458578
GENERAL INFORMATION:
APPLICANT: Brough, Douglas E.
TITLE OF INVENTION: Recombinant Cell Line
TILE REPERENCE: 207952
CURRENT FILING DATE: 2009-12-22
FLOR APPLICATION NUMBER: PCT/US99/14333
PRIOR PILING DATE: 1999-06-24
PRIOR PILING DATE: 1999-06-26
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PatentIn Ver: 2.0
SENGTH: 11
                 Sequence 39, Application US/09157257
Patent No. 6375954
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 81.8%;
Matches 9; Conservative
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81.8%;
                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
ORGANISM: Ehrlichia risticii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA ORGANISM: Adenovirus type 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 10.7
Best Local Similarity 81.6
Matches 9; Conservative
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US-09-157-257-39/c
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Pred. No. 2.8e+02;
0; Mismatches 2; Indels
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10.7%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 2.8e+02;
Matches 9; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 231, Application US/09475947A

Patent No. 6472154

GARRAL INFORMATION:
APPLICANT: Wren, Jonathan D.
APPLICANT: Wren, John D.
TITLE OF INVENTION: Polymorphic Repeats in Human Genes
FILE REFERENCE: USD0667

CURRENT APPLICATION NUMBER: US/09/475,947A

CURRENT FILING DATE: 1999-12-31

NUMBER OF SEQ ID NOS: 346

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Winmer, Ernst A.
APPLICANT: Werghammer, Andreas J.
APPLICANT: Berghammer, Andreas J.
APPLICANT: Ringler, Martin
TITLE OF INVENTION: Universal markers of Transgenesis
FILE REFERENCE: EX.W199-0014
CURRENT FILING DATE: 1999-08-12
NUMBER OF SEQ ID NOS: 44-
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 14
LENGTH: 11
CURRENT APPLICATION NUMBER: US/09/475,947A CURRENT FILING DATE: 1999-12-31 NUMBER OF SEQ ID NOS: 346 SOFTWARE: Patentin Ver. 2.1 SEQ ID NO 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-373-129A-14
; Sequence 14, Application US/09373129A
; Patent No. 6518481
; GENERAL INFORMATION;
                                                                                                                                                                                                                                                  10.7%;
81.8%;
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ORGANISM: Artificial Sequence
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Gaps

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Pred. No. 2.8e+02;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                          GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Abacander-Bridges, Maria C.
APPLICANT: Abacander-Bridges, Maria C.
TITLE OF INVENTION: INHIBITION OF INSULIN-
TITLE OF INVENTION: INDUCED ADIPOSIS
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
CITY: Boston
STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 50Z or 55SX
COMPUTER: WordPerfect (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/05835
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PCT-US95-09475-2; Sequence 2, Application PC/TUS9509475; GENERAL INFORMATION: GENERAL INFORMATION: TITLE OF INVENTION: Oligonuclectides TITLE OF INVENTION: Oligonuclectides CORRESPONDENCE ADDRESS: ADDRESS: ADDRESSE: AMGEN INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 00786/238001
ELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEPAX: (617) 542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/242,409
FILING DATE: 13 May 1994
ATTONNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1: Amgen Inc.
1840 Dehavilland Dr.
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     Best Local Similarity 81.8
Matches 9; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
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                                                                              935 TCCTCTTCATT 945
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EDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 rrrccccccrc 11
                                                                                                                          11 recreerer 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE
                                                                                                                                                                                                                          PCT-US95-05835-2
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APPLICANT: 1UJ CHANGDE
TITLE OF INVENTION: ANTI-HBV
TITLE OF INVENTION: ANTI-HBV
TITLE OF INVENTION: ANTI-HBV
TILE REFERENCE: 017227/0160
CURRENT APPLICATION NUMBER: US/09/529,812A
CURRENT FILING DATE: 1098-10-19
PRIOR APPLICATION NUMBER: PCT/CN98/00248
PRIOR FILING DATE: 1998-10-19
PRIOR APPLICATION NUMBER: CN 97106667.1
PRIOR APPLICATION NUMBER: CN 97106667.1
PRIOR APPLICATION NUMBER: CN 97106667.1
SACOTHWARE: PATENTION DATE: 1997-10-21
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PATENTIN OF: 2.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                 RESULT 536
US-09-355-017B-48

/Sequence 48, Application US/09395017B
/Sequence 48, Application US/09395017B
/Sequence 48, Application US/09395017B
/Setent No. 6642014
/GENERAL INFORMATION:
/APPLICANT: Podersen, Henrik
/APPLICANT: Kjems, Jorgen
/APPLICANT: Lund, Mette
/TITLE OF INVENTION: Substrate Reloading
/TITLE OF INVENTION: Substrate Reloading
/TITLE OF INVENTION: Substrate Reloading
/TITLE OF INVENTION: BAZYME Activity Screen With Direct
/TITLE OF INVENTION: BAZYME Activity Screen With Direct
/TITLE OF INVENTION: Substrate Reloading
/TITLE OF INVENTION: 1999-09-13
PRIOR APPLICATION NUMBER: PA 1998 01106
/PRIOR PILING DATE: 1998-09-02
/PRIOR FILING DATE: 1998-09-02
//WINBER OF SEQ ID NOS: 49
//WINBER OF SEQ ID NOS: 49
//WINBER FEATSEQ FOR Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 5, Application US/09529812A
Patent No. 6682930
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 81.8%;
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; OTHER INFORMATION: Primer US-09-395-017B-48
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                                    941 TCATTGGTTTA 951
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Batent No. 534078

GENERAL INFORMATION:

APPLICANT: GROSZ, ROW

APPLICANT: JENSEN, WARK A

TITLE OF INVENTION: JMPROYED METHOD FOR

TITLE OF INVENTION: MAPLIFICATION OF TARGETED

TITLE OF INVENTION: MESTED POLYMERASE CHAIN REACTION

NUMBER OF SEQUENCES: 22

CORRESPONDENCE ADDRESS:

ADDRESSEE B. I. du Pont de Nemours and Company

STREET: 1007 Market Street

CITY: Wilmington

STREET: 1007 Market Street

COUNTRY: U.S.A.

ZIP: 19898

COMPUTER: Macintosh

OPERATION TYPE: Diskette, 3.50 inch, 1.0 MB

COMPUTER: Macintosh

OPERATION NUMBER: US/07/990,297

FILING DATE: 19921209

SCOFTWARE: GENERAL INFORMATION:

NAME: GENERAL INFORMATION:

NAME: GENERAL INFORMATION:

NAME: GENERAL INFORMATION:

NAME: GENERAL INFORMATION:

TELECOMMUNICATION NUMBER: 35,880

REFERENCE/DOCKET NUMBER: MACINGENAL TON:

TELECOMMUNICATION NUMBER: 35,880

REFERENCE/DOCKET NUMBER: MACINGENAL TON:

TELECOMMUNICATION NUMBER: 35,880

REFERENCE/DOCKET NUMBER: MACINGENAL TON:

TELECOMMUNICATION NUMBER: 35,880

REFERENCE/DOCKET NUMBER: 35,880

REFERENCE/DOCKET NUMBER: MACINGENAL TON:

TELECOMMUNICATION NUMBER: 35,880

REPERENCE/DOCKET NUMB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2; Indels
STATE: California
COUNTRY: USA
ZIP: 91320-1789
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 in., DS, 1.4 MB
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh OS 7.0
SOFTWARE: Microsoft Word Version 5.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/09475
FILING DATE:
CLASSIFICATION DATA:
APPLICATION NUMBER: 08/282,383
FILING DATE:
CRASSIFICATION DATA:
APPLICATION TOWN SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 bases
TYPE: nucleic acid
STRANDENES: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 7.8; DB 1;
Pred. No. 2.8e+02;
0; Mismatches 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear

MOLECULE TYPE: other nucleic acid
PCT-US95-09475-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 81.8%;
Matches 9; Conservative
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TYPE: NUCLEIC ACID
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       911 TCTTTGGTCTT 921
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US-07-990-297-4/c
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                                                                                                                                                 10.7%; Score 7.8; DB 1; Length 12; ilarity 81.8%; Pred. No. 3e+02; Conservative 0; Mismatches 2; Indels
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10.7%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 3e+02;
Matches 9; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-242-409-1/c
Sequence 1, Application US/08242409
Patent No. 54960H
Patent No. 5496
Patent No. 542-8966
Patent No. 542-8966
Patent No. 542-8966
Patent No. 5406-806
Patent No. 5406
Patent No. 5406-
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GENERAL INFORMATION; GENERAL APPLICANT: Peterson, Michael G
; TOPOLOGX: Illean
; MOLECULE TYPE: DNA (genomic)
US-07-990-297-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEX: 200154
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                               950 TAATGTATCGC 960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  929 TATCCCTCCTC 939
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TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                12 TACGGTATCGC
                                                                                                                                                 Query Match
Best Local Similarity
Matches 9; Conserv
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Sequence 13, Application US/08110158

Sequence 13, Application US/08110158

Patent No. 5605821

APPLICAMT: McEver, Rodger P.
APPLICAMT: Pan, Junilang

TITLE OF INVENTION: Expression Control Sequences of the TITLE OF SEQUENCES: 17

CORRESPONDENCES: 17

CORRESPONDENCE ADDRESS:
ADDRESSEE: Patrea L. Pabst

ADDRESSEE: Patrea L. Pabst

CITY: Atlanta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match

10.7%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 3e+02;
Matches 9; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
10.7%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 3e+02;
Matches 9; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CUNTRY: USA
ZIP: 30309-4530
COMPUTER READBALE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIDLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/110,158
FILING DATE: 19330820
CLASSIFICATION DATE: 08/08/110,158
FILING DATE: 08-MAR-1989
ATPORNEY/AGENT INFORMATION:
NAME: PADSE, Patrea L.
NAME: PADSE, Patrea L.
NAME: PADSE, Patrea L.
NAME: 1935040
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 44683
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-977-9550
TELEPHONE: 212-977-9550
TELEPHONE: 212-977-9550
INFORMATION FOR SEQ ID NO: 13: 5EQUENCE CHARACTERISTICS: LENGTH: 12 base pairs LENGTH: 12 base pairs TYPE: nucleic acid STRANDEDNESS: double STRANDEDNESS: double TANDEDNESS: 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION TELEPHONE: (404)-815-6508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)
US-08-242-664-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (404)-815-6555
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          944 TTGGTTTAATG 954
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          932 CCCTCCTCTTC 942
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            nucleic acid
EDNESS: single
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                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT STREET: 4 Embarcadero Center, Suite 3400
CITY: Barcisco STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
CLASSIPICATION NUMBER: US/08/235,503B
CLASSIPICATION: 435
ATTORNEY AGENT INFORMATION:
NAME: Comman, Richard A
REGISTRATION NUMBER: 36,67
REPERPORE: (415) 781-1989
TELEPHONE: (415) 398-3249
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 base pairs
TTYPE: mucleic caid
TTYPE: mucleic caid
TYPE: mucleic caid
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US-08-242-664-13/c
US-08-242-664-13/c
Sequence 15. Application US/08242664
Patent No. 5571937
GENERAL INFORMATION:
APPLICANT: Matanabe, Kyoichi A.
APPLICANT: Ren, Wu-Yun
APPLICANT: Ren, Wu-Yun
TITLE OF INVENTION:
TITLE OF SEQUENCES:
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
                                  APPLICANT: Baichwal, Vijay R
APPLICANT: Strulovici, Berta
TITLE OF INVENTION: TRANSCRIPTION FACTOR-DNA ASSAY
NUMBER OF SEQUENCES: 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPER: 3.5 inch 1.44Mb
COMPUTER: 1BM PC COMPAIDLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/242,664
FILING DATE: May 12, 1994
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              May 12, 1994 May 1
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30 Rockefeller Plaza
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11 TGRMCYTWGCM 1
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US-08-235-503B-22
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CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               linear
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Best Local Similarity
Matches 6; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE:
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schultzl-899.rn1
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10.7%; Score 7.8; DB 1; Length 12; ilarity 81.8%; Pred. No. 3e+02; Conservative 0; Mismatches 2; Indels
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| Sequence 5, Application US/08586120
| Sequence 5, Application US/08586120
| Patent No. 5656740
| GENERAL INPORMATION:
| APPLICANT: GENSZ, RONALD
| APPLICANT: GENSZ, RONALD
| TITLE OF INVENTION: SELECTION OF DIAGNOSTIC
| TITLE OF INVENTION: GENETIC MARKERS IN
| TITLE OF INVENTION: OF A SPECIFIC MARKER
| TITLE OF INVENTION: SALMONELLA
| NUMBER OF SEQUENCES: 22
| CORRESPONDENCE ADDRESS:
| ADDRESSEE: E. I. DU PONT DE NEMOURS
| ADDRESSEE: AND COMPANY
| STREET: MILMINTON
| STREET: MILMINTON
| STATE: DELAWARE
| COUNTRY: U.S.A.
                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch 1.44Mb
COMPUTER: 12 inch 1.44Mb
COMPUTER: 12 inch 1.44Mb
COMPUTER: 12 inch 1.44Mb
COMPUTER: 12 inch 1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,138
FILING DATE: June 7, 1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 44683-Z/JPM/MJG
TELECOMMUNICATION INFORMATION:
TELEFAX: 212-97-9550
TELEFAX: 212-64-0525
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LEBNOTH: 12 base pairs
TYPE: nucleic acid
STRANDEDNES: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTY: U.S.A.

ZIP: 19898
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: MACINTOSH
OPERATING SYSTEM: MACINTOSH
OPERATING SYSTEM: MACINTOSH
SOPTWARE: MICROSOFT WORD 4.0
CURRENT APPLICATION DATA:
APPLICATION NOTAR: US/08/586,120
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: GEIGER, KATHLEEN W.
REGISTRATION NUMBER: 35,880
REPERRNCE/DOCKET NUMBER: MD-1068
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
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Best Local Similarity
Matches 9; Conserv
      STATE: New York
COUNTRY: U.S.A.
ZIP: 10036
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18-08-14-656E-24/C

18-08-14-66E-24/C

18-08-
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10.7%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 3e+02;
Matches 9; Conservative 0; Mismatches 2; Indels
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US-08-484-138-13/c
US-08-484-138-13/c
Sequence 13, Application US/08484138
Fatench No. 5652350
GENERAL INFORMATION:
APPLICANT: Watanabe, Kyoichi A.
APPLICANT: Ren, Wu-Yun
APPLICANT: Weil, Roger
ITILE OF INVENTION: Complementary DNA and Toxins
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: DNA (genomic) US-08-147-696E-24
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2 TIGGITITAAG 12
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APPLICANT: IWAMI, MORITA
APPLICANT: ARAWORI, ICHIRO
APPLICANT: KOJO, HITOSHI
TITLE OF INVENTION: PROCESS FOR PRODUCING 7-AMINOCEPHEM
TITLE OF INVENTION: COMPOUND OR SALIS THEREOF
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESSEE: P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10.7%; Score 7.8; DB 1; Length 12; 81.8%; Pred. No. 3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1755 S. Jefferson Davis Highway, Suite 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible CORPRANTING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/314,309A FILING DATE: 30-SEP-1994
CLASSIFICATION NUMBER: US/03/631,906
FILING DATE: 21-DEC-1990
ATTONNEY/AGENT INFORMATION: APPLICATION NUMBER: 21,4188
REGISTRATION NUMBER: 24,618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
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Patent No. 5693508
GENERAL INFORMATION:
APPLICANT: CHANG.
ITILE OF INVENTION: RETROVIRAL VECTORS
NUMBER OF SEQUENCES: 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: Other nucleic acid;
DESCRIPTION: synthetic DNA
                                                                                                                                                                                                         Sequence 28, Application US/08314309A Patent No. 5677141 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 18-
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (703) 413-3000
(703) 413-2220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
950 TAATGTATCGC 960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      934 CTCCTCTTCAT 944
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE:
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                                                                                                                                                                                        US-08-314-309A-28
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10.7%; Score 7.8; DB 1; Length 12; 81.8%; Pred. No. 3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                         2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MARK A.
SELECTION OF DIAGNOSTIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENETIC MARKERS IN
MICROORGANISMS AND USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. 3e+0
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 5, Application US/08254355
Facture 5, Application US/08254355
Facture 6, Application US/08254355
Facture 70. 5660981
Factor 1 NFORMATION:
FAPPLICANT: GROSZ, RONALD
FITLE OF INVENTION: GELECTION OF DIAGNOS
FITLE OF INVENTION: GELECTION OF TITLE OF INVENTION: OF A SPECIFIC MARKER IN
FITLE OF INVENTION: OF A SPECIFIC MARKER
FITLE OF INVENTION: SALMONELLA
FITLE OF INVENTION: S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: MACINTOSH
OPERATING SYSTEM: MACINTOSH SYSTEM 6.0
SOFTWARE: MICROSOSPT WORD 4.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/254,355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OF A SPECIFIC MARKER
FOR DETECTION OF
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TELECOMOUNICATION UNPORMATION
TELEPHONE: 302-892-8112
TELEFAX: 302-892-7949
                                                                                                                                                                                                                                                    TOPOLOGY: linear // MOLECULE TYPE: DNA (genomic) US-08-586-120-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: GEIGER, KATHLEEN W
REGISTRATION NUMBER: 35,8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEX: 835420
INFORMATION FOR SEQ ID NO: 5
SEQUENCE CHARACTERISTICS:
LENGTH: 12 base pairs
TYPE: nucleic acid
      302-892-8112
                                    TELEFAX: 302-892-7949
TELEX: 835420
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTER.ESTICS:
LENGTH: 12 base pairs
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Best Local Similarity 81.8
Matches 9, Conservative
                                                                                                                                                                                                                                                                                                                                                                              Ouery Match 10.7
Best Local Similarity 81.8
Matches 9; Conservative
                                                                                                                                                       LENGTH: 12 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        950 TAATGTATCGC 960
                                302-892-7949
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12 TACGGTATCGC 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19898
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   TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 548
US-08-254-355-5/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-254-355-5
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US-08-411-727-6/c

| Sequence 6, Application US/08411727 |
| Patent No. 5705161 |
| APPLICANT | POOLMAN |
| POOLMANT | On Theunis |
| APPLICANT | POOLMAN |
| APPLICANT | POOLMAN |
| APPLICANT | POOLMAN |
| PATENT | POOLMAN |
| APPLICANT | POOLMAN |
| PATENT | POOLMAN |
| PATENT | POOLMAN |
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CUDNIER: U.S.A.

CUDNIER: U.S.A.

MEDIUM TYPE: Floppy disk

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/411,727

FILING DATE: 02-0CT-1992

RILNG APPLICATION DATA:

APPLICATION NUMBER: WO PCT/NL93/00163

RILNG APPLICATION DATA:

APPLICATION NUMBER: BO 38275

RESERRACE/DOCKET NUMBER: BO 38275

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELEFEXX: 703-68-0573

TELEFEXX: 703-68-0573
WO PCT/NL93/00163
                        FILING DATE: 30-JUL-1993

ATTORNEY/AGENT INFORMATION:
NAME: PATCH, Andrew J.
REGISTRATION NUMBER: 32925
REFERENCE/DOCKET NUMBER: BO 382
REFERENCE/DOCKET NUMBER: BO 382
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-521-2297
TELERAX: 703-685-0573
TELERAX: 704-685-0573
TELERAX: 704-685-0573
TYPE: nucleic acid
STRANDEDNESS: single
TYPE: nucleic acid
STRANDEDNESS: single
TYPE: MOLECULE TYPE: DNA (genomic)
US-08-411-727-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 81.8
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         959 GCTACCAACGG 969
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APPLICATION NUMBER:
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JOS-08-411-72,-5

Patent No. 5705161

APPLICANT: WAN DER LEY, Peter Andre

APPLICANT: POCORANTON: Theuris

APPLICANT: POCORANTON: Deter Theuris

APPLICANT: POCORANTON: NAMINGENIC MENINGCOCCCAL LPS AND OTHER

TITLE OF INVENTION: IMMUNOGENIC MENINGCOCCCAL LPS AND VACCINE THEREFROM

NUMBER OF INVENTION: MEMBRANE VESICLES AND VACCINE THEREFROM

NUMBER OF INVENTION: AT HOMPSON

STREET: 745 SOUTH 237d Street, Suite 200

CITY: Arlington

STREET: VIGINIA

CONTURY: U.S.A.

ZIP: 22202

COMPUTER: ISM PC Compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIN NUMBER: US/08/411,727

FILING DATE: 01-MAY-1995

CLASSIFICATION NUMBER: NL 9201716

FILING DATE: 02-07-1992

REDICATION NUMBER: NL 9201716

FILING DATE: 02-07-1992

REIGN APPLICATION DATA:

APPLICATION NUMBER: NL 9201716

FILING DATE: 02-07-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10.7%; Score 7.8; DB 1; Length 12; 81.8%; Pred. No. 3e+02;
            CORRESPONDENCE ADDRESS:
STREET: 220 MONTGOMERY STREET, SUITE 2200
STREET: 220 MONTGOMERY STREET, SUITE 2200
STATE: 220 MONTGOMERY STREET, SUITE 2200
STATE: CALIFORNIA
COUNTRY: UNITED STATES OF AMERICA
201P: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Flopy disk
COMPUTER: IBM PC compatible
OPERATION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/336,132
FILING DATE: 07-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: CARROLL, PETER G.
RESISTRATION NUMBER: 13,637
REFERENCE/DOCKET NUMBER: 2,837
REFERENCE/DOCKET NUMBER: 3,837
REFERENCE/DOCKET NUMBER: 3,765-8410
TELEPHONE: (415) 397-338
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-336-132-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 81.8
Matches 9; Conservative
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CORRESPONDENCE ADDRESS
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US-08-411-727-5
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Sequence 18, Application US/08608881A
Patent No. 5/47257
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: GENERIC MARKERS
TITLE OF INVENTION: THE DETECTION OF
TITLE OF INVENTION: SEROTYPE-0157:H7
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: E. I. DU PONT
STREET: 1007 MARKET STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 41, Application US/08360125
| Betent No. 5767246
| GENERAL INFORMATION:
| APPLICANT: Saiko HOSOKAWA
| APPLICANT: Toshiaki TAGAWA
| APPLICANT: Toshiaki TAGAWA
| APPLICANT: Tokhiaki TAGAWA
| APPLICANT: Wow 5767246ihiko ITO
| TITLE OF INVENTION: Human Monoclona TITLE OF INVENTION: Specifically Bit TITLE OF INVENTION: GLI Membrane NUMBER: OF SEQUENCES: 42
| CORRESPONDENCE ADDRESS: ADDRESSEE: ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: FLOYD. LINDA A
REFERENCE/DOCKET NUMBER: MD1C
TELECOMMUNICATION INFORMATION:
TELEFHONE: 302-892-8112
TELEFAX: 302-892-8112
INFORMATION FOR SEQ ID NO: 18: SEQUENCE CHARACTERISTICS:
LENGTH: 12 base pairs
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MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10.7%;
81.8%;
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Best Local Similarity 81.8
Matches 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12 racedrarcec 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: WILMINGTON
STATE: DELAWARE
COUNTRY: U.S.A.
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                                             JS-08-608-881A-18/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-360-125-41/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE:
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Patent No. 273379
GENERAL INFORMATION:
APPLICANT: REFF, Mitchell E.
TITLE OF INVENTION: IMPAIRED DOMINANT SELECTABLE MARKER
TITLE OF INVENTION: SEQUENCE AND INTRONIC INSERTION STRATEGIES FOR ENHAN
TITLE OF INVENTION: OF EXPRESSION OF GENE PRODUCT AND EXPRESSION VECTOR
TITLE OF INVENTION: OF SYSTEMS COMPRISING SAME
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                  Score 7.8; DB 1; Length 12;
Pred. No. 3e+02;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10.7%; Score 7.8; DB 1; Length 12; 81.8%; Pred. No. 3e+02; tive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 07-JUN-1995
CLASSIFICATION DATA:
FILING DATE: 07-JUN-1995
RIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/147,696
FILING DATE: 03-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/977,691
FILING DATE: 13-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: TESKLA, ROBIN L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 35,030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS STREET: P.O. BOX 1404
CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
; TYPE: nucleic acid
; STRANDENNESS: single
TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-411-727-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 24:
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: United States
                                                                                                                                                                                                                                  Query Match
Best Local Similarity 81.8
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy di
                                                                                                                                                                                                                                                                                                                                                                                              959 GCTACCAACGG 969
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 553
US-08-484-334-24/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-484-334-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
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Specifically Binding to Surface Antigen of Cancer
Cell Membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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MARK A GENETIC MARKERS AND METHODS FOR THE DETECTION OF E. COLI SEROTYPE-0157:H7
                                                                                                                                                                                                                    ZIP: 19998
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/608,881A
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 7.8; DB 1;
Pred. No. 3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Wenderoth, Lind & Ponack
805 Fifteenth Street, N.W., #700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
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Sequence 2; Application US/08545785
Patent No. 5770713
GENERAL INFORMATION:
APPLICAMY: Imbach and Rayner
TITLE OF INVENTION: And Method of Preparation
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSE: Woodcock Washburn Kurtz Mackiewicz & No. 5770713ris LLP
STREET: On Liberty Place - 46th Floor
CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ô
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-41-897A-71

Sequence 71, Application US/08441887A

Patent No. 5837832

GENERAL INFORMATION:
PAPLICANT: Cronin, Maureen T.
APPLICANT: Fodor: Stephen P.A.
APPLICANT: Hubbell, Kabhua X.
APPLICANT: Hubbell, Rarl A.
APPLICANT: Lipshutz, Robert J.
APPLICANT: Libshutz, Robert J.
APPLICANT: Maddonald S.
APPLICANT: Maddonald S.
APPLICANT: Maddonald S.
APPLICANT: Sheldon, Edward L.
TITLE OF INVENTION: Biological Chips
NUMBER OF SEQUENCES: 360
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Twomsend and Townsend and Crew Lip
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE: PA

COUNTRY: U.S.A.

ZIP: 19103

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch disk, 1.44 Mb

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDFREECT 6.1

CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US.08/545,785
FILING DATE: 17-0AN-1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: JOSSPI LUCCI
REGISTRATION NUMBER: 33,307
REPERBNCE/DOCKST NUMBER: ISIS-2114
TELEFONE: 215-568-3100
TELEFAX: 2115-568-3100
TELEFAX: 2115-56
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                                                                                        RESULT 556
US-08-545-785-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-545-785-2
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STRAIN:
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
HARLOTYPE:
TISSUE TYPE:
CELL TYPE:
CELL LINE:
ORGANELLE:
IMMEDIATE SOURCE:
LIBRARY:
CLONE:
CROWOSOME/SEGMENT:
MAP POSITION:
MAP POSITION:
FEATURE:
FEATUR
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COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DDS
SOFWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/360,125
                                                                                                                                                                                                   FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION DATA:
FILING DATE:
TING DATE: June 29, 1992
APPLICATION NUMBER: 07/905,534
APPLICATION NUMBER:
FILING DATE: TORNATION:
NAME: WAITEN INCORVATION:
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELEPHONE: 202-371-8850
TELEPHONE: 202-371-8850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             JOURNAL:
VOLUME:
VOLUME:
VOLUME:
PAGES:
DATE:
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
US-08-360-125-41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         41:
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SEQUENCE CHARACTERISTICS:
LENGTH: 12 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION:
PUBLICATION INFORMATICN:
AUTHORS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               905 TCATTTTCTTT 915
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: CDNA HYPOTHETICAL:
ANTI-SENSE:
PRAGMENT TYPE:
ORIGINAL SOURCE:
ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11 rcAcrercrrr 1
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81.8%; Pred. No. 3e+02;
cive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Lipshutz, Robert J.
APPLICANT: Libshan, Peter E.
APPLICANT: Mortis, Macdonald S.
APPLICANT: Mortis, Macdonald S.
APPLICANT: Sheldon, Edward L.
TITLE OF INVENTION: Arrays of Nucleic Acid Probes on TITLE OF SEQUENCES: 360
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Townsend and Townsend and Townsend Corrections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CAMPUTER FELAL
COMPUTER FLORY disk
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
COPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/441,887A
FILING DATE: 16-MAY-1995
CLASSIFICATION: 435
                                                                            PUCASIFICATION: 435
PRICAR APPLICATION DATA:
APPLICATION NUMBER: US 08/143,312
FILING DATE: 26-0CT-1993
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/082,937
FILING DATE: 25-UTN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Liebeschuetz, Joseph O.
REGISTRATION NUMBER: 37,505
REFERENCE/DOCKET NUMBER: 37,505
REFERENCE/DOCKET NUMBER: 018547-004160US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-326-2402
INFORMATION FOR SEQ ID NO: 91:
SEQUENCE CHARACTERISTICS:
LENGTH 12 base pairs
FILING DATE: 16-MAY-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/143,312
FILING DATE: 26-0CT-1993
CLASSIFICATION: 435
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Patent No. 5837832
GENERAL INFORMATION:
APPLICANT: Chee, Mark
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chee, Mark
Cronin, Maureen T.
Fodor, Stephen P.A.
Huang, Xiaohua X.
Hubbell, Earl A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear MOLECULE TYPE: DNA (probe)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 81.8
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                927 TITAICCTIC 937
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11 TTTTCCCCTCC 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-441-887A-103/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10.7%; Score 7.8; DB 1; Length 12; 81.8%; Pred. No. 3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Cronin, Maureen T.
APPLICANT: Cronin, Maureen T.
APPLICANT: Cronin, Maureen T.
APPLICANT: Huang, Xiaohua X.
APPLICANT: Hubbell, Barl A.
APPLICANT: Hubbell, Barl A.
APPLICANT: Lobban, Peter E.
APPLICANT: Macdonald S.
APPLICANT: Marays of Nucleic Acid Probes on TITLE OF INVENTION: Arrays of Nucleic Acid Probes on TITLE OF INVENTION: Biological Chips
NUMBER OF SEQUENCES: 360
CORRESPONDENCE ADDRESS:
                                                                                                                                                 OPERATING SYSTEM: PC-UCS/MS-UCS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/441,887A
FILING DATE: 16-MAY-1995
CLASSIPICATION: 435
RIGHT APPLICATION TAMBER: US 08/143,312
APPLICATION NUMBER: US 08/143,312
FILING DATE: 26-OCT-1993
CLASSIPICATION: 435
PRICK APPLICATION: DATA:
APPLICATION NUMBER: US 08/082,937
FILING DATE: 25-UN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Liebeschuetz, Joseph O.
REGISTRATION NUMBER: 37,505
REFERENCE/DOCKET NUMBER: 0188547-004160US
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEE: Townsend and Townsend and Crew LLP: Two Embarcadero Center, 8th Floor San Francisco California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 558
US-08-441-887A-91/c
; Sequence 91, Application US/08441887A
; Eatent No. 5837832
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 650-326-2422
INFORMATION FOR SEQ ID NO: 71:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: DNA (probe)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 81.8
Matches 9, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                single
                                                                    COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 TAGCAGCGGTG 11
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-441-887A-71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE: Ca
                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET:
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Query Match 10.7%; Score 7.8; DB 1; Length 12; Best Local Similarity 81.8%; Pred. No. 3e+02; Matches 9; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Chee, Mark
APPLICANT: Cronin, Maureen T.
APPLICANT: Podor, Stephen P.A.
APPLICANT: Hubbell, Kabhua X.
APPLICANT: Lipshutz, Robert J.
APPLICANT: Lipshutz, Robert J.
APPLICANT: Lipshutz, Robert J.
APPLICANT: Sheldon, Peter E.
APPLICANT: Sheldon, Edward L.
TITLE OF INVENTION: Arrays of Nucleic Acid Probes on TITLE OF INVENTION: Alboration Arrays of SQUENCES: 360
CORRESPONDENCE ADDRESS:
ADDRESSEE: TOWNSOND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Flopy disk
MEDIUM TYPE: Flopy disk
COMPUTER: IBM PC compatible
SOFTWARE: Batentin Release #1.0, Version #1.25
SOFTWARE: Batentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US 08/143,312
FILING DATE: 26-COT-1993
CLASSIFICATION NUMBER: US 08/082,937
FILING DATE: 25-UN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Liebeschuetz, Joseph O.
REGISTRATION NUMBER: 01867-004160US
REGISTRATION NUMBER: 01867-004160US
TELECOMMUNICATION INFORMATION:
MATERIARICALION NUMBER: 01867-004160US
TELECOMMUNICATION INFORMATION:
MATERIARICALION NUMBER: 01867-004160US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Townsend and Townsend and Crew STREET: Two Embarcadero Center, 8th Floor CITY: San Francisco STARE: California COUNTRY: USA
                                                                                     LENGTH: 12 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (probe)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 650-326-2422
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 base pairs
                                  INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 base pairs
                                                                                                                                                                                                                                                                                                                                                                                          950 TAATGTATCGC 960
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             inear
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US-08-441-887A-135
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Pred. No. 3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Cree, Mark
APPLICANT: Croin, Maureen T.
APPLICANT: Fodor, Stephen P.A.
APPLICANT: Huang, Xiaohua X.
APPLICANT: Hubbell, Earl A.
APPLICANT: Lipshutz, Robert J.
APPLICANT: Lipshutz, Robert J.
APPLICANT: Sheldon, Beter B.
APPLICANT: Morris, Macdonald S.
APPLICANT: Sheldon, Edward L.
TITLE OF INVENTION: Biological Chips
NUMBER OF SEQUENCES: 360
CORRESPONDENCE ADDRESS:
ADDRESSED: Townsend and Townsend and Crew LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: Two Embarcadero Center, 8th Floor
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111
COMPUTER EXADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/441,887A
FILING DATE: 16-MAY-1995
RIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/143,312
FILING DATE: 26-OCT-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/082,937
FILING DATE: 25-OUT-1993
ATTORNEY/AGENT INFORMATION:
NAME: Liebeschuetz, Joseph O.
RESTERRALION NUMBER: 37,505
REFERRENT NUMBER: 37,505
REFERRENT NUMBER: 37,505
REFERRENT NUMBER: 37,005
APPLICATION NUMBER: US 08/082,937
FILING DATE: 25-UN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Liebeschuetz, Joseph O.
REGISTRATION NUMBER: 37,505
REFERENCE/DOCKET NUMBER: 018547-004160US
TELEPAN: 650-326-2400
TELEPAN: 650-326-3260
TENGTH: 12 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              018547-004160US
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-41-887A-135/c
; Sequence 135, Application US/08441887A
; Patent No. 5837832
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: 01
ELECOMMUNICATION INFORMATION:
TELEPHONE: 650-326-2400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 81.8%;
Matches 9; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear MOLECULE TYPE: DNA (probe)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          956 ATCGCTACCAA 966
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Sequence 14, Application US/08661330A

Patent No. 5849485

GENERAL INFORMATION:
APPLICANT: Sladek, Frances M.
APPLICANT: Zhong, Weimin Jar., James F.
TITLE OF INVENTION: LIVER ENRICHED TRANSCRIPTION FACTOR
NUMBER OF SEQUENCE: 17

CORRESPONDENCE ADDRESS:
ADDRESSE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
STREET: Now Jersey
COUNTRY: USA

COUNTRY: USA

COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER TRADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/661,330A
FILING DATE: 14-JUN-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-030A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 7.8; DB 1;
Pred. No. 3e+02;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
US-08-450-578-41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 14: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 81.8%;
Matches 9; Conservative
                                                                                                     POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
UNITS:
FEATURE:
NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION:
PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  905 TCATITICITY 915
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CELL LINE:
ORGANELLE:
IMMEDIATE SOURCE:
LIBRARY:
                                                                                                                                                                                                                                                                                                                                        AUTHORS:
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Sequence 41, Application US/08450578

Patent No. 5837845

GENERAL INFORMATION:
Saiko HOSOKAWA
APPLICANT: Saiko HOSOKAWA
APPLICANT: Yoko HIRAKAWA
APPLICANT: No. 5837845ihiko ITO
APPLICANT: Kazuhiro NAGAHKE
TITLE OF INVENTION: Human Monoclonal Antibody
TITLE OF INVENTION: Specifically Binding to Surface Antigen of Cancer
TITLE OF INVENTION: Cell Membrane
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
                                                                                            Gaps
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                                            10.7%; Score 7.8; DB 1; Length 12; 81.8%; Pred. No. 3e+02; tive 0; Mismatches 2; Indels
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CELL TYPE: Hybridoma producing human antibody 1-3-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500 kb COMPUTER: Inal Compatible COMPUTER: Inal Compatible OPERATING SYSTEM: MS-DOS SOFTWARE: WordPerfect 5.1 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/450,578 FILING DATE: May 25, 1995 CLASSIFICATION 100: 435 PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/360,125 FILING DATE: December 20, 1994 FILING DATE: December 20, 1994 FILING DATE: December 20, 1994 FILING DATE: JUNE 20, 1994 FILING DATE: JUNE 20, 1995 ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 07/905,534 ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 33,367 REFERENCE/DOCKET NUMBER: TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEE: Wenderoth, Lind & Ponack
: 805 Fifteenth Street, N.W., #700
Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                               Query Match 10.7
Best Local Similarity 81.8
Matches 9; Conservative
                                                                                                                                         934 CTCCTCTTCAT 944
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DEVELOPMENTAL STAGE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: line
MOLECULE TYPE: (
HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FRAGMENT TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                      RESULT 562
US-08-450-578-41/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE:
STREET: 80
       US-08-441-887A-334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ANTI-SENSE:
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TYPE: nucleic acid
STRANDEDNESS: double stranded
     909 TITCITIGGIC 919
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Best Local Similarity
Matches 9; Conserv
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MOLECULE TYPE: other nucleic acid
DESCRIPTION: third strand derived from
DESCRIPTION: retinoblastoma sequence region in Seq ID No. 586124483
                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
10.7%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 3e+02;
Matches 9; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-173-489C-84

| Sequence 84, Application US/08173489C|
| Patent No. 5861244|
| Application US/08173489C|
| Patent No. 5861244|
| Applicant: Wang, C. -G.
| Applicant: Wang, C. -G.
| Applicant: Wang, C. -G.
| TITLE OF INVENTION: TRIPLE-STRAND FORMATION.
| TITLE OF INVENTION: TRIPLE-STRAND FORMATION.
| OF SEQUENCES: 365
| CORRESPONDENCE ADDRESS:
| ADDRESSEE: PROFILE DIAGNOSTIC SCIENCES, INC., CITY: NEW YORK
| STATE: NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ANTI-SENSE: No
publication information:
RELEVAT RESIDUES IN SEQ ID NO: 84 :FROM 1 TO 12
US-08-173-489C-84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: Use.

ZIP: 10021.
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44Mb storage
COMPUTER: IBM PC/XT/AT
OPERATING SYSTEM: MS-DOS version 6.2
SOFTWARE: Wordperfect Version 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/173,489C
FILING DATE: 22 DEC 1993
CLASSIFICATION NUMBER: US 07/968,436
FILING DATE: 29 OCT 1992
ATTORNEY/AGENT INFORMATION:
NAME: Handelman, Joseph H.
REGISTRATION NUMBER: 26,179
REPERENCE/DOCKET NUMBER: 26,179
REPERENCE/OFFICE (attorney) (212) 708-188C
TELEFAX: (attorney) (212) 708-188C
TELEFAX: (attorney) (212) 246-8959
INFORMATION FOR SEQ ID NO: 84:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 bases
TYPE: Nucleic Acid
STRANDEDNESS: single stranded
TOPOLOGY: linear
                                                                                    MOLECULE TYPE: other nucleic acid
BESCRIPTION: /desc = "HNF-4 Consensus"
US-08-661-330A-14
12 base pairs
                                                                                                                                                                                                                                                                                                                  915 IGGICTITICC 925
                       TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                            ||: |:|:|:
11 TGRMCYTWGCM 1
                                                                        linear
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LENGIH:
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Gaps
RESULT 565
US-08-173-489C-119
i Sequence 119, Application US/08173489C
j Patent No. 5861244
j GENERAL INFORMATION:
APPLICANT: WANG, C. -G.
APPLICANT: WEBURN, A. G.
TITLE OF INVENTION: TRIPLE-STRAND FORMATION.
NUMBER OF SEQUENCES: 365
CORRESPONDENCE ADDRESS:
ADDRESSEE: APOFILE DIAGNOSTIC SCIENCES, INC.,
STREET: 510 EAST 73RD STREET,
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10.7%; Score 7.8; DB 1; Length 12; llarity 81.8%; Pred. No. 3e+02; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: genomic DNA
DESCRIPTION: beta-globin gene (accession # V00499)
DESCRIPTION: nucleotides 1284 to 1295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DATE: 1980
RELEVANT RESIDUES IN SEQ ID NO: 119 :FROM 1 TO 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    O'Connell,
                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: USA
ZIP: 1021.

COMPUTER REABABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44Mb storage
COMPUTER: IBM PC/XT/AT
OPERATING SYSTEM: MS-DOS version 6.2
SOFTWARE: Wordeperfect Version 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/173,489C
FILING DATE: 22 DEC 1993
CLASSIFATIONIN MERR: US 07/968,436
FILING DATE: 29 OCT 1992
ATTORNEY/AGENT INFORMATION:
NAME: Handelman, Oseeph H.
REGISTRATION NUMBER: US 0.179
REFERENCE/DOCKET NUMBER: US 1.79
RELEPAX: (attorney) (212) 246-8959
SEQUENCE CHARACTERISTICS:
LENGTH: 12 base pairs
TVDF: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Efstratiadis, A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ANTI-SENSE: no
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
PUBLICATION INFORMATION:
AUTHORS: Lawn, R M, Efstratiadis, A
AUTHORS: C, Maniatis, T
TITLE: The nucleotide sequence of
JOURNAL: Cell
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12 CCTTTCACCCC 2

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MOLECULE TYPE: genomic DNA
DESCRIPTION: 23s rRNA gene from Escherichia coli
DESCRIPTION: (Accession # M25458) nucleotides 785 to 796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10.7%; Score 7.8; DB 1; Length 12; 81.8%; Pred. No. 3e+02; tive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               structures of Escherichia coli MRE 600 23S ribosomal RNA Comparison with models of secondary structure for maize chloroplast 23S ERNA and for large portions of mouse and human 16S mitochondrial rRNAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PUBLICATION INFORMATION:
AUTHORS: Branlant, C, Krol, A, Machatt, M, A,
AUTHORS: Pouyet, J, Ebel, J P, Edwards, K, Koessel,
                              Sequence 219, Application US/08173489C
Patent No. 5861244
GENERAL INFORMATION:
APPLICANT: WANG, C. -G.
APPLICANT: WANG, C. -G.
TITLE OF INVENTION: GENETIC SEQUENCE ASSAY USING DNA TITLE OF INVENTION: TRIPLE-STRAND FORMATION.
NUMBER OF SEQUENCES: 365
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        , RELEVANT RESIDUES IN SEQ ID NO: 219 :FROM 1 TO 12 US-08-173-489C-219
                                                                                                                                                                                                                                                     ADDRESSEE: PROFILE DIAGNOSTIC SCIENCES, INC., STREET; 510 EAST 73RD STREET, CITY: NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44Mb storage
COMPUTER: 1BM PC/XT/Ah,
COMPUTER: 1BM PC/XT/Ah,
COMPUTER: 1BM PC/XT/Ah,
COMPUTER: 1BM PC/XT/Ah,
SOFTWARE: Wordperfect Version 5.1
CURRENT APPLICATION DATA:
PILING DATE: 22 DEC 1993
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (attorney) (212) 708-1880 TELEFAX: (attorney) (212) 246-8959 INFORMATION FOR SEQ ID NO: 219: SEQUENCE CHARACTERISTICS: LENGTH: 12 base pairs TYPE: nucleic acid stranbedness: double stranded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/968,436
FILING DATE: 29 OCT 1992
ATTOCNEY/AGENT INFORMATION:
NAME: Handelman, Joseph H.
REGISTATION NUMBER: 26,195
REFERENCE/DOCKET NUMBER: U9518-6
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Primary and secondary
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Best Local Similarity 81.8
Matches 9; Conservative
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                                                                                                                                                                                                                                                                                                                               STATE: NEW YORK
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RESULT 566
US-08-173-489C-219/c
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ANTI-SENSE: n
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Pred. No. 3e+02;
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RESULT 567
US-08-173-489C-246
; Sequence 246, Application US/08173489C
; Patent No. 5861244
; GENERAL INFORMATION:
; APPLICANT: WANG, C. -G.
; TITLE OF INVENTION: TRIPLE-STRAND FORMATION.
; TITLE OF INVENTION: TRIPLE-STRAND FORMATION.
; NUMBER OF SEQUENCES: 365
; CORRESPONDENCES: 365
; ADDRESSEE: PROFILE DIAGNOSTIC SCIENCES, INC.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-173-489C-292
Sequence 292, Application US/08173489C
Sequence 292, Application US/08173489C
Patent No. 5861244
Patent INVERATION:
APPLICANT: WANG, C. -G.
APPLICANT: HERBURN, A. G.
TITLE OF INVENTION: TRIPLE-STRAND FORMATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RELEVANT RESIDUES IN SEQ ID NO: 246 :FROM 1 TO 12 US-08-173-489C-246
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third strand derived from M. luteus
23s region in Seq ID No. 5861244245
                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44Mb storage
COMPUTER: 18M PC/XT/AT
OPERATING SYSTEM: MS-DOS version 6.2
SOFTWARE: Wordperfect Version 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/173,489C
FILING DATE: 2 DEC 1993
CLASSIFICATION 1435
PRIOR APPLICATION 1435
PRIOR APPLICATION 1978: 20 OCT 1992
ATTORNEY/AGENT INFORMATION:
NAME: Handelman, Joseph H.
REGISTRATION NUMBER: 26,179
REFERENCE/DOCKET NUMBER: 19518-6
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
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(212) 246-8959
O: 246:
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STRANDEDNESS: single stranded
                                                                                                                                                                                                                                                                                    510 EAST 73RD STREET
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Best Local Similarity 81.8%;
Matches 9; Conservative
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TELEFAX: (attorney) (2)
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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PUBLICATION INFORMATION:
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NEW YORK
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Patent No. 5871697
GENERAL INFORMATION:
APPLICANT: Rothberg, Jonathan
APPLICANT: School Sequences in a Sample Without TITLE OF INVENTION: Method for the Determination and TITLE OF INVENTION: Classification of DNA Sequences in a Sample Without TITLE OF INVENTION: Sequencing NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSE: Pennie and Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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MOLECULE TYPE: other nucleic acid
DESCRIPTION: third strand derived from C.
DESCRIPTION: pasteurianum 16s region in Seq ID No. 5861244291
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; ANTI-SENSE: no
; PUBLICATION INFORMATION:
; FELEVANT RESIDUES IN SEQ ID NO: 292 :FROM 1 TO 12
US-08-173-489C-292
NUMBER OF SEQUENCES: 365
CORRESPONDENCE ADDRESS:
ADDRESSEE: PROFILE DIAGNOSTIC SCIENCES, INC.,
STREET: 510 EAST 73RD STREET,
CITY: NEW YORK
STRATE: NEW YORK
COUNTRY: USA
                                                                                                                                              ZIP: 10021
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44Mb storage
COMPUTER: 1BM FC/XT/AT
OPERATING SYSTEM: MS-DOS version 6.2
SOSTWARE: WORDERFECT VERSIOn 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/173,489C
FILING DATE: 22 DEC 1993
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION WORBER: US 07/968,436
FILING DATE: 29 OCT 1992
ATTORNEY/AGENT INFORMATION:
NAME: Handelman, Joseph H.
REFERENCE/DOCKET NUMBER: US-180
TELEPHONE: (attorney) (212) 708-1880
TELEPHONE: (attorney) (212) 708-1880
TELEFRATION FOR SEQ ID NO: 292:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 bases
TYPE: mocleic acid
STRANDEDDRESS: single stranded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
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COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10.7%;
81.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 10.7
Best Local Similarity 81.8
Matches 9; Conservative
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US-08-547-214-13
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US-08-751-243C-27/C

Sequence 27, Application US/08761243C

Sequence 27, Application US/08761243C

Sequence 27, Application US/08761243C

Patent No. 5879879

TITLE OF INVENTION: No. 5879879el Cis-Acting Element In The Human LDL Receptor Proving Sequences. 28

CORRESPONDENCES. 28

ADDRESSEE: Benjamin Aaron Adler, Ph.D.,J.D.

STREET: 8011 Candle Lane
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION DATA:
TLING DATE: 24-OCT-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leelie
REGISTRATION NUMBER: 18,872
REGISTRATION NUMBER: 18,872
REGISTRATION NUMBER: 19,999
TELEFANCK/DOCKET NUMBER: 7934-015-999
TELEFANCK/DOCKET NUMBER: 7934-015-999
TELEFANCK/DOCKET NUMBER: 12,299
TELEFANCK/DOCKET NUMBER: 12,299
TELEFANCK/DOCKET NUMBER: 13,884
TELEFAN: (212)-699-884
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADTRET: 8011 Candle Lane
CITY: Houston
STATE: Texas
COMPUTE: Texas
COMPUTER TEADABLE FORM:
MEDIUM TYPE: FLOPPY disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM:
MACINTOSH MACINTOSH
OPERATING SYSTEM:
SOFTWARE: MICTOSOFT WORD ATA:
APPLICATION NUMBER: US/08/761,243C
FILNG DATE: December 6, 1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: BENJAMIN AARON Adler, Ph.D., J.D.
REGISTRATION NUMBER: 35,423
REGISTRATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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TELEPHONE: 713-77-6908
TELEFAK: 713-77-6908
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 bp
TYPE: nucleic acid
STRANDEDNESS: single-stranded
"""DATOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            other nucleic acid
No
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81.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 81.8
Best Local 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          943 ATTGGTTTAAT 953
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; MOLECULE TYPE:
US-08-547-214-13
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APPLICANT: Simpson, John
TITLE OF INVENTION: METHOD AND APPARATUS FOR IDENTIFYING,
TITLE OF INVENTION: CLASSIFYING, OR QUANTIFYING DNA SEQUENCES IN A SAMPLE
TITLE OF INVENTION: WITHOUT SEQUENCING
TITLE OF INVENTION: WITHOUT SEQUENCING
CORRESPONDENCE 3.77
CORRESPONDENCE ADDRESS:
ADDRESSE: Pennie and Edmonds LLP
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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GENERAL INFORMATION:

APPLICANT: HORACANA, Toshiaki

APPLICANT: HIRACANA, Yoko

APPLICANT: HIRACANA, Yoko

APPLICANT: HIRACANA, Yoko

APPLICANT: HIRACANA, Yoko

APPLICANT: ITO NO. 59271hiko

APPLICANT: NAGAIKE, Kazuhiro

TITEE OF INVENTION: HUMAN MONOCICONAL ANTIBODY SPECIFICALLY BINDI

TITEE OF INVENTION: SURFACE ANTIGEN OF CANCER CELL MEMBRANE

FILE REFERENCE: 177/52736.IKH

CURRENT APPLICATION NUMBER: US/09/017,628

CURRENT APPLICATION NUMBER: 08/160,125

EARLIER FILING DATE: 1994-12-20

NUMBER OF SEQ ID NOS: 42

SOFTWARE: PALENTI VET. 2.0

SEQ ID NO 41

LENGTH: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 10.7%; Score 7.8; DB 1; Length 12; Best Local Similarity 81.8%; Pred. No. 3e+02; Matches 9; Conservative 0; Mismatches 2; Indels
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Patent No. 5990287
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (212) 869-9741/886
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          943 ATTGGTTTAAT 953
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    nucleic acid
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MOLECULE TYPE: DNA
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ORGANISM: Unknown
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                                                                                                Score 7.8; DB 1; Length 12;
Pred. No. 3e+02;
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                                                                                                                                                                    2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 571
US-08-766-439-4/c
; Sequence 4, Application US/08766439
; Patent No. 592538
; Patent No. 592538
; GENERAL INFORMATION:
APPLICANT: HAREL, JAMES WILLIAM
APPLICANT: JENSEN, MARK ANTON
; TITLE OF INVENTION: GENETIC MARKERS AND METHODS FOR
; TITLE OF INVENTION: THE DETECTION OF LISTERIA
; TITLE OF INVENTION: MONOCYTOGENES AND LISTERIA SPP.
; NUMBER OF SEQUENCES: 110
; CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEE: E. I. DU PONT DE NEMOURS AND COMPANY 1 1007 MARKET STREET WILMINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: U.S.A.

ZIP: 19998
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.50 INCH DISKETTE
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
SOFTWARE: MICROSOFT WORD 2.0C
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/766,439
                                                                                         Query Match
10.7%; Score 7.8; DB
Best Local Similarity 81.8%; Pred. No. 3e+0
Matches 9; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION: 0.243
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/745,228
FILING DATE: NOVEMBER 8, 1996
ATTORNEY/AGENT INFORMATION:
NAME: FLOYD, LINDA AXAMETHY
REGISTRATION NUMBER: 33,692
REFERRENCE/DOCKET NUMBER: MD-1065-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 302-892-8112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 572
US-08-663-823B-13
; Sequence 13, Application US/08663823B
; Patent No. 5972693
; PATENT INFORMATION:
; APPLICANT: Rothberg, Jonathan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-766-439-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 302-773-0164
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        81.8%;
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TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 81.8
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            950 TAATGTATCGC 960
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                                                                                                                                                                                                                                                                                                     11 GCTTTTTAACC 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE: DELAWARE
; ORIGINAL SOURCE:
US-08-761-243C-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET:
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Sequence 24, Application US/09013092

Sequence 24, Application US/09013092

Fatent No. 6017733

GENERAL INFORMATION

THUS OF INVENTION: SEQUENCE AND INTENDIC INSERTION STRATEGIES FOR ENHANCEMENT

TITLE OF INVENTION: SEQUENCE AND INTENDIC INSERTION STRATEGIES FOR ENHANCEMENT

TITLE OF INVENTION: SYSTEMS COMPRISING SAME

TITLE OF INVENTION: SYSTEMS COMPRISING SAME

NUMBER OF SEQUENCES: 32

ADDRESSEONDENCE ADDRESS:

ADDRESSEE: BUNNS, DOANE, SWECKER & MATHIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                   Sequence 51, Application US/08822586
Fatent No. 6015890
GENERAL INFORMATION:
FAPLICANT: WILLIAM R. JACOBS, JR., JAMES M. MUSSER AND APPLICANT: WILLIAM R. JACOBS, JR., JAMES M. MUSSER AND APPLICANT: MALIO TELENTI
ITILE OF INVENTION: MUTANTS THEREOF
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
ADDRESSED MAYERE, ROTHSTEIN & EBENSTEIN
STREET: 90 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: U.S.A.
MEDIUM TYPE: 35 INCH 1.44 Mb STORAGE
MEDIUM TYPE: DISKETTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 7.8; DB 1; Length 12;
Pred. No. 3e+02;
0; Mismatches 2; Indels
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COMPUTER: IDENTIFE: COMPATIBLE
COMPUTER: ASCII

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/822,586
FILING DATE: MARCH 20, 1997
ATTORNEY/AGENT INFORMATION:
MARE: ELIZABETH A. BOGOSIAN
REGISTRATION NUMBER: 39,911
REPERENCE/DOCKET NUMBER: 39,911
REPERENCE/DOCKET NUMBER: 96700/437
TELECOMMUTACATION INFORMATION:
TELECOMMUTACATION INFORMATION:
TELECOMMUTACATION INFORMATION:
TELECOMMUTACATION SEGORGS OF 286-0082
TELERAX: (212) 286-0854 or 286-0082
INFORMATION FOR SEQ ID NO: 51:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: other nucleic acid HYPOTHETICAL: NO
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ilarity 81.8%;
Conservative
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COUNTRY: United States
ZIP: 22313-140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           915 TGGTCTTTGCC 925
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CITY: Alexandria
STATE: Virginia
COUNTRY: United State
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 reservitede 11
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STRANDEDNESS: sing
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Best Local Similarity
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                                    US-08-822-586-51
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15-09-014-000-01/C

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15-09-014-000-01/C

15-09-014-000-01/C

15-09-014-000-01/C

15-09-014-000-01/C

15-09-014-01/C

17-00-01-01/C

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                                                         Score 7.8; DB 1; Length 12;
Pred. No. 3e+02;
0; Mismatches 2; Indels
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81.8%; Pred. No. 3e+02;
iive 0; Mismatches 2
                                                   Query Match
Best Local Similarity 81.8%;
Matches 9; Conservative
                                                                                                                                                                      905 TCATTTTCTTT 915
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Best Local Similarity 81.8
Matches 9; Conservative
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US-09-017-628-41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-014-880-41
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Sequence 84, Application US/08874825
Sequence 84, Application US/08874825
Patent No. 6057101
GENERAL INFORMATION:
APPLICANT: Nandabalan, Krishnan
APPLICANT: Rothberg, Jonathan
APPLICANT: Kang, Meijia
APPLICANT: Kang, Meijia
APPLICANT: Kalbfleisch, Theodore
APPLICANT: Kalbfleisch, Theodore
APPLICANT: Kalbfleisch, Theodore
APPLICANT: More INVENTION: IDENTIFICATION AND COMPARISON OF
TITLE OF INVENTION: PROTEIN INTERACTIONS THAT OCCUR IN POPULATIONS
TITLE OF INVENTION: AND IDENTIFICATION OF INHIBITORS OF THESE INTERACTORS
NUMBER OF SEQUENCES: 122
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
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Pred. No. 3e+02;
4; Mismatches 1; Indels
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                                                                                  MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "HNF-4 Consensus"
HYPOTHETICAL: YES
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MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FESTSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/874,825
FILING DATE: 13-UN-1997
CLASSIFICATION: 435
FILING DATE: 14-UN-1997
CLASSIFICATION NUMBER: 08/663,824
FILING DATE: 14-UN-1996
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
FEGISTRATION NUMBER: 18,872
REGISTRATION NUMBER: 18,872
REGISTRATION NUMBER: 18,972
REGISTRATION NUMBER: 18,972
FELERPAN: 212-790-9090
TELERPHONE: 212-790-9090
TELERPHONE: 212-790-9090
TELERPHONE: 212-786-8864
INFORMATION FOR SEQ ID NO: 84:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                                                                                               10.7%;
                                                                                                                                                                                                  Ouery Match 10.7
Best Local Similarity 54.5
Matches 6, Conservative
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            TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: NY
COUNTRY: USA
ZIP: 10036/2711
COMPUTER READABLE FORM:
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Best Local Similarity
Matches 9; Conserva
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                                                                                                        DESCRIPTION: HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS:
                                                                                                                                                      US-09-038-217A-14
                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-874-825-84
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Pred. No. 3e+02;
0; Mismatches 2; Indels
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US-09-038-217A-14/c
is Sequence 14 Application US/09038217A
Fatent No. 602596
GENERAL INFORMATION:
APPLICANT: Sladek, Frances M.
APPLICANT: About Weimin
APPLICANT: Darnell, Us., James F.
TITLE OF INVENTION: LIVER ENRICHED TRANSCRIPTION FACTOR
UNDMESS OF SEQUENCES: 18
CORRESPONDENCES: 18
ADDRESSEE: David A. Jackson, Esq.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
STREET: Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYEE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/038,217A
FILING DATE: March 11, 1998
CLASSIFICATION: 435
ATTORNEY AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-030B
TELECOMMUNICATION INFORMATION:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                              PRIOR APPLICATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PELING DATE: 03-NOV-1993
APPLICATION NUMBER: US 07/977,691
FILING DATE: 13-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: Teskin, Robin L.
REGISTRATION NUMBER: 012712-010
TELECOMUNICATION INFORMATION:
TELECOMUNICATION INFORMATION:
TELECOMUNICATION INFORMATION:
TELECOMUNICATION 1870-6620
TELECOMUNICATION FOR SEC 15 10 100: 24:
                                                                 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/013,092
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 201-343-1684
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10.7%;
81.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 12 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            949 TTAATGTATCG 959
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12 rraarraarcs 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
                                                                                                                  FILING DATE
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US-08-480-173A-15
### Sequence 15, Application US/08480173A
### Sequence 15, Application US/08480173A
### Sequence 15, Application US/08480173A
### APPLICANT: Thoma, Hans A
### TITLE OF INVENTION:
### APPLICANT: Thoma, Hans A
### TITLE OF INVENTION:
### APPLICANT: Thoma, Hans A
### APPLICANT: Sequence ADDRESS:
### APPLICANT: Sequence ADDRESS:
### APPLICANT: AND APPLICANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
10.7%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 38+02;
Matches 9; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                 ZIF: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: DATE: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURREMY APPLICATION DATA:
APPLICATION NUMBER: US/08/884,324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 55402

COMPUTER READALE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIWARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STAIE: D.C.
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:

CLASSIPICATION: 435

RICK APPLICATION DATA:

APPLICATION DATA:

APPLICATION NUMBER: 3P 185,305/96

FILING DATE: 27-UN-196

ATTORNEY, AGENT INFORMATION:

NAME: BROWDY, ROGET L.

REGISTRATION NUMBER: 25,618

REFERENCE/DOCKET NUMBER: 25,618

REFERENCE/DOCKET NUMBER: 25,618

TELEFAM: 202-628-5197

TELEFAM: 202-737-3528

INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTER:STICS:

LENGTH: 12 base pairs

TYPE: nucleic acid

STRANDENNES: double
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LOCATION: 1..87
IDENTIFICATION METHOD:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: Genomic ORIGINAL SOURCE: ORGANISM: human TISSUE TYPE: placenta
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-884-324-6
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                                                                                                                                                           RESULT 579
US-08-874-825-85
US-08-874-825-85
i Sequence 85, Application US/08874825
i Patent No. 6057101
i GENERAL INFORMATION:
APPLICANT: Nothberg, Jonathan
APPLICANT: Rothberg, Jonathan
APPLICANT: Yang, Meijia
i APPLICANT: Kalbfleisch, Theodore
ITILE OF INVENTION: IDENTIFICATION AND COMPARISON OF
ITILE OF INVENTION: PROTEIN-PROTEIN INTERACTIONS
ITILE OF INVENTION: AND IDENTIFICATION OF INHIBITORS OF THESE INTERACTORS
NUMBER OF SEQUENCES: 122
CORRESPONDENCE ADDRESS:
ADDRESSE: Pennie & Edmonds
ITIS Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
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COMPUTER: USA
ZIP: 10036/2711

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIBLE
SOFTWARE: FASTSEN OFS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/874,825
FILING DATE: 13-JUN-1997
CLASSIFICATION: 435
PRICE APPLICATION NUMBER: 08/663,824
FILING DATE: 14-JUN-1996
ATTORNEY FASTSEN OFS
APPLICATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 19,872
REFERENCE/DOCKET NUMBER: 18,872
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 81.8
Matches 9; Conservative
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1 CGCGTCTTCAT 11
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STRANDEDNESS: single
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; Patent No. 6083693
; General No. 6083693
; General No. 6083693
; GENERAL INFORMATION:
APPLICANT: Nandabalan, Krishnan
APPLICANT: Rothberg, Jonathan
; TITLE OF INVENTION: INFERTICATION AND COMPARISON OF PROTEIN-PROTEIN
; TITLE OF INVENTION: INFERTICATIONS THAT OCCUR IN POPULATIONS
; TITLE OF INVENTION: 1098ER: US/08/663,824
; CURRENT FILING DATE: 1996-06-14
; NUMBER OF SEQ ID NOS: 118
; SEQ ID NO 85
; LENGTH: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Nandabalan, Krishnan
APPLICANT: Nothberg, Jonathan
TITLE OF INVENTION: IDENTIFICATION AND COMPARISON OF PROTEIN-PROTEIN
TITLE OF INVENTION: INTERACTIONS THAT OCCUR IN POPULATIONS
                                                                                                                                                                                       LOCATION: 4..9—

GOTHER INFORMATION: /note= "Portion of the germline construct"

GOTHER INFORMATION: gene incorporated into the CDR3 construct"

GOS-081-037-79
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; OTHER INFORMATION: Description of Artificial Sequence: linker US-08-663-824-85
                                                                                                                                                                                                                                                                                                                                  10.7%; Score 7.8; DB 1; Length 12; 81.8%; Pred. No. 3e+02; 2; Indels :ive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 7.8; DB 1; Length 12;
Pred. No. 3e+02;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILE REFERENCE: 7934-006
CURRENT APPLICATION NUMBER: US/08/663,824
CURRENT FILING DATE: 1996-06-14
NUMBER OF SEQ ID NOS: 118
SOFTWARE: PATENTIN VET. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 84, Application US/08663824
Patent No. 6083693
GENERAL INFORMATION:
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Best Local Similarity 81.8%;
Matches 9; Conservative
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 81.0
                                                                                                                                                           NAME/KEY: misc feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                           955 TATCGCTACCA 965
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                  12 base pairs
                                         TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 cecercricar 11
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LOCATION: 1..12
OTHER INFORMATION: /note= "Adapter sequence results
OTHER INFORMATION: /note= "Adapter sequence results
OTHER INFORMATION: from oligomucleotide duplex formation with nucleotides 5-16
OTHER INFORMATION: SEQ ID NO: 16"
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STATE: C.A
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPETATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/881,037
FILING DATE: 23-UN-1997
CLASSIFICATION: 530
PRIOR APPLICATION 1997
FILING DATE: 18-MAY-1995
CLASSIFICATION: 530
PRIOR APPLICATION: 340
FILING DATE: 18-MAY-1995
CLASSIFICATION: MARER: US 08/443,540
FILING DATE: 18-MAY-1995
CLASSIFICATION: 340
FILING DATE: 18-MAY-1995
CLASSIFICATION NUMBER: 34,202
REGISTRATION NUMBER: 34,202
REFERENCE/DOCKET NUMBER: 23442110710
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 79, Application US/08881037
Fatent No. 6080588
GENERAL INFORMATION:
APPLICANT: Swanson, Patrick C.
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morrison & Poerster
STREET: 755 Page Mill Road
CITY: Plo Alto
TELECOMPONE: 612-32.

TELEPHONE: 612-334 6994
; INFORMATION FOR SEQ ID NO: 15: SEQUENCE CHARACTERISTICS: LENGTH: 12 base pairs
"VPE: nucleic acid
"VPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: DNA (synthetic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            912 CTTTGGTCTTT 922
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Best Local Similarity
Matches 9; Conserv
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US-08-881-037-79
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RESULT 587
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Pred. No. 3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10.7%; Score 7.8; DB 1; Length 12; 81.8%; Pred. No. 3e+02; cive 0; Mismatches 2; Indels
                                                                 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Robert S. Matson
APPLICANT: Robert S. Matson
TITLE OF INVENTION: USE OF URACIL-DNA GLYCOSYLASE
TITLE OF INVENTION: USE OF URACIL-DNA GLYCOSYLASE
TITLE OF INVENTION: IN GENETIC ANALYSIS
NUMBER OF SEQUENCES: 10
CORRESSEE: Beckman Instruments, Inc.
STREET: 2500 Harbor Boulevard
CITY: Fulleron
STATE: California
STATE: California
SIPE: 92834-3100
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage
COMPUTER: IBM compatible
OPERATING SYSTEM: WINDOWS 95 - WORDERFECT 7.0
SOFTWARE: ASCII (DOS) TEXT
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/959,853
FILING DATE: herewith
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: P. R. HARGER:
NAME: P.
                                                             Mismatches
                                                                                                                                                                                                                                                                                                        US-08-959-853-8/c; Sequence 8, Application US/08959853; Patent No. 6090553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-959-853-8
Query Match
Best Local Similarity 81.8%;
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (714) 773-7936
INFORMATION FOR SEQ ID NO: 8
SEQUENCE CHARACTERISTICS:
LENGTH: 12 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 81.8
Matches 9; Conservative
                                                                                                                        934 CICCICITCAT 944
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STRANDEDNESS: single
                                                                                                                                                                                  1 cragrcrrcar 11
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USA
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NAME/KEY: misc_feature
LOCATION: 1..12
UNTER INFORMATION: /note= "Adapter sequence results
OTHER INFORMATION: from oligonucleotide duplex formation with nucleotides 5-16 o
OTHER INFORMATION: SEQ ID NO: 16"
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/08/942,406
FILING DATE: 01-Oct-1997
CLASSIFICATION ATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
10.7%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 3e+02;
Matches 9; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Simpson, John
TITLE OF INVENTION: Method for the Determination and NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,408A
FILING DATE: 0'-JUN 1995
CLASSIFICATION: 435
ATTORNEY/AGBNT INFORMATION:
NAME: POPOVICH, Thomas E
REGISTRATION NUMBER: MED1003USD4
TELEPRATION FORMATION:
TELEPRATION FORMATION:
TELEPRATION FOR SEQ 1D NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 base pairs
TYPE: mucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOMESTULE TYPE: DNA (Synthetic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 7934-015-999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Pennie and Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: 08/547,214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Rothberg, Jonathan
Deem, Michael
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 13, Application US/08942406; Patent No. 6141657; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: <URKNOWN>
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      912 CTTTGGTCTTT 922
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Gaps

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US-09-281-418-71/c
| Sequence 71, Application US/09281418
| Sequence 71, Application US/09281418
| Patent No. 6287769
| GENERAL INFERMATION:
| APPLICANT: Inoue, Takakazu
| TITLE OF INVENTION: Method of Amplifying DNA Fragment, Apparatus for Amplifying DNA Fr
                                                                                                                                                                                                                                                                                                                                                                                            Determination and of DNA Sequences in a Sample Without
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Score 7.8; DB 1; Length 12;
Pred. No. 3e+02;
0; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FO COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
APPLICATION DATA:
APPLICATION NUMBER: US/09/322,617
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 7.8; DB 1;
Pred. No. 3e+02;
0; Mismatches
                                                                                                                                                                                                                Sequence 13, Application US/09322617
; Sequence 13, Application US/09322617
; Patent No. 6231812
; GENERAL INFORMATION:
APPLICANT: Deem, Michael
APPLICANT: Deem, Michael
APPLICANT: Simpson, John
TITLE OF INVENTION: Method for the Det
TITLE OF INVENTION: Sequencing
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Pennie and Edmontos
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/547,214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 79
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)-790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEX: 66441 PENNIE
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 base pairs
Query Match
Best Local Similarity 81.8%;
Matches 9; Conservative
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81.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 81.8
Matches 9; Conservative
                                                                                           949 TTAATGTATCG 959
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                                                                                                                                     12 TTAATTAATCG 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE: New York
COUNTRY: USA
ZIP: 10036-2711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-322-617-13
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US-09-24/C
1S-09-280-999-24/C

Sequence 24, Application US/09280999

Patent No. 6159730

GENERAL INFORMATION:

APPLICANT: REFF, Mitchell E.

TITLE OF INVENTION: IMPAIRED DOMINANT SELECTABLE MARKER

TITLE OF INVENTION: SEQUENCE AND INTRONIC INSERTION STRATEGIES FOR ENHAN

TITLE OF INVENTION: OF EXPRESSION OF GENE PRODUCT AND EXPRESSION VECTOR

TITLE OF INVENTION: SYSTEMS COMPRISING SAME

NUMBER OF SEQUENCES: 32

NUMBER OF SEQUENCES: 32

CORRESPONDENCE ADDRESS:

ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
                                                                                                                                                                                                                                                                                                                                                                        ..
                                                                                                                                                                                                                                                                                                                          Score 7.8; DB 1; Length 12;
Pred. No. 3e+02;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/280,999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS STREET: P.O. BOX 1404
CITY: Alexandria
                                                                                                                                                                                                        TOPOLOGY: linear

MOLECULE TYPE: DNA
SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-08-942-466-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-010
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 24:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
PILING DATE:
APPLICATION NUMBER: US/08/147,696
FILING DATE: 03-NOV-1993
APPLICATION NUMBER: US 07/977,691
FILING DATE: 13-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
                          TELEFACONE: (212)-790-9090
TELEFAX: (212)-869-8864
TELEX: 66441 PENNIE
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 base pairs
       TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/013,092
                                                                                                                                                                  TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                          10.7%;
81.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Alexander STATE: Virginia COUNTRY: United States Z19:1404
                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 81.8
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                    943 ATTGGTTTAAT 953
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 12 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 AGTGGCTTAAT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  nucleic acid
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APPLICANT: Scherman, Daniel
APPLICANT: Wils, Pierre
APPLICANT: Wils, Pierre
APPLICANT: Blanche, Francis
TITLE OF INVENTION: PURPERCATION OF A TRIPLE HELIX FORMATION WITH AN
TITLE OF INVENTION: PURPERCATION OF A TRIPLE HELIX FORMATION WITH AN
TITLE OF INVENTION: IMMOBILIZED OLIGONUCLEOTIDE
FILS REFERENCE: 03804.0138-01
CURRENT FILING DATE: 1090-00-028
PRIOR FILING DATE: 1097-06-09
PRIOR FILING DATE: 1995-11-08
NUMBER OF SEQ ID NOS: 36
SOUTHARE: Patentin Ver. 2.1
SEQ ID NO 28
LENGTH: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10.7%; Score 7.8; DB 1; Length 12; 81.8%; Pred. No. 3e+02;
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OTHER INFORMATION: Description of Artificial Sequence:
OTHER INFORMATION: binding region
US-08-849-567A-42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; OTHER INFORMATION: Description of Artificial Sequence: , OTHER INFORMATION: oligonucleotide US-09-580-923-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: JOYCE, Gerald F.
APPLICANT: JOYCE, Gerald R.
APPLICANT: BOXCE, Gerald R.
TITLE OF INVENTION: ENZYMATIC DNA MOLECULES
FILE REFERENCE: SCR19438
CURRENT PAPLICATION NUMBER: US/08/849,567A
CURRENT FILING DATE: 1997-08-25
PRIOR APPLICATION NUMBER: PCT/US95/15580
PRIOR APPLICATION NUMBER: 08/472,194
PRIOR APPLICATION NUMBER: 08/472,194
PRIOR APPLICATION NUMBER: 08/499,023
PRIOR APPLICATION NUMBER: 08/349,023
PRIOR FILING DATE: 1994-12-02
NUMBER OF SEQ ID NOS: 101
SEQ ID NO 42
LENGTH: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-849-567A-42; Sequence 42, Application US/08849567A; Patent No. 6326174
                                                                                                                           RESULT 592
US-09-580-923-28
Sequence 28, Application US/09580923
Patent No. 6319672
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA ORGANISM: Artificial Sequence
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      12 CCTTACCTTTT
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Best Local Similarity
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US-09-417-455-28/C
Sequence 28, Application US/09417455
PATENT NO. 6294655
PATENT NO. 6294655
GENERAL INFORMATION:
APPLICANT: Pord, John
TITLE OF INVENTION: A NOVEL INTERLEUKIN-1 RECEPTOR ANTAGONIST AND USES THEREOF
FILE REFERENCE: 28110/36328
CURRENT PAPLICATION NUMBER: US/09/417,455
CURRENT PAPLICATION NUMBER: US/09/418,942
PRIOR FILING DATE: 1999-00-13
FRIOR FILING DATE: 1999-04-05
FRIOR PAPLICATION NUMBER: US 09/287,210
FRIOR PAPLICATION NUMBER: US 09/22-17
FRIOR PAPLICATION NUMBER: US 09/22-17
FRIOR FILING DATE: 1998-04-05
FRIOR PAPLICATION NUMBER: US 09/22-17
FRIOR FILING DATE: 1998-06-19
FRIOR APPLICATION NUMBER: US 09/092,818
FRIOR FILING DATE: 1998-06-19
FRIOR APPLICATION NUMBER: US 09/092,818
FRIOR FILING DATE: 1998-06-15
FRIOR FILING 
TITLE OF INVENTION: agment, Method of Assaying Microorganisms, Method of Analyzing I
TITLE OF INVENTION: nisms and Method of Assaying Contaminant
FILLE REFERENCE: 9982.7
CURRENT APPLICATION NUMBER: US/09/281,418
CURRENT APPLICATION NUMBER: UP/1998/87651
EARLIER APPLICATION NUMBER: UP/1998/87651
EARLIER FILING DATE: 1999-03-16
NUMBER OF SEQ ID NOS: 216
NUMBER OF SEQ ID NOS: 216
LENGTH: 12
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Pred. No. 3e+02;
0; Mismatches 2; Indels
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81.8%;
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Best Local Similarity 81.8%;
Matches 9; Conservative
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Best Local Similarity 81.8
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: Primer US-09-281-418-71
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US-09-417-455-28
                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
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Sequence 84, Application US/09231303
| Sequence 84, Application US/09231303
| Sequence 84, Application US/09231303
| Patent No. 6395476
| GENERAL INFORMATION:
| APPLICANT: Nandabalan, Krishnan
| APPLICANT: Nandabalan, Krishnan
| TITLE OF INVENTION: IDENTIFICATION AND COMPARISON OF PROTEIN-PROTEIN
| TITLE OF INVENTION: IDENTIFICATION OF INHIBITORS OF THESE INTERACTIONS
| TITLE OF INVENTION: IDENTIFICATION OF INHIBITORS OF THESE INTERACTIONS
| FILE REFERENCE: 7934-087
| CURRENT APPLICATION NUMBER: US/09/231,303
| CURRENT ELING DATE: 1999-01-12
| EARLIER FILING DATE: 1996-06-14
| NUMBER OF SEQ ID NOS: 118
| SOFTWARE: PATENTIN VET: 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; CTHER INFORMATION: Description of Artificial Sequence: linker
US-09-231-303-84
                                                                                                                                                Score 7.8; DB 1; Length 12;
Pred. No. 3e+02;
0; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Nathery, Jonathan M
APPLICANT: Nathery, Girish N
APPLICANT: Hu, Xinghua
APPLICANT: Hu, Xinghua
TITLE OF INVENTION: Methods and Devices for Measuring
TITLE OF INVENTION: Differential Gene Expression
FILE REPERENCE: 7934-052
CURRENT APPLICATION NUMBER: US/09/203,231B
CURRENT FILING DATE: 1998-12-02
FRIOR FILING DATE: 1997-12-03
NUMBER OF SEQ ID NOS: 88
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 17
LENGTH: 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 17, Application US/09203231B Patent No. 6355423 GENERAL INFORMATION:
ORGANISM: Artificial Sequence
                                                                                                                                                Query Match
Best Local Similarity 81.8%;
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA ORGANISM: Artificial Sequence
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Best Local Similarity 81.8
Matches 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GTHER INFORMATION: Primer US-09-203-231B-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        943 ATTGGTTTAAT 953
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                                                       ); OTHER INFORMATION: TBD US-09-348-942-28
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LENGTH: 12
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US-09-348-942-28/C
US-09-348-942-28/C
Sequence 28, Application US/09348942
Patent No. 6337072
GENERAL INPORMATION:
JAPPLICANT: JOHN PORE
TILE REPRENCE: 28110/35011
CURRENT APPLICATION NUMBER: US/09/348,942
CURRENT APPLICATION NUMBER: US/09/348,942
CURRENT APPLICATION NUMBER: US/09/348,942
CURRENT FILING DATE: 1999-04-05
BARLIER FILING DATE: 1999-04-05
BARLIER PLING DATE: 1999-01-13
BARLIER PLING DATE: 1998-02-17
BARLIER PLING DATE: 1998-02-17
BARLIER PLING DATE: 1998-06-13
BARLIER PLING DATE: 1998-05-20
BARLIER PLING DATE: 1998-05-30
BARLIER PLING DATE: 1998-05-30
BARLIER PLING DATE: 1998-05-31
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APPLICANT: Bloch, William
APPLICANT: Bloch, William
APPLICANT: Bloch, William E.
APPLICANT: Bloch, Michael
APPLICANT: Explain, Michael
APPLICANT: Myers, Rene L.
TITLE OF INVENTION: Compositions of Solvents and High
TITLE OF INVENTION: Concentrations of Nucleic Acid Analogs
FILE REPERENCE: 4444
CURRENT APPLICANT: 1999-05-13
NUMBER OF SEQ ID NOS: 6
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 6
LENGTH: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 1; Length 12;
   Indels
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10.7%; Score 7.8; DB 1;
Best Local Similarity 81.8%; Pred. No. 3e+02;
Matches 9; Conservative 0; Mismatches
Mismatches
                                                                                                                                                                                                                                                                      ; Sequence 6, Application US/09311079; Patent No. 6331618
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9; Conservative
                                                              952 ATGIATCGCIA 962
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                                                                                                                      2 ATGTGACGCTA 12
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                                                                                                                                                                                                                     RESULT 594
US-09-311-079-6/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
Matches
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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SEQUENCE CHARACTERISTICS:
LENGTH. 12 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 81.0
                                                                                                                                                                                                                                                                                                                                                                                                                                926 TTTTATCCCTC 936
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TYPE: nucleic acid
STRANDEDNESS: single
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ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12 rrrrcrrccrc 2
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US-08-927-165A-16
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US-09-751-561-13
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                                                                                                                                                                           NESULT 598

US-09-231-303-85

i Sequence 85, Application US/09231303

patent No. 6395478

i GENERAL INFORMATION:

i GENERAL INFORMATION:

i APPLICANT: Nandabalan, Krishnan

i APPLICANT: Nandabalan, Krishnan

i TITLE OF INVENTION: INFORMATION INFORMATION OF PROTEIN-PROTEIN

TITLE OF INVENTION: INFORMATION OF INFORMATIONS AND

TITLE OF INVENTION: INDENTIFICATION OF INFIBITORS OF THESE INTERACTIONS

TITLE OF INVENTION: 1994-067

CURRENT APPLICATION NUMBER: 08/09/231,303

CURRENT FILING DATE: 1996-01-12

EARLIER FILING DATE: 1996-06-14

NUMBER OF SEQ ID NOS: 118

SEQ ID NO 85

LENGTH: 12
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OTHER INFORMATION: Description of Artificial Sequence: linker
US-09-231-303-85
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Score 7.8; DB 1; Length 12;
Pred. No. 3e+02;
0; Mismatches 2; Indels
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Sequence 16, Application US/08927165A

Patent No. 6410226

GENERAL INFORMATION:
APPLICANT: Kmiec, Eric B.
APPLICANT: Rice, Milliam K.
APPLICANT: Rice, Michael C.
APPLICANT: Smith, Sheryl T.
APPLICANT: Shu, Zhigang

TITLE OF INVENTION: Mammalian and Human Rec2
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/927,165A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: USA
ZIP: 18940
COMPUTER REDABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATINE
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Kimeragen, Inc. STREET: 300 Pheasant Run
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA ORGANISM: Artificial Sequence
  10.7%;
81.8%;
                                          9; Conservative
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 CTAGTCTTCAT 11
                                                                                                                        1 CGCGTCTTCAT 11
    Query Match
Best Local Similarity
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CITY: Newtown
STATE: PA
                                          Matches
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Sequence 13, Application US/09751561

Sequence 13, Application US/09751561

Sequence 13, Application US/09751561

GENERAL INFORMATION:
APPLICANT: Rothberg, Jonathan
APPLICANT: Simpson, John
ITILE OF INVENTION: Method for the Determination and
ITILE OF INVENTION: Classification of DNA Sequences in a Sample Without
ITILE OF INVENTION: Classification of DNA Sequences in Sequencing
NUMBER OF SEQUENCES: 59

CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie and Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STREET: New York

CONTAINS New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
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CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/751,561

FILING APPLICATION DATA:

PRICK APPLICATION DATA:

PRICK APPLICATION NUMBER: 08/547,214

FILING APPLICATION NUMBER: 08/547,214

FILING APPLICATION NUMBER: 18,872

ATTORNEY/AGENT INFORMATION:

NAME: Misrock, S. Leslie

REGISTRATION NUMBER: 18,872

REFRENCE/DOCKET NUMBER: 1934-015-999

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELETEX: 66441 FENNIE

INFORMATION FOR SEQ 1D NO: 13:

SEQUIENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                         10.7%; Score 7.8; DB 1;
81.8%; Pred. No. 3e+02;
ATTORNEY/AGENT INFORMATION:
MAME: Hansburg, Daniel
REGISTATION NUMBER: 36156
REFERENCE, DOCKET NUMBER: 7991-010-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-504-4444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
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US-08-450-363-41/c

US-08-450-363-41/c

Sequence 41, Application US/08450363

Sequence 41, Application US/08450363

Sequence 41, Application US/08450363

APPLICANT: Saiko HOSOKAWA

APPLICANT: Yoko HIRAKAWA

APPLICANT: Kazuhiro NAGANA

TITLE OF INVENTION: Specifically Binding to Surface Antigen of Cancer

TITLE OF INVENTION: Cell Membrane

TITLE OF INVENTION: Cell Membrane

NUMBER OF SEQUENCES: 42

CORRESPONDENCE ADDRESS:

ADDRESSES: Wenderoth, Lind & Ponack
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 7.8; DB 1; Length 12;
Pred. No. 3e+02;
0; Mismatches 2; Indels
                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/724,385
FILING DATE: 28-NO. 6432361-2000
CLASSIFICATION, «Unknown»
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 09/322,617
FILING DATE: «Unknown»
ATTORNEY/AGENT INFORMATION:
NAME: Miscork S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 7934-015-99
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION:
TELEPHONE: (212)-790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Diskette, 5.25 inch, 500 kb COMPUTER: IBM Compatible OPERATING SYSTEM: MS-DOS SOFTWARE: WordPerfect.5.1 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/450,363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Wenderoth, Lind & Ponack
805 Fifteenth Street, N.W., #700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: DNA
SEQUENCE DESCRIPTION: SEQ ID NO: 13:
                                                                                                                            ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 base paire
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81.8%;
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COMPUTER READABLE FORM:
MEDIUM TYPE: Distriction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 10.7
Best Local Similarity 81.8
Matches 9; Conservative
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FILE REFERENCE: 28110/36010

CURRENT PAPLICATION NUMBER: US/09/457,626

CURRENT FILING DATE: 1999-10-13

EARLIER APPLICATION NUMBER: US 09/417,455

EARLIER FILING DATE: 1999-10-13

EARLIER PEPLICATION NUMBER: US 09/24291

EARLIER PEPLICATION NUMBER: US 09/287,210

EARLIER PEPLICATION NUMBER: US 09/281,370

EARLIER PELING DATE: 1999-04-05

EARLIER APPLICATION NUMBER: US 09/251,370

EARLIER PELING DATE: 1999-04-13

EARLIER PELING DATE: 1999-01-13

EARLIER PEPLICATION NUMBER: US 09/229,591

EARLIER PEPLICATION NUMBER: US 09/229,591

EARLIER PEPLICATION NUMBER: US 09/229,591

EARLIER PEPLICATION NUMBER: US 09/029,818

EARLIER FILING DATE: 1998-01-13

EARLIER FILING DATE: 1998-05-10

EARLIER PELING DATE: 1998-05-10

EARLIER PELING DATE: 1998-05-10

EARLIER PELING DATE: 1998-05-10

EARLIER PELING DATE: 1998-05-15

EARLIER FILING DATE: 1998-05-15

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                           Score 7.8; DB 1; Length 12;
Pred. No. 3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1; Length 12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 7.8; DB 1;
Pred. No. 3e+02;
                                                                                       0; Mismatches
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                                                                                                                                                                                                                                                                                                                                       Sequence 28, Application US/09457626
Patent No. 6426191
GENERAL INFORMATION:
APPLICANT: Ford, John
APPLICANT: Pace, Ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 13, Application US/09724385
Patent No. 6432361
GENERAL INFORMATION:
APPLICANT: Rothberg, Jonathan
Deem, Michael
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10.7%;
81.8%;
Ouery Match
Best Local Similarity 81.0
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Best Local Similarity 81.0
                                                                                                                                              943 ATTGGTTTAAT 953
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US-09-457-626-28/c
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COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Eloppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/09/757,528
FILING DATE: 10-Jan-2001
FILING DATE: 10-Jan-2001
FILING DATE: 10-Jan-2001
PRIOR APPLICATION NUMBER: 08/547,214
PRIDRE APPLICATION NUMBER: 08/547,214
PRIDRE MARE: Mistrock, S. Leslie
REGISTRATION NUMBER: 18/872
REFERENCE/DOCKET NUMBER: 7934-015-999
TELEFAXION INFORMATION:
TELEFAXION INFORMATION:
TELEFAXI (212)-790-9090
TELEFAX: (5441 PENNIE
INFORMATION FOR SEQ 1D NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 Dase pairs
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                                                   APPLICANT: Rothberg, Jonathan
Deem, Michael
Simpson, John
TITLE OF INVENTION: Method for the Determination and
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie and Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear;
MOLECULE TYPE: DNA
SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-09-757-528-13
Sequence 13, Application US/09757528
Patent No. 6453245
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
STRANDEDNESS: single
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10.7%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 3e+02;
Matches 9; Conservative 0; Mismatches 2; Indels
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DEVELOPMENTAL STAGE:
HAPLOTYPE:
TISSUE TYPE:
CELL TYPE:
CELL INE:
     PILING DATE: nay L. CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 08/360,125
FILING DATE: December 20, 1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/905,534
FILING DATE: June 29, 1992
ATTORNEY/AGRAT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEPHONE: 202-371-8850
TELEFEX:
INFORMATION FOR SEQ ID NO: 41:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL:
ANTI-SENSE:
CREAMENT TYPE:
ORGANISM:
ORGANISM:
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RELEVANT RESIDUES IN SEQ ID NO:
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CHROMOSOME/SEGMENT:
MAP POSITION:
UNITS:
FEATURE:
NAME/KRY:
LOCATION:
LOCATION:
DENTIFICATION METHOD:
OTHER INPORMATION:
AUTHORS:
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DOCUMENT NUMBER:
FILING DATE:
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MMEDIATE SOURCE:
LIBRARY:
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VOLUME:
ISSUE:
PAGES:
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RESULT 604 US-09-757-528-13

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; Sequence 28, Application US/09576008; Patent No. 6541623
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Ford, John APPLICANT: Ho, Alice Suk-Yue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 10.7
Best Local Similarity 81.8
Matches 9; Conservative
                                                                                                                                                                                                                                                                                  915 TGGTCTTTGCC 925
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                                                                                                                                                      US-09-447-034-14
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Patent No. 6500672

GENERAL INFORMATION:
APPLICANT: Sladek, Frances M.
Zhong, Weimin
Darnell, Jr., James F.

TITLE OF INVENTION: LIVER ENRICHED TRANSCRIPTION FACTOR
NUMBER OF SEQUENCES: 18

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 07601

COMPUTER READABLE FORM:
MEDLUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOTWARE: Patentin Release #1.0, Version #1.30
CURRINT APPLICATION DATA:
APPLICATION NOWBER: US/09/447,034
FILING DATE: 22-No. 6500672-1999
CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 7.8; DB 1; Length 12;
Pred. No. 3e+02;
0; Mismatches 2; Indels
SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/059.625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/038,217
FILING DATE: March 11, 1998
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-030B
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
                                                                         FILICATION WOLDER:
FILING DATE: 14-APR-1998
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MUCCINO, RICHARD R
REGISTRATION NUMBER: 32,538
REFERENCE/DOCKET NUMBER: UMD1-040
TELECHONICATION INFORMATION:
TELEFPHONE: 908-273-4988
TELEFRX: 908-273-4988
TELEFRX: 908-273-4679
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
                                                            JMBER: US/09/059,625
14-APR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                      DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 81.8%;
Matches 9; Conservative
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SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: New Jersey
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                          LENGTH: 12 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Hackensack
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   948 TTTAATGTATC 958
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                                                                                                                                                                                                                                                                                                                                                                                             unknown
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                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; ANTI-SENSE: NO
US-09-059-625-31
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US-09-447-034-14/c
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JUNEARL INVERTALION:

JUNEARL INVERTALION:

APPLICANT: SHAW, LYNN C.

APPLICANT: SHAW, LYNN C.

APPLICANT: GRAW, LYNN C.

APPLICANT: GRAW, LYNN C.

TITLE OF INVENTION: THE TREATMENT OF RETINAL DISEASES

TITLE OF INVENTION: THE TREATMENT OF ASSOCIATED OF ASSOCIATION OF AS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 7.8; DB 1; Length 12;
Pred. No. 3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
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AMPLIFICATION OF
TARGETED SEGMENTS OF
NUCLEIC ACID USING
NESTED POLYMERASE CHAIN
REACTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; LOCATION: (). ()
; OTHER INFORMATION: SYNTHETIC OLIGONUCLECTIDE US-09-814-601-137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2; Mismatches
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OPERATING SYSTEM: Macintosh 6.0
SOFTWARE: PATENTIN RELEASE #1.0,
SOFTWARE: VERSION #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/11702
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: IMPROVED METHOD F
TITLE OF INVENTION: AMPLIFETCATION OF
TITLE OF INVENTION: TARGETED SEGMENTS
TITLE OF INVENTION: NUCLEIC ACID USIN
TITLE OF INVENTION: NESTED POLYMERASE
TITLE OF INVENTION: REACTION
NUMBER OF SEQUENCES: 2
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 4, Application PC/TUS9311702; GENERAL INFORMATION:
Application US/09874601
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 63.6%;
Matches 7; Conservative 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Artificial Sequence
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TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              961 TACCAACGGTG 971
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Best Local Similarity
Matches 9; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: RNA
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Sequence 136, Application US/09874601

Sequence 136, Application US/09874601

Setent No. 6632057

GENERAL INFORMATION:

APPLICANT: LEWIN, ALFRED S.

APPLICANT: SHAW, LYNN C.

TITLE OF INVENTION: ADENO-ASSOCIATED VIRUS-DELIVERED RIBOZYME COMPOSITIONS AND METHOD TITLE OF INVENTION: THE TREATHENT OF RETINAL DISEASES

TITLE OF INVENTION: ADENO-ASSOCIATED VIRUS-DELIVERED RIBOZYME COMPOSITIONS AND METHOD TITLE OF INVENTION: THE TREATHENT OF RETINAL DISEASES

FILE REFREENCE: 4300.014100

CURRENT APPLICATION NUMBER: US/09/874,601

CURRENT FILING DATE: 1999-04-21

PRIOR PILING DATE: 1997-04-21

PRIOR FILING DATE: 1997-04-21

PRIOR FILING DATE: 1997-04-21

NUMBER OF SEQ ID NOS: 182

SEQ ID NO 136

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LEMETH: 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 7.8; DB 1; Length 12
Pred. No. 3e+02;
0; Mismatches 2; Indels
                                                                                                                                              Sequence 57, Application US/09512563C
Fatent No. 6579969
GENERAL INFORMATION:
APPLICANT: Saus, Juan
TITLE OF INVENTION: Goodpasture Binding Protein
FILLE REFERENCE: 98-733-A
FURRENT APPLICATION NUMBER: US/09/512,563C
CURRENT FILING DATE: 2000-02-24
FRICR APPLICATION NUMBER: 60/121,483
FRICR APPLICATION NUMBER: 60/121,483
FRICR APPLICATION NUMBER: 60/121,483
FRICR APPLICATION UNMBER: 60/121,483
FRICR APPLICATION UNM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 81.8%;
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   961 TACCAACGGTG 971
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA ORGANISM: Homo sapiens
                                                                                                                                 US-09-512-563C-57/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 610
US-09-874-601-137
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10.7%;
Best Local Similarity 81.8%;
Matches 9; Conservative C
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
PCT-US95-05835-1
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                                                                                           FGENERAL INFORMATION:

Sequence 22, Application PC/TUS9505265

Sequence 22, Application PC/TUS9505265

GENERAL INFORMATION:

TITLE OF INVENTION:

TITLE OF INVENTION:

TORRESPONDENCES: 74

CORRESPONDENCES: 74

CORPUTE: California

COUNTY: San Francisco

STAIE: 9411-4187

COMPUTER: READABLE FORM:

MOMPUTER: Flopy disk

COMPUTER: PALPATION AINS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION NUMBER: PCT/US95/05265
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
CLASSIFICATION
PRIOR PAPELICATION
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/235,503
FILING DATE: 29-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: OSman, Richard A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: FP-59232-PC/RAO
TELECHOME: (415) 781-1989
TELEFRONE: (415) 398-3249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1, Application PC/TUS9505835
Sequence 1, Maphication PC/TUS9505835
SEREAL INFORMATION:
APPLICANT: Alexander-Bridges, Maria C.
APPLICANT: Zhao, Hui-Fen
TITLE OF INVENTION: INHIBITION OF INSULIN-
TITLE OF INVENTION: INDUCED ADIPOSIS
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEX: 910 277299
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
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TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 10.7
Best Local Similarity 54.5
Matches 6; Conservative
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CITY: Boston
STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
12 TACGGTATCGC 2
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PCT-US95-05835-1/c
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SOFTWARE: WASTER CVERSION 5:1)

CHERRY PRILOCATION BATH:

PRUING DATE:

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PRUING DATE:

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Search completed: October 18, 2004, 14:27:52 Job time : 3 secs
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5212296-13/c
Fatent No. 5212296
Fatent No. 5212296
FATELCANT DEAN, CAROLINE, HARDER, PATRICIA A., LETO, KENNETH
JJ.; O'KEEPE, DANIEL P.; OMER, CHARLES A., ROMESSER, JAMES A.
; TEPPERMAN, JAMES M.
; TITLE OF INVENTION: EXPRESSION OF HERBICIDE METABOLIZING
;
                                                                                          Query Match 10.7%; Score 7.8; DB 1; Length 12; Best Local Similarity 81.8%; Pred. No. 3e+02; Matches 9; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 10.7%; Score 7.8; DB 1; Length 12; Best Local Similarity 81.8%; Pred. No. 3e+02; Matches 9; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                  SELECTION OF DIAGNOSTIC
GENETIC MARKERS IN
MICROORGANIGNS AND USE
OF A SPECIFIC MARKER
SALMONELLA
1: 22
                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
TITLE OF INVENTION: SELECTION OF DIAGNOTITLE OF INVENTION: MICROORGANISMS AND TITLE OF INVENTION: MICROORGANISMS AND TITLE OF INVENTION: POR A SPECIFIC MARKET ITLE OF INVENTION: POR DETECTION OF TITLE OF INVENTION: SALMONELLA NUMBER OF SEQUENCES: 22
COMPUTER READABLE FORM: MEDIUM TYPE: DISKETTE, 3.50 INCH OF TITLE OF SEQUENCES: 22
COMPUTER: MACINTOGH OF SOFTWARE: MACINTOGH OF SOFTWARE: MACINTOGH OF SOFTWARE: MICROSOFT WORD, 4.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/06704
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 19
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/569,781
FILING DATE: 23-AUG-1990
PRIOR APPLICATION NUMBER: 464,499
FILING DATE: 12-JAN-1990
APPLICATION NUMBER: 405,605
FILING DATE: 11-SEP-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: GEIGER, KATHLEEN W.
REGISTRATION NUMBER: 35,880
REFERENCE/DOCKET NUMBER: MD-1068
INFORMATION FOR SEQ ID NO; 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 base pairs
TYPE: Nucleic acid
STRANDENNES: single
                                                                                                                                                                                                                                                                                                  RESULT 615
PCT-US95-06704-5/c
; Sequence 5, Application PC/TUS9506704
; GENERAL INFORMATION:
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
PCT-US95-06379-13
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MOLECULE TYPE: DNA (genomic)
PCT-US95-06704-5
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10.7%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 3e+02;
Matches 9; Conservative 0; Mismatches 2; Indels
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;SEQ ID NO:13:
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LENGTH: 12
5212296-13
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